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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND HBL 100 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human HBL 100 cells is described. Also, described are single exon nucleic acid probes expressed in the HBL 100 cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND HBL 100
CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the 10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of 15 UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
20 REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in 25 triplicate, containing a file named pto_HBL100.txt, created 24 January 2001, having 11,029,597 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In 35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human HBL 100 cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had 10 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane 20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308 (5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes 30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of 35 mRNA – are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this 5 approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of 10 the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot 15 be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing 20 approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic 25 sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and 30 apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 35 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al., *Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known,
5 however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may
15 need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the
20 expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in
25 Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1) (suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes 5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of 10 yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally 15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic 20 factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have 25 polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human breast, particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional 35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel 5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids 10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single 15 exon nucleic acid probes for measuring gene expression in a sample derived from human Breast, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,074 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably 25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality 30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,058 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, 10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane 30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, 35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
5 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of 10 amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

15 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon 20 probes that include specifically-hybridizable fragments of SEQ ID Nos. 5,075 - 10,058, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,074.

25 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 30 5,074 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a 35 nucleotide sequence as set out in any of SEQ ID NOs.: 5,075

- 10,058 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast 5 which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,059 - 15,009 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

10 Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, 15 suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

25 Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 35 and Cy5 although other suitable dyes will be known to those

skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and 5 bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is 10 provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

15 wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Breast, comprising:

20 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then

25 measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

30 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are 35 derived from mRNA from the Breast of said eukaryote, said

probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the 5 invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

10 identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using 15 hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single 20 gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 10,058 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is 25 provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 5,075 - 10,058, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any 30 of SEQ ID NOS.: 1 - 5,074.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,059 - 15,009.

35 Accordingly in a eleventh aspect of the invention

there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 10,059 - 15,009, or fragment thereof.

In another aspect, the invention provides means 5 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated 10 sequence.

Detailed Description of the Invention

15 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately 20 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach 25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1) (suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the 30 term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner 35 et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);

in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid 5 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution 10 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the 15 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

20 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop 25 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

30 As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

35 As used herein, the term "peptide" refers to a

sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: . The codons 5 encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a 10 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present 15 within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is 20 meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , 25 preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display 30 of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

35 As used herein, a "Mondrian" means a visual

display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and 10 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in 15 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

20 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

30 FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the

expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25 Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than

human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

5 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, 10 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing 15 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which 20 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

25 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic 30 assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

35 The subset of sequences output from process 300

is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

5 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
10 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
15 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process
20 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
25 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
30 substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.
35 Often, data will be stored after each, or at least a

plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to 5 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be 10 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction 15 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of 20 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend 25 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the 30 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in 35 subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently 5 long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment 10 length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal 15 number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according 20 to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate 25 a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been 30 described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is 35 possible to query the database for newly added sequence,

either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic,
5 temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts
10 that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST
15 and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

20 If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.
25

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to
30 report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional
35 preprocessing 24, suitable and specific for the desired

analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as 5 processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis.

10 Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

15 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using 20 programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified 25 algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can 30 be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the 35 undesired sequence as, for example, by converting the

specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, 5 leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered 10 occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

15 Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived 20 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the 25 input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, 30 where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after 35 transcription into mRNA, regulating message splicing after

transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X 5 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, 10 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described 15 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene 20 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and 25 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For 30 the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 35 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase 5 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to 15 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report 20 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% 25 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

30 Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process 35 can be repeated on the same input sequence, or subset

thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, 5 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done 10 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional 15 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental 20 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the 25 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses 30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify 35 and select those ORFs that appear most likely successfully

to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that 5 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, 10 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

15 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

20 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The 25 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In 30 particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

35 Putative ORFs as predicted by a consensus of gene

calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is 5 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) 10 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 15 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more 20 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 25 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs 30 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at 35 amplifying pieces of such ORFs is low, and that such

putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been

obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology 5 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 10 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material 15 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the 20 absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial 25 advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support 30 substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

35 Typically, the support substrate will be glass,

although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 10 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached 15 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

20 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 25 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays 30 typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 35 32 *E. coli* genes suffice to provide a robust measure of

background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural 5 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the 10 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, 15 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

20 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.

Further, gene expression can also be confirmed using 25 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid 30 probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For 35 example, each standard microscope slide can include at

least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

5 Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as
10 is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3)
20 those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived – either directly or indirectly – from expressed message. As discussed above,
25 it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question,
30 R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries,
35 shown herein to represent only a fraction of expressed

genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message 5 successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression 10 measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences 15 that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, 20 optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor 25 cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from 30 genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST 35 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

5 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a
10 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
15 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,
20 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical
25 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the
30 probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from
35 genomic DNA. Typically, therefore, at least about 50, 60,

- 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.
- 5 Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including
- 10 probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.
- 15 As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes
- 20 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.
- As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific
- 25 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the
- 30 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even
- 35 smaller amount of nonspecific sequence that would

contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the

probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-
5 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure
10 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

15 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons
20 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic
25 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn
30 from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

35 The genome-derived single exon microarrays of the

present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

5 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
10 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the
15 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
20 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

25 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
30 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large
35 percentage differences in the theoretically optimum

stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the 5 range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the 10 quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present 15 substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* – that is, only about 4 20 - 5% – have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the 25 ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm 30 expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% 35 of protein-encoding genes have introns. In preferred

embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about 5 one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present 10 invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, 15 through hybridization to genome-derived single exon microarrays prepared as above-described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the 20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single 25 cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased 30 commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a 35 fluorophore (fluorochrome; fluor; fluorescent dye); the

reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes 5 prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned 10 using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain 15 of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for 20 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention 25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is 30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher 35 density arrays, such as are provided by microtiter plates

having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-
5 noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each 10 probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, 15 different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be 20 packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a 25 genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the 30 genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation 35 information, such as gene expression data. Such recordable

media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in 5 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should 10 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and 15 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic 20 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected 25 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, 30 SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - 35 including information on identical sequences and

information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, 5 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such 10 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or 15 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

20 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the 25 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively 30 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an 35 annotated sequence, representation of individual

nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention 5 herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian 10 visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of 15 rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, 20 as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession 25 number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is 30 anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual 35 display 80 is used as a graphical user interface to

computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

5 Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle
10 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach
15 identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of
20 horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the
25 functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or
30 approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from
35 GRAIL or GRAIL II, rectangles 83b can represent the results

from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where 15 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by 20 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 25 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as 30 many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. 35 However, the increased visual complexity occasioned by such

display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of

bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as

can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute

expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

30 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present

invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of 5 single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present 10 invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon 15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,074 of these ORFs in HBL 100 cells.

The HBL 100 human breast cancer cell line was 20 established in vitro from milk of an apparently healthy woman. The cells express a variant of SV40 large T antigen, and genomic DNA from HBL 100 cells possesses transforming activity associated with the viral information. The HBL100 cell line is nontumorigenic, and 25 acquires the capacity to invade normal tissues and to replace them by proliferation in vitro only at high passage levels (HPL); these epithelial cells are thus are a useful model for studying breast tumor progression in vitro. HBL 30 100 cells bind both epidermal growth factor (EGF) and glucocorticoids but are progesterone receptor negative.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in HBL 100 cells is currently available for use 35 in measuring the level of its ORF's expression in Breast.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies.

For example, according to the American Cancer Society (ACS), carcinoma of the breast is the second most common cancer in women and, after lung cancer, is the second deadliest. The ACS estimates that in the U.S. there occurred 182,800 new cases of malignant breast cancer in 2000, and about 40,800 deaths from the disease. Although incidence of breast cancer is said to have declined, the disease clearly continues to represent a serious risk to the health and life of American women. Indeed, about one in nine U.S. women will develop breast cancer in her lifetime, and at present mortality rates, about a third of such women will eventually die from the disease.

A variety of factors are known to increase the risk of breast carcinoma. Sex is one: breast cancer in men is rare. Age is another: as women age, their risk for developing breast cancer increases, a 70 year old woman having three times the risk of developing cancer and five times the risk of dying from the disease as compared to a 40 year old woman. Most breast cancers occur after age 50, although in women with a genetic susceptibility, breast cancer tends to occur at an earlier age than in sporadic cases. Reproductive and menstrual history are also known to affect risk, with risk increasing with early menarche and late menopause, and is reduced by early first full term pregnancy. Additional risk factors, oft-times termed "lifestyle factors", include weight gain, obesity, fat intake, alcohol consumption, and level of physical

activity.

That genetic factors underlie the etiology of breast cancer is suggested by the approximately two-fold increased risk for development of breast cancer by women 5 with a first-degree relative who has also developed breast cancer. After gender and age, a positive family history is the strongest known predictive risk factor for breast cancer. Genetic linkage analysis in families with high rates of inherited cancer have facilitated the 10 identification of several genes in which mutations can be shown to contribute substantially to the development and progression of breast cancer, including BRCA1, BRCA2, p53, and PTEN/MMAC1. Further study has made clear, however, that these genes are not alone sufficient to explain all 15 genetic contributions to breast cancer.

For example, BRCA1 appears to be responsible for disease in up to 90% of families with both breast and ovarian cancer, but in only 45% of families with multiple cases of breast cancer without occurrence of ovarian 20 cancer. And mutations in BRCA2, localized to the long arm of chromosome 13, are thought to account for only approximately 35% of multiple case breast cancer families. Furthermore, despite the strong correlation between 25 germline mutations in BRCA1 or BRCA2 and development of breast cancer, only weak connections have been made between these genes and sporadic breast cancer.

Epistatic effects of BRCA1 and BRCA2 mutations on other genetic loci, only some of which have been identified, have been postulated to account for some of the 30 deleterious effects of mutations in these two genes.

Thus, mutations in p53 seem to be much more frequent in BRCA1 breast cancers (20/26) and somewhat more frequent in BRCA2-associated breast cancers (10/22) than in grade-matched sporadic cancers (7/20). BRCA mutation- 35 associated cancers contain p53 mutations not typically

found in sporadic breast cancer, and 12 individual hereditary breast cancers have been shown to contain more than a single p53 mutation. Mutations of BRCA1 and BRCA2 may thus confer a "mutator" phenotype permitting the 5 accumulation of genetic abnormalities, with p53 inactivation selected during tumor progression.

Additionally, genome-wide screening for chromosomal gains or losses in breast cancers harboring BRCA1 or BRCA2 mutations demonstrated more regions that 10 were amplified or deleted compared to controls, suggesting a generalized increase in large-scale genomic instability. Chromosomes 5q, 4q, and 4p had very frequent loss of heterozygosity in BRCA1 tumors, while BRCA2 tumors were characterized by losses at 13q (near the BRCA2 locus 15 itself) and 6q, and chromosomal gains at 17q (outside of the HER2/neu locus) and 20q.

Mutations of other genes have also been implicated in susceptibility to development or aggressiveness of breast cancer. For example, germline 20 mutations in the ATM gene, localized to chromosome 11q22-23, result in an increased risk of breast cancer among female heterozygote carriers with an estimated relative risk of 3.9 to 6.4; it is unclear, however, if mutations in the ATM gene itself contribute to breast 25 cancer.

Normal allelic variation in a variety of genes, as opposed to frank mutation, may also influence susceptibility to developing breast carcinoma and the propensity for the disease to progress. Such 30 polymorphisms may thus explain why particular women or ethnic groups who do not otherwise bear mutations in genes known to be linked to breast cancer are at greater risk, especially in the context of exposure to environmental agents and other nonhereditary risk factors.

35 Polymorphically expressed genes may code for enzymes that

metabolize estrogens or detoxify drugs and environmental carcinogens.

For example, molecular epidemiologic studies of cancer of the breast have examined associations with p450 cytochrome genotypes including CYP1A1, CYP2D6, and CYP17. The CYP1A1 gene, located on chromosome 15q, encodes the enzyme aryl hydrocarbon hydroxylase (AHH), present in breast tissue, and which catabolizes polycyclic aromatic hydrocarbons and arylamines. AHH is strongly inducible, i.e., greater enzymatic activity is seen with greater exposure to substrates. AHH catalyzes the monooxygenation of polycyclic aromatic hydrocarbons to phenolic products and epoxides that may be carcinogenic. AHH is also involved in the conversion of estrogen to hydroxylated conjugated estrogens such as 2-hydroxyestradiol.

Three polymorphisms in the CYP1A1 gene have been identified: an MspI RFLP of the 3' end of the gene (MspI); an adenine to guanine mutation in exon 7, causing an isoleucine to valine substitution (Ile-Val); and a polymorphism of the CYP1A1 gene identified among Negroids. The frequencies of the MspI and Ile-Val polymorphisms vary considerably by race, being higher among Japanese and Hawaiian populations as compared with Caucasians and Negroids.

The CYP2D6 gene is located on chromosome 22q and encodes the enzyme debrisoquine hydroxylase, which metabolizes a variety of drugs and other xenobiotics. Like other polymorphically expressed p450 enzymes, it may activate procarcinogens or, conversely, detoxify carcinogens. A number of alleles have been characterized at the CYP2D6 locus. The "poor metabolizer" phenotype (CYP2D6 mutant/mutant genotype), which is rare in Asians, occurs in about 5% to 10% of Caucasians and in 2% of Negroids.

As another example, the N-acetyl transferase-1

(NAT1) and N-acetyl transferase-2 (NAT2) genes are located on chromosome 8q. Allelic variation in the NAT genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to compounds present in tobacco. NAT2 detoxifies or, conversely, activates aromatic amines found in tobacco smoke such as 4-aminobiphenyl. Both phenotypic assays and genotypic assays for NAT2 can be used to classify individuals as rapid or slow acetylators. Genetic variants of the NAT2 gene have been cloned and 6 alleles at this locus have been identified: the F1 allele confers the fast acetylator phenotype. The distribution of NAT1 and NAT2 alleles differs widely between racial and ethnic groups.

As yet another example, the glutathione S-transferase-M1 (GSTM1) gene is located on chromosome 1 and the gene for glutathione S-transferase-T1 (GSTT1) is located on chromosome 11q. A glutathione S-transferase P1 (GSTP1) gene has also been identified.

Glutathione S-transferases detoxify a variety of carcinogens and cytotoxic drugs (for example, benzo(a)pyrene, monohalomethanes such as methyl chloride, ethylene oxide, pesticides, and solvents used in industry) by catalyzing the conjugation of a glutathione moiety to the substrate. Allelic variation in the glutathione-S-transferase genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to environmental toxins. Individuals homozygous for deletions in the GSTM1, GSTT1, or GSTP1 genes may have a higher risk of cancer of the breast and other sites because of their impaired ability to metabolize and eliminate carcinogens.

GSTM1 is polymorphically expressed and 3 alleles at the GSTM1 locus have been identified: GSTM1-0

(homozygous deletion genotype), GSTM1a, and GSTM1b. The null allele (GSTM1-0) is present in about 38% to 67% of Caucasians and 22% to 35% of Negroids. GSTM is not expressed in breast tissue at high levels. Two functionally different genotypes at the GSTT1 locus have been described: GSTT1-0 (homozygous deletion genotype) and GSTT1-1 (genotypes with 1 or 2 undeleted alleles). A polymorphism of the GSTP1 gene, A313G (changing codon 105 from Ile to Val), has been identified. The GSTT1-0 allele has been associated with accelerated age of first breast cancer diagnosis as compared with the GSTT1-1 allele.

Many other genes have been suggested to be involved in the development and/or progression of breast cancer, either as a result of gain of function or loss of function mutations, or as a result of normal allelic variation within different populations. A nonexhaustive list of such genes, each followed by the gene's chromosomal location, if known, follows: AMPII 7p14-p13; AMPHL (BIN1, SH3P9) 2q14; API4 (survivin, SVV) 17q25(?); ARHA (ARH12, RhoA) 3p21.3; ARHC (RhoC) 1p21-p13; ATM (ATA, ATC) 11q22.3; BAG1 9p12; BARD1 2q34-q35; BCAR1 16q23.1; BCAR2; BCAR3 (NSP2); BCAS1 (NABC1, AIBC1) 20q13.2-q13.3; BRCA1 17q21; BRCA2 13q12.3; CCND1 (D11S287E, Cyclin D, PRAD1) 11q13; CD44 (MDU3, HA, MDU2) 11pter-p13; CD9 (p24, MIC3, BA2) 12p13; CDKN1B (KIP1, P27) 12p13; CDKN2A (P16, INK4A, MTS1) 9p21; COMT 22q11.2; COT (MAP3K8, TPL-2, EST) 10p11.2; CSK (c-src) 15q23-q25; CTSD (CPSD) 11p15.5; CYP17 10q24.3; CYP19 15q21.1; CYP1A1 (CYP1) 15q22-q24; CYP1B1 (GLC3A) 2p22-p21; EFNB2 (EPLG5, LERK5, ephrin-B2) 13q33; EIF3S6 (INT6) 8q22-q23; EIF4E (EIF-4E) 4q21-q25; EMS1 11q13; ERBB2 (HER2, NEU) 17q11.2-q12; ERBB3 (HER3) 12q13; ESR1 (ESRA) 6q25.1; ESR2 (ESRB, ERBeta) 14q; FGF8 (AIGF) 10q24; GSTM1 (GST1, MU) 1p13.3; GSTP1 (FAEES3, GST3, PI) 11q13; GSTT1 22q11.23; HRAS 11p15.5; HSPB1 (HSP27) 7q; HSPCA (HSP90A, HSPC1); HSPCB (HSP90B, HSPC2) 6p12; IGF1

12q22-q24.1; IGF1R (JTK13) 15q25-q26; IGF2
11p15.5; IL6 (IFNB2) 7p21; ING1 13q34; KISS1 (KiSS-1) 1q32;
KLK3 (PSA, APS) 19q13; LASP1 (MLN50) 17q11-q21.3; LIBC
6q22; MAP2K4 (MKK4, SEK1, JNKK1) 17p11.2; MKI67 (Ki-67)
5 10q25-qter; MMP11 (STMY3, STR3) 22q11.2; MMP2 (CLG4A, CLG4,
GELA) 16q13; MUC1 (PUM, PEM) 1q21; MYC (CMYC, C-MYC)
8q24.12-q24.13; NOTCH4 (INT3, NOTCH3) 6p21.3; PCNA 20p12;
PI5 (maspin) 18q21.3; PLAU (uPA , URK) 10q24; PSEN2
10 (Rb) 13q14.2; S100A4 (MTS1, P9KA, metastasin) 1q21;
SLC22A1L (BWSCR1A, ORCTL2, IMPT1) 11p15.5; SNCG (BCSG1)
10q23.2-q23.3; SRD5A2 2p23; STIP1 (HSP70) 11?; STK11 (LKB1,
PJS) 19p13.3; TFAP2A (AP2 , AP2TF) 6p24; TFAP2B (AP2B)
6p12; TFAP2C 20q13.2; TFF1 (D21S21, BCEI) 21q22.3; TGFB2
15 3p22; TIMP2 17q25; TP53 (p53 , P53) 17q13.1; TPD52 (D52)
8q21; TPD52L1 (D53, hD53) 6q22-q23; TSG101 11p15.2-p15.1.

The etiology of non-cancerous disorders of the breast may also involve genetic factors. Such disorders include disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease, and non-carcinoma tumors.

Disorders of development of the breast include supernumerary nipples or breasts; accessory axillary breast tissue; congenital inversion of the nipples; and 25 macromastia.

Inflammatory diseases of the breast include acute mastitis; periductal mastitis, also called recurrent subareolar abscess and squamous metaplasia of the lactiferous ducts; mammary duct ectasia; fat necrosis; and 30 granulomatous mastitis, including granulomatous lobular mastitis. Systemic granulomatous diseases that can affect the breast include Wegener granulomatosis and sarcoidosis.

Proliferative breast diseases include epithelial hyperplasia; sclerosing adenosis; and small duct 35 papillomas. Non-carcinoma tumors include stomal tumors

including fibroadenoma and phyllodes tumor, and sarcomas that include angiosarcoma, rhabdomyosarcoma, liposarcoma, leiomyosarcoma, chondrosarcoma and osteosarcoma. Other breast tumors include epithelial cell tumors including 5 large duct papillomas.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human breast, particularly those 10 diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed at detectable levels in human breast cancer cells, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide 15 exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of 20 a given breast disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 25 patient's breast to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the . 30 function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be 35 used to interrogate genomic DNA, rather than pools of

expressed message; this latter approach permits predisposition to and/or prognosis of breast disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human breast. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the HBL 100 cells has been demonstrated are useful for both measurement in the Breast and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or

tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

5 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

10 Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

15 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell 20 Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999)); 25 Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for

example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., 5 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and 10 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the 15 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

20 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, 25 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway 30 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter 35 a gene's expression level is evidence that the drug does

not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in HBL 100 cells. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the

hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to 5 PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the 10 range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be 15 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be 20 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first 25 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe 30 composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the 35 present invention will typically average at least about

100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the 5 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first 10 bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that 15 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable 20 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention 25 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,075 - 10,058, respectively, for probe SEQ ID NOS. 1 - 5,074. The minimum amount of ORF required to be included in the probe of the present invention in order to 30 provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,075 - 10,058 individually by routine experimentation using standard high stringency conditions.

35 Such high stringency conditions are described,

inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded

probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural 5 individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 10 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 15 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon 20 probes can usefully include a plurality of probes chosen for the common attribute of expression in the human HBL 100 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, 25 as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid 30 amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays 35 useful for gene expression analysis, where the term

"microarray" has the meaning given in "the "definitional" section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human HBL 100 cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 5,074.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,074 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,075 - 10,058, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 5,074 can be used, or that portion thereof in SEQ ID NOS. 5,075 - 10,058

used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially
5 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter 15 alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7), Oxford Univ. Press 20 (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence 25 translated from SEQ ID NOS.: 5,075 - 10,058. Such amino acid sequences are set out in SEQ ID NOS: 10,059 - 15,009. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate 30 antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
5 in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
10 immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
15 reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
Markoff model, and DICTION, a program proprietary to
20 Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

The three gene finding programs yielded a range
25 of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
genomic sequence called as coding region.

30 The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
That is, 0.25% of the genomic sequence was identified by
35 all three of the programs as containing putative coding

region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

10

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant

further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon 5 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® 10 green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

15 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue 20 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR 25 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR 30 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of 35 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less

than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

15 Table 1

| Total | V6 chip | V7 chip | Function Predicted from Comparative Sequence Analysis |
|-------|---------|---------|---|
| 211 | 96 | 115 | Receptor |
| 120 | 43 | 77 | Zinc Finger |
| 30 | 11 | 19 | Homeobox |
| 25 | 9 | 16 | Transcription Factor |
| 17 | 11 | 7 | Transcription |
| 118 | 57 | 61 | Structural |
| 95 | 39 | 56 | Kinase |
| 36 | 18 | 18 | Phosphatase |
| 83 | 31 | 52 | Ribosomal |
| 45 | 19 | 26 | Transport |
| 21 | 17 | 14 | Growth Factor |
| 17 | 12 | 5 | Cytochrome |
| 50 | 33 | 17 | Channel |

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 35 After 2 hours, the first strand cDNA was isolated by adding

1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

5 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2
10 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by

the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic

expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity

for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all 5 sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the 10 ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large 15 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA 20 library.

The significant point is that presence of the 25 gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic 30 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific 35 gene expression patterns as measured by the microarray

experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray

hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

| Function of the Most Highly Expressed Genes Expressed Only in Brain | | | | |
|--|--------------------------|----------------------|--|---|
| Microarray Sequence Name | Normal ized Signal | Expressi on Ratio | Homology to EST present in GenBank | Gene Function as described by GenBank |
| AP000217-1 | 5.2 | +7.7 | High | S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system |
| AP000047-1 | 2.3 | | High | Unknown Function |
| AC006548-9 | 1.7 | | High | Similar to mouse membrane glyco-protein M6, expressed in central nervous system |
| AC007245-5 | 1.5 | | High | Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21 |
| L44140-4 | 1.2 | +2.0 | High | Endothelial actin-binding |

| | | | | protein found in nonmuscle filamin |
|------------|-----|------|------|--|
| AC004689-9 | 1.2 | +3.5 | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |
| AL031657-1 | 1.2 | +3.0 | High | Unknown function/ Contains the anhyrin motif, a common protein sequence motif |
| AC009266-2 | 1.1 | +3.7 | Low | Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain |
| AP000086-1 | 1.0 | +2.7 | Low | Unknown, very poor homology to collagen |
| AC004689-3 | 1.0 | | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |

Of the ten sequences studied by these latter

confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca²⁺ binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

35 Other interesting genes highly expressed in brain

were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

| Comparison of Expression Ratio, for each tissue, of GAPDH | | |
|---|------------------|-----------------|
| | AC006064 (n = 4) | Control (n = 5) |
| Bone Marrow | -1.81 ± 0.11 | -1.85 ± 0.08 |
| Brain | -1.41 ± 0.11 | -1.17 ± 0.05 |
| BT474 | 1.85 ± 0.09 | 1.66 ± 0.12 |
| Fetal Liver | -1.62 ± 0.07 | -1.41 ± 0.05 |
| HBL100 | 1.32 ± 0.05 | 2.64 ± 0.12 |

| | | |
|----------|--------------|--------------|
| Heart | 1.16 ± 0.09 | 1.56 ± 0.10 |
| HeLa | 1.11 ± 0.06 | 1.30 ± 0.15 |
| Liver | -1.62 ± 0.22 | -2.07 ± |
| Lung | -4.95 ± 0.93 | -3.75 ± 0.21 |
| Placenta | -3.56 ± 0.25 | -3.52 ± 0.43 |

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases

25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

5 As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

10 Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

15 The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We
20 selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression
25 patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they
30 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
35 turquoise = α_1 anti-chymotrypsin (P01011); mauve = 40S

ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

5 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

The protocols set forth in Examples 1 and 2,
10 supra, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in HBL 100 cells.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid,
15 starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented
20 fragments of each of the 5,074 single exon probes, each fragment corresponding to an extension product from one of
25 the two amplification primers.)

The structures of the 5,074 unique single exon probes are clearly presented in the Sequence Listing as SEQ
30 ID Nos.: 1 - 5,074. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,075 - 10,058,
35 respectively. It will be noted that some amplicons have

more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 10 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the 20 duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than 25 median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified 30 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

35 This means that, assuming that the data is

distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. 5 Example 5 presents the subset of probes that is significantly expressed in the human HBL 100 cells and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human HBL 100 cells.

10 The sequence of each of the exon probes identified by SEQ ID NOS.: 5,075 - 10,058 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because 15 the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

20 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as 25 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be 30 expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, 35 the accession number of the database sequence that yielded

the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1×10^{-5}) and 1e-100 (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary:

in Example 2, *supra*, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 5,074) and probe exon (SEQ ID NOS.: 5,075 - 10,058, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human HBL 100 cells

5

Table 4 (209 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human HBL 100 cells, a hormone sensitive human breast cancer cell line.

10

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--|
| 447 | 5484 | 10501 | 4.37 | | | | |
| 878 | 5896 | 10937 | 8.5 | | | | |
| 1028 | 6038 | | 2.62 | | | | |
| 1283 | 6282 | 11324 | 8.84 | | | | |
| 1577 | 6574 | 11636 | 3.1 | | | | |
| 1596 | 6592 | 11653 | 4.71 | | | | |
| 1687 | 6683 | 11758 | 2.18 | | | | |
| 1710 | 6705 | 11781 | 1.16 | | | | |
| 1717 | 6712 | 11789 | 7.06 | | | | |
| 1850 | 6839 | 11928 | 1.12 | | | | |
| 1933 | 6919 | 12018 | 1.75 | | | | |
| 2101 | 7082 | 12197 | 1.88 | | | | |
| 2216 | 7193 | 12315 | 4.79 | | | | |
| 3112 | 8128 | 13148 | 3.32 | | | | |
| 3366 | 8374 | 13394 | 1.09 | | | | |
| 3437 | 8445 | 13471 | 12.48 | | | | |
| 3481 | 8489 | | 1.38 | | | | |
| 3573 | 8580 | 13586 | 1.16 | | | | |
| 3844 | 8846 | | 1.1 | | | | |
| 4074 | 9068 | 14058 | 1.73 | | | | |
| 4139 | 9134 | 14117 | 6.13 | | | | |
| 4211 | 9204 | | 1.28 | | | | |
| 4689 | 9674 | 14667 | 1.1 | | | | |
| 4879 | 9858 | 14829 | 4.14 | | | | |
| 4888 | 9867 | 14837 | 1.25 | | | | |
| 2595 | 7558 | 12672 | 0.93 | 9.4E+00 | L11433.1 | NT | Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds |
| 2595 | 7558 | 12673 | 0.93 | 9.4E+00 | L11433.1 | NT | Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds |
| 2853 | 7873 | 12888 | 3.02 | 9.4E+00 | AB043785.1 | NT | Mus musculus AT3 gene for antithrombin, complete cds |
| 437 | 5475 | 10491 | 2.23 | 8.4E+00 | 5031804 | NT | Homo sapiens insulin receptor substrate 1 (IRS1) mRNA |
| 2909 | 7928 | 12946 | 3.48 | 7.2E+00 | L12051.1 | NT | Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 2909 | 7928 | 12947 | 3.48 | 7.2E+00 | L12051.1 | NT | Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 3445 | 8453 | | 0.71 | 5.8E+00 | 7666557 | NT | Homo sapiens DESC1 protein (DESC1), mRNA |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4640 | 9625 | 14617 | 1.32 | 5.3E+00 | L43128.1 | NT | Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds |
| 3949 | 8947 | | 11.08 | 4.8E+00 | AF185255.1 | NT | Eunice australis histone H3 (H3) gene, partial cds |
| 287 | 5345 | 10357 | 2.26 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5' |
| 288 | 5345 | 10357 | 1.89 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5' |
| 3200 | 8216 | 13237 | 1.53 | 4.7E+00 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 3469 | 8477 | | 1.24 | 4.0E+00 | P38229 | SWISSPROT | GLC7-INTERACTING PROTEIN 1 |
| 3424 | 8432 | 13458 | 4.3 | 3.9E+00 | X64518.1 | NT | N.tabacum chitinase C gene 50 for class I chitinase C |
| 4194 | 9187 | | 0.7 | 3.9E+00 | AF055466.1 | NT | Mus musculus seminal vesicle secretory protein 9g (MSVSP9g) gene, promoter region |
| 2857 | 7522 | | 1.46 | 3.8E+00 | AE001562.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 3912 | 8912 | 13907 | 11.92 | 3.7E+00 | AL161539.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39 |
| 5050 | 10021 | | 1.5 | 3.7E+00 | AF216290.1 | NT | Mus musculus heterochromatin protein 1 alpha mRNA, complete cds |
| 588 | 5619 | 10617 | 3.88 | 3.6E+00 | AV761056.1 | EST_HUMAN | AV761055 MD3 Homo sapiens cDNA clone MDSBUE10 5' |
| 3174 | 8190 | 13211 | 0.95 | 3.5E+00 | AF221588.1 | NT | Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds |
| 1881 | 6478 | 11534 | 2.26 | 3.4E+00 | AF254577.1 | NT | Brassica napus RPB5d mRNA, complete cds |
| 497 | 5533 | 10540 | 1.62 | 3.2E+00 | X86422.1 | NT | Danio rerio zp-50 F OU gene |
| 4588 | 9576 | 14567 | 1.44 | 3.2E+00 | | | Homo sapiens carcinomaembryonic antigen-related cell adhesion molecule 1 (liliary glycoprotein) (CEACAM1), mRNA |
| 2764 | 7785 | 12809 | 2.05 | 3.0E+00 | 8923984 | NT | Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA |
| 1961 | 6947 | 12049 | 1.6 | 2.9E+00 | AE002225.2 | NT | Chlamydomonas pneumophila AR39, section 53 of 94 of the complete genome |
| 1430 | 6427 | 11485 | 4.89 | 2.8E+00 | AF186398.1 | NT | Buxus harlandii maturose K (matK) gene, partial cds; chloroplast gene for chloroplast product |
| 1593 | 6589 | | 1.65 | 2.8E+00 | AL161552.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52 |
| 230 | 5293 | 10301 | 19.61 | 2.7E+00 | | 6679306 | Mus musculus per-hexameric repeat gene 3 (Phx3), mRNA |
| 230 | 5293 | 10302 | 19.61 | 2.7E+00 | | 6679306 | Mus musculus per-hexameric repeat gene 3 (Phx3), mRNA |
| 4538 | 9528 | 14514 | 5.78 | 2.6E+00 | AF068749.1 | NT | Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds |
| 1436 | 6433 | 11489 | 2.05 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |
| 1436 | 6433 | 11490 | 2.05 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |
| 2944 | 7963 | 12983 | 0.8 | 2.4E+00 | M24282.1 | NT | Chicken alpha-3 collagen type VI mRNA, 3' end |
| 4752 | 9737 | 14723 | 5.52 | 2.4E+00 | 4503352 | NT | Homo sapiens double C2-like domains, alpha (DOC2A) mRNA |
| 1234 | 6232 | 11276 | 13.73 | 2.3E+00 | Z16724.1 | NT | G.domesticus artificial single chain antibody gene (L3) |
| 4002 | 8998 | | 1.54 | 2.3E+00 | AJ401081.1 | NT | Bos taurus partial cytb gene for cytochrome b |
| 3910 | 8910 | 13806 | 1.11 | 2.2E+00 | AF020528.1 | NT | Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds |
| 4186 | 9179 | 14162 | 4.03 | 2.2E+00 | D67071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| 4186 | 9179 | 14163 | 4.09 | 2.2E+00 | D67071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| 564 | 7724 | 10597 | 7.72 | 2.1E+00 | AF132612.2 | NT | Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--|--|
| | | | | | | | | |
| 2948 | 7967 | 12985 | 1.2 | 2.1E+00 | AF208532.1 | NT | Homo sapiens fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds | U1-H-B13-alk-e-08-0-UI-s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734550 3' |
| 3507 | 8515 | | 0.83 | 2.1E+00 | AW449366.1 | EST_HUMAN | | |
| 1177 | 6179 | 11215 | 2.45 | 2.0E+00 | AF180527.1 | NT | Homo sapiens p122Dokdel (DOKDEL) mRNA, complete cds | |
| 1177 | 6179 | 11216 | 2.45 | 2.0E+00 | AF180527.1 | NT | Homo sapiens p122Dokdel (DOKDEL) mRNA, complete cds | |
| 1315 | 6312 | 11361 | 1.07 | 2.0E+00 | AF204927.1 | NT | Oryctolagus cuniculus Na ⁺ -K ⁺ -ATPase beta 1 subunit mRNA, complete cds | |
| 1540 | 6538 | | 3.99 | 2.0E+00 | P25582 | SWISSPROT | PUTATIVE RNA METHYLTRANSFERASE SPB1 | |
| 2088 | 7069 | 12182 | 8.21 | 2.0E+00 | Z78279.1 | NT | R.norvegicus tRNA for collagen alpha1 type I | |
| 2088 | 7069 | 12183 | 8.21 | 2.0E+00 | Z78279.1 | NT | R.norvegicus tRNA for collagen alpha1 type I | |
| 3984 | 8982 | 13967 | 1.95 | 2.0E+00 | AW664496.1 | EST_HUMAN | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); | hi13c05.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 |
| 3984 | 8982 | 13968 | 1.95 | 2.0E+00 | AW664498.1 | EST_HUMAN | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); | hi13c05.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 |
| 3019 | 8036 | 13046 | 1.75 | 1.8E+00 | P21004 | SWISSPROT | PROTEIN B8 PRECURSOR | Synechococcus sp. PC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 3047 | 8064 | 13072 | 2.44 | 1.8E+00 | U04356.1 | NT | Synechococcus sp. PC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds | |
| 3047 | 8064 | 13073 | 2.44 | 1.8E+00 | U04356.1 | NT | LEVANSUFRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) SUCROSE 6-FRUCTOSYL TRANSFERASE | |
| 1091 | 6098 | 11127 | 1.65 | 1.7E+00 | Q60114 | SWISSPROT | | Homo sapiens chromosome 21 segment HS21C080 |
| 2209 | 7180 | 12308 | 2.62 | 1.7E+00 | AL163280.2 | NT | | ox43h05.x1 Soares, NIH/MPU_S1 Homo sapiens cDNA clone IMAGE:1678137 3' |
| 2312 | 7287 | 12408 | 1.36 | 1.7E+00 | AI141057.1 | EST_HUMAN | | |
| 1983 | 6968 | 12074 | 8.04 | 1.6E+00 | AF198339.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds | |
| 1992 | 6977 | 12081 | 2.96 | 1.6E+00 | AF077374.1 | NT | Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds | |
| 1996 | 6980 | 12085 | 1.09 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcII gene, exon 2 | |
| 2220 | 7197 | | 4.52 | 1.6E+00 | X98373.1 | NT | B.napus gene encoding endo-polylacturonase zd25f01.r1 Soares, fetal heart_NbII-H19W Homo sapiens cDNA clone IMAGE:341689 5' similar to | |
| 2891 | 7910 | 12931 | 1.57 | 1.6E+00 | W58426.1 | EST_HUMAN | gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN); | |
| 3921 | 8921 | | 5.49 | 1.6E+00 | BF570077.1 | EST_HUMAN | 6021860951 NIH MGIC_45 Homo sapiens cDNA clone IMAGE:4310591 3' | |
| 4226 | 9220 | 14199 | 1.68 | 1.6E+00 | AF155827.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds | |
| 4226 | 9220 | 14200 | 1.68 | 1.6E+00 | AF155827.1 | NT | Homo sapiens ST6GalNAcIII gene, exon 2 | |
| 4911 | 9890 | 14863 | 2.77 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcIII gene, exon 2 | |
| 4911 | 9890 | 14864 | 2.77 | 1.6E+00 | Y11344.1 | NT | Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds | |
| 33 | 5113 | 10069 | 4.61 | 1.5E+00 | U53449.1 | NT | Chlamydomonas AR39, section 32 of 94 of the complete genome | |
| 231 | 5294 | 10303 | 1.98 | 1.5E+00 | AE002201.2 | NT | | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 616 | 5643 | | | 1.7 | 1.5E+00 | 6752961 | NT |
| 2544 | 7318 | 12438 | 1.68 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA complete genome, isolate U |
| 2444 | 7414 | 12530 | 1.67 | 1.5E+00 | 6678350 | NT | Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA |
| 3065 | 7318 | 12438 | 2.59 | 1.6E+00 | AJ131402.1 | NT | Potato virus A RNA complete genome, isolate U |
| 30 | 5110 | 10095 | 1.17 | 1.4E+00 | 7661685 | NT | Homo sapiens DKFZP5B86M0122 protein (DKFZP5B86M0122), mRNA |
| 30 | 5110 | 10096 | 1.17 | 1.4E+00 | 7661685 | NT | Homo sapiens DKFZP5B86M0122 protein (DKFZP5B86M0122), mRNA |
| 2272 | 7248 | | 7.96 | 1.4E+00 | U67922.1 | NT | Ovis aries prf1: protein gene, complete cds |
| 2598 | 7560 | 12677 | 1.44 | 1.4E+00 | X74463.1 | NT | Human papillomavirus type 7 genomic DNA |
| 2701 | 7658 | 12771 | 3.21 | 1.4E+00 | AF064564.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 2701 | 7658 | 12772 | 3.21 | 1.4E+00 | AF064564.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 3259 | 8272 | | 0.89 | 1.4E+00 | 54531733 | NT | Homo sapiens Mad4 homolog (MAD4) mRNA |
| 4453 | 9443 | | 1.34 | 1.4E+00 | BFE81547.1 | EST_HUMAN | 60215668Y1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5' |
| 4994 | 9986 | 14944 | 1.02 | 1.4E+00 | BE972426.1 | EST_HUMAN | 60165225Y1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3995556 5' |
| 565 | 5568 | | 1.44 | 1.3E+00 | Z73640.1 | NT | M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase |
| 891 | 5909 | 10949 | 2.13 | 1.3E+00 | AJ271192.1 | NT | Cantharellus sp. partial 26S rRNA gene, isolate Tibet |
| 1112 | 6118 | | 19.14 | 1.3E+00 | Y19213.1 | NT | Homo sapiens putative psn1bA pseudogene for hair keratin, exons 2 to 7 |
| 1278 | 6277 | 11318 | 14.53 | 1.3E+00 | 4507998 | NT | Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA |
| 1278 | 6277 | 11319 | 14.53 | 1.3E+00 | 4507998 | NT | Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA |
| 1338 | 63346 | | 1.06 | 1.3E+00 | U6730.2 | NT | Cat lacrmejobi dihydropicolinate synthase (dapA) gene, complete cds |
| 1574 | 6571 | | 2.03 | 1.3E+00 | AE002338.2 | NT | Chlamydia muridarum, section 68 of the complete genome |
| 2479 | 7448 | | 1.67 | 1.3E+00 | BE986735.2 | EST_HUMAN | 60166123R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3' |
| 3517 | 8525 | 13536 | 0.68 | 1.3E+00 | AF016494.1 | NT | Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c> |
| 642 | 5670 | 10674 | 8.78 | 1.2E+00 | AA676246.1 | EST_HUMAN | Z122d08.81 Scares fetal liver spleen 1NF1 S1 Homo sapiens cDNA clone IMAGE:431535 3' |
| 813 | 5834 | 10887 | 0.86 | 1.2E+00 | PO5228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 813 | 5834 | 10868 | 0.86 | 1.2E+00 | PO5228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 813 | 5834 | 10889 | 0.86 | 1.2E+00 | PO5228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 867 | 5885 | | 1.83 | 1.2E+00 | 8924234 | NT | Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA |
| 1143 | 6147 | 11179 | 6.07 | 1.2E+00 | AF080245.2 | NT | Elaeis oleifera sesquiterpene synthase mRNA, complete cds |
| 1186 | 6187 | 11224 | 1.7 | 1.2E+00 | AJ252242.1 | NT | pea seed-borne mosaic virus complete genome |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 11865 | 6187 | 11225 | 1.7 | 1.2E+00 | AJ252242.1 | NT | pea seed-borne mosaic virus complete genome |
| 19950 | 6946 | 12048 | 0.97 | 1.2E+00 | AF140631.1 | NT | Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds |
| 30922 | 8103 | 13124 | 6.13 | 1.2E+00 | AL161553.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 30922 | 8103 | 13125 | 6.13 | 1.2E+00 | AL161553.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 3213 | 82228 | | 3.29 | 1.2E+00 | P54910 | SWISSPROT | CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR |
| 3277 | 8289 | 13314 | 0.73 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 3630 | 8636 | 13641 | 8.37 | 1.2E+00 | U75902.1 | NT | Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds |
| 3880 | 8881 | 13884 | 2.04 | 1.2E+00 | BF373570.1 | EST_HUMAN | MR0-FT0175-050900-203-906_1 FT0175 Homo sapiens cDNA |
| 4174 | 8289 | 13314 | 0.97 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 4273 | 9266 | 14257 | 1.01 | 1.2E+00 | 6980951 | NT | Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Gira2), mRNA |
| 4346 | 9337 | | 2.1 | 1.2E+00 | M87060.1 | NT | Rattus rattus cardiac AE3 gene, exons 1-23 |
| 4392 | 9383 | 14365 | 0.99 | 1.2E+00 | AL161509.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21 |
| 4429 | 9419 | 14405 | 1.92 | 1.2E+00 | AF158495.1 | NT | Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds |
| 4456 | 9446 | | 5.44 | 1.2E+00 | Y09200.1 | NT | T. pennatum chloroplast rbcL gene, partial |
| 461 | 5498 | 10509 | 1 | 1.1E+00 | D86580.1 | NT | Human mRNA for KIAA0227 gene, partial cds |
| 1725 | 6720 | 11798 | 1.36 | 1.1E+00 | AW995393.1 | EST_HUMAN | QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA |
| 3255 | 8268 | 13280 | 7.24 | 1.1E+00 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3255 | 8268 | 13291 | 7.24 | 1.1E+00 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3406 | 8415 | 13443 | 0.72 | 1.1E+00 | 8922641 | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| 3479 | 8487 | 13849 | 2.43 | 1.1E+00 | 8922973 | NT | Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA |
| 3499 | 8507 | 13522 | 0.93 | 1.1E+00 | AB08360.1 | EST_HUMAN | wf54h11.x1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 '3' similar to SW:P531_HUMAN Q12888 P53 BINDING PROTEIN 53BP1 ; |
| 3636 | 8642 | 13647 | 1.32 | 1.1E+00 | AE003886.1 | NT | Xylella fastidiosa, section 32 of the complete genome |
| 3636 | 8642 | 13648 | 1.32 | 1.1E+00 | AE003886.1 | NT | Xylella fastidiosa, section 32 of the complete genome |
| 3840 | 8842 | 13849 | 0.95 | 1.1E+00 | 8922641 | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| 3913 | 8913 | 13908 | 0.88 | 1.1E+00 | 6755205 | NT | Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA |
| 4094 | 9083 | | 8.1 | 1.1E+00 | 5835331 | NT | R. unicornis complete mitochondrial genome |
| 4834 | 9818 | 14796 | 4.26 | 1.1E+00 | U18466.1 | NT | African swine fever virus, complete genome |
| 4899 | 9878 | 14847 | 1.11 | 1.1E+00 | X78425.1 | NT | E. faecalis ppp5 gene |
| 5024 | 9995 | 14963 | 0.71 | 1.1E+00 | P25396 | SWISSPROT | TELLURITE RÉSISTANCE PROTEIN TEHA |
| 5058 | 10028 | 14996 | 0.97 | 1.1E+00 | AJ251835.1 | NT | Mus musculus Kcnq1, Lrp5, Mash2, Tspy-1, Tssc4 and Tssc6 genes, alternative transcripts |
| 98 | 5175 | | 3.83 | 1.0E+00 | U23808.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 113 | 5185 | 10194 | 2.17 | 1.0E+00 | DBB425.1 | NT | Cavia cobaya mRNA for sarco(endo)thelial kinase, complete cds |
| 415 | 5452 | | 2.22 | 1.0E+00 | AB021684.1 | NT | Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA |

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 Table 4
 Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--|
| 571 | 5604 | 10602 | 1.57 | 1.0E+00 | AJ251660.1 | NT | Girardia tigrina mRNA for homeodomain transcription factor (so gene) |
| 669 | 5694 | 10703 | 9.1 | 1.0E+00 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 670 | 5695 | | 0.89 | 1.0E+00 | AF125984.1 | NT | Aedes aegypti mucin-like protein MUC1 mRNA, complete cds |
| 1365 | 7746 | | 3.02 | 1.0E+00 | X80416.1 | NT | V. carteri Algal-CAM mRNA |
| 1719 | 6714 | 11791 | 1.39 | 1.0E+00 | AB006531.1 | NT | Plautia stali Intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds |
| 2414 | 7385 | 12504 | 1.05 | 1.0E+00 | P48355 | SWISSPROT | DNA GYrase SUBUNIT B |
| 2414 | 7385 | 12505 | 1.05 | 1.0E+00 | P48355 | SWISSPROT | DNA GYrase SUBUNIT B |
| 2806 | 7826 | 12841 | 3.99 | 1.0E+00 | P24008 | SWISSPROT | 3-Oxo-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2806 | 7826 | 12842 | 3.99 | 1.0E+00 | P24008 | SWISSPROT | 3-Oxo-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2897 | 7916 | | 0.98 | 1.0E+00 | O14226 | SWISSPROT | HYPOTHETICAL 67.9 kD PROTEIN C6F12.0BG IN CHROMOSOME 1 |
| 3126 | 8142 | 13163 | 0.82 | 1.0E+00 | AA620453.1 | EST_HUMAN | af26q08_s1_Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element; |
| 3519 | 5175 | | 0.92 | 1.0E+00 | U23808.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 3597 | 8604 | 13612 | 1.71 | 1.0E+00 | AJ223816.1 | NT | Agaricus bisporus mRNA for tyrosinase |
| 3956 | 8954 | 13943 | 1 | 1.0E+00 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4153 | 9148 | | 1.07 | 1.0E+00 | 8922245 | NT | Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA |
| 4660 | 9645 | 14633 | 1.73 | 1.0E+00 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 4751 | 9736 | | 1.35 | 1.0E+00 | U75741.1 | NT | Taenia ovis 45W antigen (ToW4) gene, complete cds |
| 4859 | 9840 | | 0.93 | 1.0E+00 | D10852.1 | NT | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |
| 4978 | 9954 | | 1.12 | 1.0E+00 | AF200817.1 | NT | Pilot whale morbillivirus phosphoprotein (P) gene, partial cds |
| 5031 | 10002 | | 1.36 | 1.0E+00 | AJ245481.2 | NT | Human immunodeficiency virus type 1 proviral complete genome, Isolate 95ML84 |
| 2566 | 7529 | 12647 | 0.95 | 9.9E-01 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 3524 | 8531 | | 0.82 | 9.9E-01 | AF174585.1 | NT | Apple mosaic virus RNA 2 putative polymerase gene, complete cds |
| 519 | 5554 | 10557 | 0.97 | 9.8E-01 | P22567 | SWISSPROT | AMINO ACID ACETYLTRANSFERASE (N-ACETYLGUTAMATE SYNTHASE) (AGS) (NAGS) |
| 2729 | 7686 | | 0.98 | 9.8E-01 | AF17464.1 | NT | Xenopus laevis rac GTPase mRNA, complete cds |
| 4315 | 9307 | 14291 | 0.68 | 9.6E-01 | AF197925.1 | NT | Bromus inermis putative cytosolic phosphoglucomutase [pgm1] mRNA, complete cds |
| 4315 | 9307 | 14292 | 0.68 | 9.6E-01 | AF197925.1 | NT | Bromus inermis putative cytosolic phosphoglucomutase [pgm1] mRNA, complete cds |
| 4336 | 9327 | 14312 | 1.34 | 9.6E-01 | AW789674.1 | EST_HUMAN | PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA |
| 2404 | 7375 | 12495 | 1.44 | 9.5E-01 | 7705591 | NT | Homo sapiens CGI-125 protein (LOC51003), mRNA |
| 3694 | 8698 | 13699 | 2.08 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675639F-1 NIH_MGGC_21 Homo sapiens cDNA clone IMAGE:39558473 5' |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3694 | B698 | 13700 | 2.08 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675639FT1 NIH MGCC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 3128 | 8144 | | 3.87 | 9.4E-01 | AF165990.1 | NT | Bartonella claridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds |
| 3146 | 8162 | | 1.76 | 9.4E-01 | AF080595.1 | NT | Plimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds |
| 1694 | 6689 | | 1.02 | 9.3E-01 | AF242382.1 | NT | Homo sapiens phytanoyl-CoA hydroxylase (PHYH1) gene, exon 5 |
| 2662 | 7526 | 12644 | 2.29 | 9.3E-01 | BE071172.1 | EST_HUMAN | RC5-BT0503-271189-011-B01 BT0503 Homo sapiens cDNA |
| 3166 | 8182 | 13205 | 3.17 | 9.2E-01 | BE622702.1 | EST_HUMAN | 601441338T1 NIH MGCC_72 Homo sapiens cDNA clone IMAGE:3916184 3' |
| 2065 | 7047 | | 2.24 | 9.1E-01 | 8923056 | NT | Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA |
| 3132 | 8148 | 13168 | 0.83 | 9.1E-01 | T26418.1 | EST_HUMAN | AB200GBR Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200GBR 5' |
| 3132 | 8148 | 13169 | 0.83 | 9.1E-01 | T26418.1 | EST_HUMAN | AB200GBR Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200GBR 5' |
| 4254 | 9248 | 14232 | 1.01 | 9.0E-01 | AF099810.1 | NT | Homo sapiens neutrophil-1-alpha gene, partial cds |
| 4111 | 9401 | 14386 | 2.16 | 8.8E-01 | O26350 | SWISSPROT | PUTATIVE F420-DEPENDENT NADP REDUCTASE |
| 462 | 5459 | 10510 | 1.83 | 8.7E-01 | AF106953.2 | NT | Homo sapiens SOS1 (SOS1) gene, partial cds |
| 2804 | 7824 | 12839 | 5.88 | 8.7E-01 | AA595863.1 | EST_HUMAN | nn05111.s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877 |
| | | | | | | | Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbB (ohbB), OhbC (ohbC), ortho-halobenzene 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put> |
| 4847 | 9829 | | 4 | 8.7E-01 | AF121970.1 | NT | Rat IgfII gene for insulin-like growth factor II |
| 471 | 5507 | | 1.63 | 8.6E-01 | X7012.1 | NT | |
| 848 | 5867 | 10908 | 8.21 | 8.6E-01 | W69059.1 | EST_HUMAN | zd44e03.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:313516 5' |
| 3539 | 8545 | 13552 | 0.72 | 8.6E-01 | AL161585.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 3710 | 8714 | 13716 | 1.03 | 8.6E-01 | U49724.1 | NT | Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds |
| 732 | 5755 | 10776 | 2.07 | 8.3E-01 | M93437.1 | NT | Thermus thermophilus cytochrome c-552 (cytC) and CytB (cytB) genes, complete cds |
| 3021 | 8038 | 13047 | 3.04 | 8.3E-01 | AL161506.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 3905 | 8905 | 13903 | 2.61 | 8.3E-01 | Y19177.1 | NT | Streptomyces antibioticus polyketide biosynthetic gene cluster |
| 1599 | 6982 | 12086 | 1.66 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 2608 | 7570 | | 1.22 | 8.2E-01 | AW376990.1 | EST_HUMAN | IL3-CT0219-61198-031-C08 CT0219 Homo sapiens cDNA |
| 3819 | 8821 | 13828 | 0.93 | 8.2E-01 | AF063417.1 | NT | Tanystylum orbiculare elongall factor 1-alpha mRNA, partial cds |
| 4935 | 9912 | 14890 | 0.99 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 2664 | 7642 | | 0.93 | 8.1E-01 | AF191839.1 | NT | Mus musculus TANK binding kinase TBK1 (TBK1) mRNA, complete cds |
| 3376 | 8384 | 13404 | 2.84 | 8.1E-01 | AF055086.1 | NT | Homo sapiens MHC class 1 region |
| 3376 | 8384 | 13405 | 2.84 | 8.1E-01 | AF055066.1 | NT | Homo sapiens MHC class 1 region |
| 176 | 5240 | | 2.17 | 8.0E-01 | AJ271510.1 | NT | Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15 |
| 286 | 5344 | 10356 | 8.83 | 8.0E-01 | AJ132772.1 | NT | Bos taurus fib and rtf genes |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--------------------|
| 1984 | 6969 | | | 1.42 | 8.0E-01 | BF530982.1 | EST HUMAN |
| 3003 | 8021 | 13034 | | 1.22 | 8.0E-01 | AF127897.1 | NT |
| 3239 | 8252 | 13273 | | 1.18 | 8.0E-01 | AB006193.1 | NT |
| 3621 | 8628 | | | 1.19 | 8.0E-01 | AL162758.2 | NT |
| 4402 | 9393 | 14377 | | 7.03 | 8.0E-01 | X83739.2 | NT |
| 4822 | 9806 | 14788 | | 1.12 | 8.0E-01 | 7657352 | NT |
| 451 | 5488 | 10503 | | 1.35 | 7.9E-01 | D11476.1 | NT |
| 705 | 5729 | | | 0.79 | 7.9E-01 | AE002130.1 | NT |
| 1568 | 6365 | | | 14.05 | 7.9E-01 | AB040885.1 | NT |
| 2201 | 7179 | 12302 | | 8.75 | 7.9E-01 | AB004816.1 | NT |
| 2202 | 7180 | 12303 | | 1.53 | 7.9E-01 | AF130459.1 | NT |
| 3438 | 8446 | 13472 | | 2.93 | 7.9E-01 | AF228664.1 | NT |
| 4176 | 9170 | | | 0.79 | 7.9E-01 | BE263612.1 | EST HUMAN |
| 4479 | 9469 | 14449 | | 1.35 | 7.9E-01 | 6753746 | NT |
| 4479 | 9469 | 14450 | | 1.35 | 7.9E-01 | 6753745 | NT |
| 865 | 5883 | | | 2.29 | 7.8E-01 | Z43785.1 | EST HUMAN |
| 2213 | 7190 | 12311 | | 2.82 | 7.8E-01 | AW959567.1 | EST HUMAN |
| 4563 | 9551 | 14537 | | 0.79 | 7.8E-01 | U87305.1 | NT |
| 4871 | 9830 | | | 1.51 | 7.8E-01 | AW753353.1 | EST HUMAN |
| 143 | 5209 | 10223 | | 4.43 | 7.7E-01 | AF184345.1 | NT |
| 716 | 5739 | | | 1.61 | 7.7E-01 | AF050157.1 | NT |
| 2640 | 7600 | 12714 | | 1.56 | 7.7E-01 | O33915 | SWISSPROT |
| 3520 | 8527 | 13338 | | 3.71 | 7.7E-01 | AF118085.1 | NT |
| 4272 | 9265 | 14255 | | 3.89 | 7.7E-01 | AF199488.1 | NT |
| 4272 | 9265 | 14256 | | 3.89 | 7.7E-01 | AF199488.1 | NT |
| 509 | 5544 | | | 1.38 | 7.5E-01 | AL163301.2 | NT |
| 579 | 5611 | 10610 | | 1 | 7.5E-01 | AF020503.1 | NT |
| 5070 | 10039 | 15006 | | 0.95 | 7.5E-01 | 6981387 | NT |
| 1113 | 6119 | 11147 | | 1.25 | 7.4E-01 | A1598146.1 | EST HUMAN |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2281 | 7257 | 12375 | 0.97 | 7.4E-01 | AB011106.1 | NT | Homo sapiens mRNA for KIAA0534 protein, partial cds |
| 3643 | 8649 | 13655 | 0.87 | 7.4E-01 | AF112538.1 | NT | Malva pusilla actin (Act1) mRNA, complete cds |
| 4114 | 9177 | 14161 | 8.61 | 7.4E-01 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 5013 | 9984 | 14960 | 1.07 | 7.4E-01 | AW270642.1 | EST_HUMAN | xp83d04.x1 NCI CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2746951 3' similar to contains element MER35 MER35 repetitive element; |
| 4483 | 9473 | 14453 | 0.84 | 7.3E-01 | AE001166.1 | NT | Borrelia burgdorferi (section 52 of 70) of the complete genome |
| 4552 | 9550 | 14536 | 4.94 | 7.3E-01 | AF225421.1 | NT | Homo sapiens HT017 mRNA, complete cds |
| 5046 | 10017 | 14986 | 0.92 | 7.3E-01 | AI400861.1 | NT | Cicer arietinum partial mRNA for putative UDP-glycoside |
| 821 | 5841 | | 2.09 | 7.2E-01 | I29281.1 | NT | Rattus norvegicus Initiation factor-2 kinase (elf-2a) mRNA, complete cds |
| 1917 | 6903 | 11987 | 3.43 | 7.2E-01 | X79140.1 | NT | N labacum Naf1F-4A13 mRNA |
| 2392 | 7363 | 12485 | 1.25 | 7.2E-01 | AB009605.1 | NT | Gallus gallus gene for melanocortin 2-receptor, complete cds |
| 2933 | 8011 | 13023 | 1.4 | 7.2E-01 | AF198100.1 | NT | Fowlpox virus, complete genome |
| 3370 | 8378 | 13398 | 2.78 | 7.2E-01 | AF065606.1 | NT | Glardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds |
| 3553 | 8539 | 13545 | 0.98 | 7.2E-01 | AB002307.1 | NT | Human mRNA for KIAA0309 gene, partial cds |
| 3780 | 8783 | 13787 | 2.44 | 7.2E-01 | BF338356.1 | EST_HUMAN | 602035589f1 NCI CGAP_Bin64 Homo sapiens cDNA clone IMAGE:4183222 5' |
| 4624 | 9609 | 14597 | 3.41 | 7.2E-01 | D90314.1 | NT | L-mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7) |
| 4919 | 8926 | 14904 | 1.37 | 7.2E-01 | AF196779.1 | NT | Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α 2 |
| 4949 | 9926 | 14905 | 1.37 | 7.2E-01 | AF196779.1 | NT | Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α 2 |
| 4975 | 9951 | 14929 | 0.78 | 7.2E-01 | P33066 | SWISSPROT | NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I) |
| 683 | 5707 | 10719 | 9.06 | 7.1E-01 | D21070.1 | NT | Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds |
| 2989 | 8007 | 13020 | 14.39 | 7.1E-01 | AJ270777.1 | NT | Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16 |
| 4086 | 9080 | 14070 | 3.49 | 7.1E-01 | 7305360 | NT | Mus musculus otogelin (Otg), mRNA |
| 4086 | 9080 | 14071 | 3.49 | 7.1E-01 | 7305360 | NT | Mus musculus otogelin (Otg), mRNA |
| 1209 | 6209 | 11248 | 2.58 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0614 protein, partial cds |
| 1209 | 6209 | 11249 | 2.58 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0614 protein, partial cds |
| 2381 | 7353 | 12474 | 1.03 | 7.0E-01 | N62412.1 | EST_HUMAN | yZ73e07_s1 Soares_multiple_sclerosis_2NbHMSp Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alt repetitive element, |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|---|
| 2381 | 7353 | 12475 | 1.03 | 7.0E-01 | NC_062412.1 | EST_HUMAN | y73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708_3' similar to contains Alu repetitive element; |
| 4889 | 9868 | | 1.81 | 7.0E-01 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 955 | 5971 | 11004 | 15.93 | 6.9E-01 | UJ69674.1 | NT | Candida albicans: squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 955 | 5971 | 11005 | 15.93 | 6.9E-01 | U69674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 1291 | 6290 | 11334 | 1.72 | 6.9E-01 | AA583530.1 | EST_HUMAN | mn28e09.s1 NC_ CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176_3' |
| 3148 | 8164 | 13184 | 1.56 | 6.9E-01 | AE002271.2 | NT | Chlamydia muricatum, section 3 of 85 of the complete genome |
| 942 | 5959 | 10992 | 2.14 | 6.8E-01 | AF017784.1 | NT | Giardia intestinalis carbamate kinase gene, complete cds |
| 2603 | 7565 | | 1.2 | 6.8E-01 | DR00917.1 | NT | Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470 |
| 4439 | 9429 | 14413 | 1.39 | 6.8E-01 | JQ0762.1 | NT | Rat(hooded) prolactin gene: exon III and flanks |
| 236 | 5353 | 10366 | 24.4 | 6.7E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 337 | 5389 | 10396 | 21.87 | 6.7E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 2086 | 7067 | 12179 | 1.15 | 6.7E-01 | AA451864.1 | EST_HUMAN | zx12g12.s1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:786310_3' similar to contains element TAR1 repetitive element; |
| 2102 | 7763 | 12198 | 2.56 | 6.7E-01 | AF186073.1 | NT | Drosophila melanogaster Ms185C gene, complete cds; NMDMC Isoform (Nmmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced |
| 2927 | 7946 | 12963 | 4 | 6.7E-01 | 6678560 | NT | Mus musculus Wiskott-Aldrich syndrome protein (Wasp) mRNA |
| 4331 | 9322 | 14308 | 0.7 | 6.7E-01 | XJ74421.1 | NT | S. tuberosum mRNA for glucose-6-phosphate dehydrogenase |
| 2628 | 7588 | 12700 | 1.28 | 6.6E-01 | AF199339.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 3409 | 8418 | 13446 | 0.93 | 6.6E-01 | 4506680 | NT | Homo sapiens sema domain, seven thrombospondin repeats (type I and type II-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA |
| 3574 | 8581 | 13567 | 3.48 | 6.6E-01 | Y07669.1 | NT | C. albicans random DNA marker, 282bp |
| 3993 | 8990 | | | | | | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoR γ t gene, and sodium phosphate transporter (NP13) gene, complete cds |
| 618 | 5645 | 10647 | | | | | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 618 | 5645 | 10648 | | | | | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 3348 | 8357 | 13375 | | | | | Mus musculus gene for Tab2, complete cds |
| 4159 | 9154 | 14137 | | | | | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--------------------|
| 4894 9873 | 14840 | 2.32 | 6.5E-01 | U28921.1 | NT | Phascolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds | |
| 5073 10042 | 15008 | 1.39 | 6.5E-01 | 8924057 | NT | Homo sapiens hypothetical protein PRO1580 (PRO1580), mRNA | |
| 250 5310 | 10321 | 8.85 | 6.4E-01 | U48848.1 | NT | Drosophila melanogaster 8kd dynein light chain mRNA, complete cds | |
| 2611 7479 | 12594 | 0.9 | 6.4E-01 | AF161184.1 | NT | Pseudomonas fluorescens trypophan halogenase (prmA) gene, complete cds | |
| 3374 8382 | 13402 | 3.74 | 6.4E-01 | U48854.2 | NT | Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds | |
| 3771 8774 | 13778 | 1.19 | 6.4E-01 | AB046827.1 | NT | Homo sapiens mRNA for KIAA1607 protein, partial cds | |
| 4364 9355 | 14334 | 0.74 | 6.4E-01 | Y12488.1 | NT | M.musculus Wn gene | |
| 4364 9355 | 14335 | 0.74 | 6.4E-01 | Y12488.1 | NT | M.musculus Wn gene | |
| 431 5469 | 10488 | 3.16 | 6.3E-01 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFIHRP-III) | |
| 531 5566 | 10569 | 1.73 | 6.3E-01 | U32689.1 | NT | Haemophilus influenzae Rd section 4 of 163 of the complete genome | |
| 2098 7079 | 12193 | 25.01 | 6.3E-01 | U81136.1 | NT | Shigella flexneri multi-antibiotic resistance locus | |
| 2603 7471 | 12587 | 1.82 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds | |
| 2603 7471 | 12588 | 1.82 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds | |
| 2649 7968 | | 0.67 | 6.3E-01 | Y17275.1 | NT | Lycopersicon esculentum p69a gene, complete CDS | |
| 2330 7304 | | 3.53 | 6.1E-01 | 6678076 | NT | Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA | |
| 4405 8396 | 14379 | 0.98 | 6.1E-01 | 45575338 | NT | Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA | |
| 491 5527 | 10535 | 1.08 | 6.0E-01 | D87675.1 | NT | Xenopus DNA for amyloid precursor protein, complete cds | |
| 557 5591 | | 2.78 | 6.0E-01 | 5802999 | NT | Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA | |
| 1345 6342 | 11393 | 1.38 | 6.0E-01 | AF065233.1 | NT | Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds | |
| 3725 8729 | 13727 | 0.81 | 6.0E-01 | AJ233396.1 | NT | Viral hemorrhagic septicemia virus N, P, M, G, N, L genes, French strain 07-71 | |
| 3623 8923 | 13914 | 2.18 | 8.0E-01 | X16842.1 | NT | Xenopus mRNA for desmin | |
| 4064 9058 | | 1.03 | 8.0E-01 | AF058885.1 | NT | Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28 | |
| 985 6000 | 11031 | 1.03 | 5.9E-01 | U32701.1 | NT | Haemophilus influenzae Rd section 16 of 163 of the complete genome | |
| 3196 8212 | 13233 | 9.18 | 5.9E-01 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 | |
| 3196 8212 | 13234 | 9.18 | 5.9E-01 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 | |
| 4100 9094 | | 3 | 5.9E-01 | AF1622756.1 | NT | Rattus norvegicus cavinin 2 mRNA, partial cds | |
| 1666 6885 | 11943 | 1.05 | 5.8E-01 | P40472 | SWISSPROT | SIM1 PROTEIN | |
| 3876 8877 | 13880 | 0.97 | 5.8E-01 | B16957538.1 | EST_HUMAN | 601852474F1 NIH MGIC_56 Homo sapiens cDNA clone IMAGE:4076131'5' | |
| 4383 9374 | 14353 | 4.1 | 5.8E-01 | AB009077.1 | NT | Vigna radiata mRNA for proton pyrophosphatase, complete cds | |
| 4652 9637 | | 1.31 | 5.8E-01 | AF110846.1 | NT | Megapedia sexifaria sex-lethal homolog (Megsl) gene, partial cds, alternatively spliced products | |
| 4775 9759 | | 2.29 | 5.8E-01 | AW769483.1 | EST_HUMAN | h64f10.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:30065995 3' | |
| 1463 6460 | 11518 | 1.04 | 5.7E-01 | P06727 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) | |
| 1463 6460 | 11519 | 1.04 | 5.7E-01 | P06727 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit No. | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|---------------|-----------------------|-------------------------|--|
| 3152 | 8168 | 13188 | 1.38 | 5.7E-01 | Q9WTJ2 | | SWISSPROT | PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A) |
| 3425 | 8433 | | - | 2.37 | 5.7E-01 | AB033503.1 | NT | Populus euramericana peacs-2 mRNA for 1-amino cyclopropane-1-carboxylate synthase, complete cds |
| 5042 | 10013 | 14982 | .0.95 | 5.7E-01 | I41867.1 | NT | | Drosophila extra sex comb gene, exon 1-4, complete cds |
| 3283 | 8295 | 13320 | 1.11 | 5.6E-01 | AB018283.2 | NT | | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3283 | 8285 | 13321 | 1.11 | 5.6E-01 | AB018283.2 | NT | | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 4117 | 9111 | 14095 | 2.28 | 5.6E-01 | D83135.1 | NT | | Chicken TBP gene, exon 8, complete cds |
| 1192 | 6193 | 11230 | 1.79 | 5.5E-01 | 8393912 | NT | | Rattus norvegicus Propion Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA |
| 2629 | 7589 | 12701 | 2.21 | 5.5E-01 | P03341 | | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2629 | 7589 | 12702 | 2.21 | 5.5E-01 | P03341 | | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2848 | 7968 | 12884 | 0.79 | 5.5E-01 | 5902085 | NT | | Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA |
| 2992 | 8010 | | 1.33 | 5.5E-01 | H46219.1 | EST_HUMAN | | y018a10_s1 Soares adult brain N2b5-HB55Y Homo sapiens cDNA clone IMAGE:178266_3 |
| 3163 | 8179 | 13201 | 3.6 | 5.5E-01 | AF227240.1 | NT | | Rabbit oral papillomavirus, complete genome |
| 3608 | 8615 | 13624 | 1.37 | 5.5E-01 | P48755 | | SWISSPROT | FOS-RELATED ANTIGEN-1 |
| 4982 | 9857 | 14935 | 0.99 | 5.5E-01 | U69097.1 | NT | | Bos taurus MHC class II beta-chain Bcl-A-DIB1 gene, partial cds |
| 144 | 5210 | 10224 | 13.58 | 5.4E-01 | 7657266 | NT | | Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 144 | 5210 | 10225 | 13.58 | 5.4E-01 | 7657266 | NT | | Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 580 | 5612 | 10611 | 1.77 | 5.4E-01 | AF232006.1 | NT | | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes |
| 580 | 5612 | 10612 | 1.77 | 5.4E-01 | AF232006.1 | NT | | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes |
| 1252 | 6250 | 11291 | 2.4 | 5.4E-01 | AW896087.1 | EST_HUMAN | | QV4-NN0040-07040-0160-04 NN0040 Homo sapiens cDNA |
| 2048 | 7030 | | 2.35 | 5.4E-01 | AE002247.2 | NT | | Chlamydomonas AR39, section 74 of 94 of the complete genome |
| 2193 | 7172 | 12293 | 1.53 | 5.4E-01 | AJ276882.1 | NT | | Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene) |
| 512 | 5547 | 10552 | 1.61 | 5.3E-01 | AF019413.1 | NT | | Homo sapiens IHLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, > |
| 2710 | 7667 | 12779 | 10.07 | 5.3E-01 | 4506328 | NT | | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 2710 | 7667 | 12780 | 10.07 | 5.3E-01 | 4506328 | NT | | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 3169 | 8185 | 13206 | 3.67 | 5.3E-01 | AF087658.1 | NT | | Homo sapiens :secreted C-type lectin precursor (SLC1) gene, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|---|---|
| 4090 8084 | 806 | 5827 | 1.22 | 5.3E-01 U39887.1 | NT | | Mycoplasma genitalium section 9 of 51 of the complete genome |
| 1146 6150 | 11182 | 11182 | 11.32 | 5.2E-01 Q9WV30 | NT | SWISSPROT | NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NFAT5) |
| 1171 6174 | 11208 | 11208 | 6.03 | 5.2E-01 AF224492.1 | NT | | (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5) |
| 1847 6836 | | | 4.17 | 5.2E-01 AL163285.2 | NT | Homo sapiens phospholipid scramblase 1 gene, complete cds | Homo sapiens chromosome 21 segment HS21C085 |
| 2085 7066 | 12178 | | 1.52 | 5.2E-01 AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds | |
| 3046 8063 | 13071 | | 1.72 | 5.2E-01 U65942.1 | NT | Chlamydophila abortus strain S26/3 POMP90A precursor, genes, complete cds | |
| 3321 8331 | | | 11.56 | 5.2E-01 AL116780.1 | NT | Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation | |
| 3360 8368 | 13387 | | 2.52 | 5.2E-01 AA984165.1 | EST_HUMAN | | am77g05.s1 St-atagene schizo brain S1 Homo sapiens cDNA clone IMAGE:1616504 3' |
| 3547 8554 | | | 0.79 | 5.2E-01 AF020269.1 | NT | | Medicago sativa chloroplast malate dehydrogenase precursor (p11mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds |
| 4358 9349 | | | 1.46 | 5.2E-01 AF093796.1 | NT | | Avian infectious bronchitis virus isolate variant 2 S1 spike glycoprotein gene, partial cds |
| 4960 9937 | | | 1.01 | 5.2E-01 AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 | |
| 613 5640 | 10643 | | 1.9 | 5.1E-01 M58509.1 | NT | | Human adenoxitin reductase gene, exons 3 to 12 |
| 640 5668 | 10671 | | 3.68 | 5.1E-01 AJ233944.1 | NT | Polyangium vitellinum (strain PI v1) 16S rRNA gene | |
| 640 5668 | 10672 | | 3.68 | 5.1E-01 AJ233944.1 | NT | Polyangium vitellinum (strain PI v1) 16S rRNA gene | |
| 3963 8961 | 13951 | | 4.37 | 5.1E-01 AI858485.1 | EST_HUMAN | w39612.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2427263 3' | |
| 4062 9056 | 14043 | | 2.47 | 5.1E-01 P96380 | SWISSPROT | TRANSCRIPTION REPAIR COUPLING FACTOR (TRCF) | |
| 2076 7058 | 12167 | | 1.03 | 5.0E-01 | 4885552 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2076 7058 | 12168 | | 1.03 | 5.0E-01 | 4885552 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2083 7064 | 12174 | | 1.08 | 5.0E-01 AF008210.1 | NT | | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnabA), ATP operon (atpCDGAHFEFB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 2083 7064 | | | | | | | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnabA), ATP operon (atpCDGAHFEFB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 3740 8744 | 13744 | | 1.11 | 5.0E-01 L38483.1 | NT | | Rattus norvegicus jagged protein mRNA, complete cds |
| 3782 8785 | 13788 | | 2.97 | 5.0E-01 AB033010.1 | NT | | Homo sapiens mRNA for KIAA1184 protein, partial cds |
| 781 5802 | 10832 | | 2.67 | 4.9E-01 BF5/1462.1 | EST_HUMAN | | 602076649F1 NIH MGIC_62 Homo sapiens cDNA clone IMAGE:4243860 5' |
| 1619 6616 | 11682 | | 4.93 | 4.9E-01 AJ243955.1 | NT | Xenopus laevis mRNA for c-Jun protein, 1978 BP | |
| 1864 6853 | 11941 | | 1.9 | 4.9E-01 U40868.1 | NT | Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds | |
| 3460 8468 | | | 1.14 | 4.8E-01 AA912842.1 | EST_HUMAN | ol32a09.s1 Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3' | |
| 3658 8664 | 13689 | | 1.62 | 4.6E-01 BF693301.1 | EST_HUMAN | | 602081103F1 NIH MGIC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3658 | 8664 | 13670 | | 1.62 | 4.6E-01 | BF693300.1 | EST_HUMAN 602081103f1 NIH MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 2799 | 7819 | 12836 | | 4.48 | 4.5E-01 | AA677086.1 | EST_HUMAN 3f55d02_s1 Scares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3' |
| 3243 | 8256 | 13277 | | 4.25 | 4.5E-01 | Q05793 | SWISSPROT BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC) |
| 3293 | 8304 | 13329 | | 1.39 | 4.5E-01 | AF126378.1 | NT Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12 |
| 3917 | 8917 | | | 1.06 | 4.5E-01 | Q28247 | SWISSPROT COLLAGEN ALPHA 5(V) CHAIN |
| 4052 | 10058 | | | 5.38 | 4.5E-01 | AW873495.1 | EST_HUMAN hg60g02_x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:38666023 3' |
| 4786 | 9770 | 14754 | | 1.55 | 4.5E-01 | BE963445.2 | EST_HUMAN 601657225R1 NIH MGC_67 Homo sapiens cDNA clone IMAGE:11map1, mRNA |
| 111 | 1985 | 6970 | | 2.19 | 4.4E-01 | 6680503 | NT Mus musculus integral membrane-associated protein 1 (lmap1), mRNA |
| | 2325 | 7299 | | 4.73 | 4.4E-01 | P49765 | SWISSPROT VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR) |
| | 3241 | 8254 | | 1.19 | 4.4E-01 | AF058790.1 | NT Reitius norvegicus SynGAP-b mRNA, complete cds |
| | 3241 | 8254 | | 1.19 | 4.4E-01 | AF058790.1 | NT Reitius norvegicus SynGAP-b mRNA, complete cds |
| | 3245 | 8258 | | 1.81 | 4.4E-01 | BT056728.1 | EST_HUMAN 7f91d02_y1 NCI CGAP_Bt16 Homo sapiens cDNA clone IMAGE:3398795 5' |
| | 4113 | 9107 | | 1.55 | 4.4E-01 | BE3718707.1 | EST_HUMAN 601237139f1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5' |
| | 4938 | 9915 | | 8.65 | 4.4E-01 | U61154.1 | NT Buzura suppressaria nucleopophedrostis/fus ecdisysteroid UDP-glucosyltransferase (egt) gene, complete cds |
| | 4048 | 5445 | | 1.95 | 4.3E-01 | AF165218.1 | NT Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| | 4048 | 5445 | | 1.95 | 4.3E-01 | AF165218.1 | NT Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| | 2801 | 7821 | | 1.34 | 4.3E-01 | AW935269.1 | EST_HUMAN CM2-DT0003-01/0200-077-c01 D10003 Homo sapiens cDNA MRO-BN0070/27/0300-008-g04 BN0070 Homo sapiens cDNA |
| | 2986 | 8004 | | 0.72 | 4.3E-01 | AW999477.1 | EST_HUMAN MRO-BN0070/27/0300-008-g04 BN0070 Homo sapiens cDNA |
| | 4028 | 9024 | | 1.2 | 4.3E-01 | J00306.1 | Human somatosatin I gene and flanks |
| | 4282 | 5445 | | 1.07 | 4.3E-01 | AF155218.1 | NT Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| | 4282 | 5445 | | 1.07 | 4.3E-01 | AF155218.1 | NT Callithrix jacchus MW/LW opsin gene, upstream flanking region |
| | 4944 | 9921 | | 1.08 | 4.3E-01 | Q635250 | NT Xestia c-nigrum granulomus, complete genome |
| | 1341 | 7745 | | 1.24 | 4.2E-01 | Q39102 | SWISSPROT CELL DIVISION PROTEIN FISH-HOMOLOG PRECURSOR |
| | 3528 | 8534 | | 3.83 | 4.2E-01 | AE003947.1 | NT Xylophagidae fastidiosa, section 93 of 229 of the complete genome |
| | 3552 | 8559 | | 2.9 | 4.2E-01 | AI280338.1 | EST_HUMAN qf94b01_x1 Scares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876945 3' |
| | 3629 | 10057 | | 0.86 | 4.2E-01 | NB12203.1 | EST_HUMAN 788IE1 fetal brain cDNA Homo sapiens cDNA clone IMAGE:788IE1-K similar to R07819, Z40498 |
| | 4558 | 9546 | | 5.45 | 4.2E-01 | AA534093.1 | EST_HUMAN nigroho1_s1 INGI CGAP_P710 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600_HLA CLASS II HISTOCOMATIBILITY ANTIGEN DR-1 BETA CHAIN (HUMAN) |
| | 4636 | 9621 | | 3.8 | 4.2E-01 | R13467.1 | EST_HUMAN yf77e01_11 Scares Infant brain 1NIB Homo sapiens cDNA |
| | 1077 | 6084 | | 1.52 | 4.1E-01 | AI905481.1 | EST_HUMAN RC-BT091-210_189-142 BT091 Homo sapiens cDNA |
| | 1086 | 6093 | | 2.09 | 4.1E-01 | AV705243 | ADB Homo sapiens cDNA clone ADBAHF08 5' |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--|
| 1086 | 6093 | 11123 | 2.09 | 4.1E-01 | AV705243 | EST_HUMAN | ADBAHF08 5' |
| 1573 | 6570 | 11632 | 0.94 | 4.1E-01 | AI905949.1 | EST_HUMAN | PM-BT103-270499-684 BT103 Homo sapiens cDNA |
| 2638 | 7598 | 12712 | 1.1 | 4.1E-01 | 7705283 | NT | Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA |
| 2869 | 7888 | 12908 | 2.49 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 2869 | 7888 | 12909 | 2.49 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 3229 | 8244 | 13266 | 0.7 | 4.1E-01 | AA906344.1 | EST_HUMAN | 094d08_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3' |
| 4152 | 9147 | 14131 | 2.75 | 4.1E-01 | AJ249207.1 | NT | Rhodococcus sp. A45 isoG, IsoH, IsoI, IsoJ, IsoA, IsoB, isoC, isoD, IsoE and IsoF genes |
| 4178 | 9172 | | 0.74 | 4.1E-01 | AA909257.1 | EST_HUMAN | dm33d02_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3' |
| 4532 | 9522 | 14509 | 1.37 | 4.1E-01 | AV747880 | NC_Pt Homo sapiens cDNA clone NPCBDI10 5' | |
| 1022 | 6031 | 11061 | 0.81 | 4.0E-01 | 8404656 | NT | Laqueus rubellus mitochondrion, complete genome |
| 1319 | 6317 | 11365 | 1.16 | 4.0E-01 | AF203478.1 | NT | Drosophila melanogaster Dalmatian (dm1) mRNA, complete cds |
| 1454 | 6451 | | 3.09 | 4.0E-01 | 6679258 | NT | Mus musculus platelet-derived growth factor receptor, beta polypeptide (Pdgfb), mRNA |
| 2733 | 5207 | 10222 | 2.12 | 4.0E-01 | 6678490 | NT | Mus musculus ubiquitin-protein ligase E3 component n-recognin (Ubr1), mRNA |
| 2898 | 7917 | 12937 | 1.16 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2898 | 7917 | 12938 | 1.16 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| | | | | | | | Streptococcus pneumoniae YIC (yIC), YID (yID), penicillin-binding protein 2x (ppb2x), and undecaprenyl-phosphate-UDP-N-acetylpeptidyl-phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds |
| 3612 | 8619 | 13629 | 2.74 | 4.0E-01 | AF068903.1 | NT | Ovis aries partial ID2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 3737 | 8741 | 13740 | 3.44 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial ID2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 3737 | 8741 | 13741 | 3.44 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial ID2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 4672 | 9657 | | 8.6 | 4.0E-01 | Q31849 | SWISSPROT | NADH-PLASTOCIUNONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST |
| 1359 | 6356 | 11407 | 1.57 | 3.9E-01 | AF206618.1 | NT | Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds |
| 2571 | 12651 | | 2.87 | 3.9E-01 | AB033019.1 | NT | Homo sapiens mRNA for KIAA1193 protein, partial cds |
| 2633 | 7593 | 12705 | 2.98 | 3.9E-01 | XB2032.1 | NT | H. sapiens B-myb gene |
| 2633 | 7593 | 12706 | 2.98 | 3.9E-01 | XB2032.1 | NT | H. sapiens B-myb gene |
| 3023 | 8040 | 13049 | 4.17 | 3.9E-01 | AJ225896.1 | NT | Sinorhizobium meliloti egl, syrB2, cya3 genes and ori3 |
| 3964 | 8962 | 13952 | 1.39 | 3.9E-01 | BF592611.1 | EST_HUMAN | 7161d01 x1 NCL CGAP_B16 Homo sapiens cDNA clone IMAGE:3339169 3' |
| 159 | 5225 | | 27.46 | 3.8E-01 | 7019488 | NT | Homo sapiens protein kinase PKNbeta (pknbeta), mRNA |
| 502 | 5537 | | 3.87 | 3.8E-01 | AB039291.1 | NT | Mus musculus Pcb-1 mRNA for pericentriolar material-1, complete cds |
| 2496 | 7464 | 12579 | 3.42 | 3.8E-01 | AF214117.1 | NT | Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds |
| 2560 | 7775 | 12641 | 3.09 | 3.8E-01 | 6678002 | NT | Mus musculus solute carrier family 1, member 8 (Slc1a6), mRNA |
| 2933 | 7952 | | 0.82 | 3.8E-01 | AJ251057.1 | NT | Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213) |
| 2974 | 7992 | 13007 | 2.37 | 3.8E-01 | AF043383.1 | NT | Pleurocytes americanus aminopeptidase N (ampN) gene, partial cds |
| 3403 | 8412 | 13438 | 8.3 | 3.8E-01 | AL161518.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe Seq ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3461 | 8469 | | | 0.77 | AI807219.1 | EST_HUMAN | W38b12.x1_Searcs_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3671 | 8676 | 13679 | 0.93 | 3.8E-01 | BE154080.1 | EST_HUMAN | PM0-HT0339-201400-010-G01 HT0339_Homo sapiens cDNA |
| 2410 | 7381 | 12499 | 5.9 | 3.7E-01 | AB037831.1 | NT | Homo sapiens mRNA for KIAA1410 protein, partial cds |
| 3378 | 8386 | 13407 | 10.03 | 3.7E-01 | AF056336.1 | NT | Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds |
| 3779 | 8782 | 13786 | 1.12 | 3.7E-01 | AA319482.1 | EST_HUMAN | EST21715_Adrenal gland tumor Homo sapiens cDNA 5' end |
| 4108 | 9102 | 14089 | 7.57 | 3.7E-01 | AI218707.1 | EST_HUMAN | ok39c07.x1_Searcs_NSF_F8_9W_O_PA_P_S1_Homo sapiens cDNA clone IMAGE:1510188 3' |
| 4193 | 9186 | 14167 | 1.55 | 3.7E-01 | AW878037.1 | EST_HUMAN | MR3-OT0007-08300-104-b02 OT0007_Homo sapiens cDNA |
| 4265 | 9258 | 14248 | 3.38 | 3.7E-01 | AE002408.1 | NT | Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome |
| 980 | 5995 | | | 8.26 | U89241.1 | NT | Human mlnbp gene, partial cds |
| 1295 | 6293 | 11339 | 2.38 | 3.6E-01 | T80255.1 | EST_HUMAN | yd03e05.r1_Searcs_Infant brain 1NIB_Homo sapiens cDNA clone IMAGE:24443 5' |
| 1295 | 6293 | 11340 | 2.38 | 3.6E-01 | T80255.1 | EST_HUMAN | yd03e05.r1_Searcs_Infant brain 1NIB_Homo sapiens cDNA clone IMAGE:24443 5' |
| 1872 | 6861 | 11949 | 3.81 | 3.6E-01 | AW590184.1 | EST_HUMAN | hg33d02.x1_NCI_CGAP_GC6_Homo sapiens cDNA clone IMAGE:2947419 3' |
| 1872 | 6861 | 11950 | 3.81 | 3.6E-01 | AW590184.1 | EST_HUMAN | hg33d02.x1_NCI_CGAP_GC6_Homo sapiens cDNA clone IMAGE:2947419 3' |
| 1912 | 6898 | 11993 | 4.6 | 3.6E-01 | AF216207.1 | NT | Mus musculus ribosomal protein S19 (Rps19) gene, complete cds |
| 2208 | 7185 | | | 0.97 | 3.6E-01 | AB002322.1 | NT |
| 2326 | 7300 | | | 2.62 | 3.6E-01 | X76725.1 | P_in regulare (P3304) gene for actin |
| 2417 | 7388 | 12508 | 0.95 | 3.6E-01 | AW812033.1 | EST_HUMAN | RC5-ST0171-181089-011-q07 ST0171_Homo sapiens cDNA |
| 2558 | 7523 | 12639 | 1.1 | 3.6E-01 | P24206 | SWISSPROT | PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) |
| 2828 | 10055 | | | 7.88 | 3.6E-01 | AF189485.1 | NT |
| 3388 | 8396 | 13420 | 1.83 | 3.6E-01 | X76758.1 | NT | Drosophila melanogaster sugar transporter 3 (slf3) mRNA, complete cds |
| 3388 | 8396 | 13421 | 1.83 | 3.6E-01 | X76758.1 | NT | H_sapiens serotonin transporter gene, exons 9 and 10 |
| 4284 | 9276 | 14264 | 0.98 | 3.6E-01 | BE707883.1 | EST_HUMAN | H_sapiens serotonin transporter gene, exons 9 and 10 |
| 4610 | 9596 | 14582 | 1.49 | 3.6E-01 | Y11526.1 | NT | RC1-HT0545-150600-014-b12 HT0545_Homo sapiens cDNA |
| 4849 | 9831 | 14806 | 2.79 | 3.6E-01 | AW339393.1 | EST_HUMAN | Z_mays mRNA for casein kinase II alpha subunit |
| 5037 | 10008 | 14978 | 1.25 | 3.6E-01 | AE001187.1 | NT | ha02g04.x1_NCI_CGAP_Lu24_Homo sapiens cDNA clone IMAGE:2872566 3' |
| 1115 | 5187 | 10196 | 0.85 | 3.5E-01 | AL161536.2 | NT | Treponema pallidum section 3 of 87 of the complete genome |
| 209 | 5273 | 10285 | 2.22 | 3.5E-01 | 6678933 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36 |
| 7115 | 5738 | 10755 | 1.11 | 3.5E-01 | 7706136 | NT | Mus musculus mannose receptor C type 2 (Mrc2), mRNA |
| 7115 | 5738 | 10756 | 1.11 | 3.5E-01 | 7706136 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 771 | 5793 | 10821 | 2.75 | 3.5E-01 | BF129796.1 | EST_HUMAN | Homo sapiens cDNA clone IMAGE:4053951 3' |
| 1580 | 6577 | 11641 | 0.92 | 3.5E-01 | BF310888.1 | EST_HUMAN | 601811050R1 NIH_MGC_48_Homo sapiens cDNA clone IMAGE:4124244 5' |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|---|
| 1600 6596 | 11657 | 2 | 3.5E-01 | U35776.1 | NT | SWISSPROT | Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds |
| 2219 7196 | 12318 | 1.43 | 3.5E-01 | P06798 | NT | HOMEobox/PROTEIN HOXA4 (HOX-1.4) (MH-3) | HOMEobox |
| 2531 7774 | 12616 | 1.81 | 3.5E-01 | AA223252.1 | EST_HUMAN | z08e09_s1 Strategene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:6508723' | |
| 3717 8721 | | 1.97 | 3.5E-01 | AA642138.1 | EST_HUMAN | inf60d03_s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:11723573' | |
| 4140 9135 | 14118 | 2.06 | 3.5E-01 | AF071253.1 | NT | Danio rerio homeobox protein (hoxdb5b) gene, complete cds | |
| 4777 9761 | 14748 | 5.2 | 3.5E-01 | M183149.1 | NT | Rat leukocyte common antigen (LCA) gene, exons 1 through 5 | |
| 697 5721 | | 1.44 | 3.4E-01 | AJ242956.1 | NT | Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line | |
| 961 5976 | 11010 | 5.81 | 3.4E-01 | Y09798.2 | NT | Pseudomorpha fluorescens colR, colS genes, orf222 and partial insA gene | |
| 1306 6304 | 11351 | 1.76 | 3.4E-01 | Y06554.1 | NT | Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element) | |
| 2338 7312 | 12433 | 1.56 | 3.4E-01 | D90909.1 | NT | Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418 | |
| 2932 7951 | 12968 | 0.8 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 | |
| 2932 7951 | 12969 | 0.8 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 | |
| 3016 8092 | 13106 | 1.04 | 3.4E-01 | D90909.1 | NT | Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418 | |
| 3088 8104 | 13119 | 7.39 | 3.4E-01 | U83905.1 | NT | Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds | |
| 3268 8281 | 13303 | 1.07 | 3.4E-01 | AF034862.1 | NT | Homo sapiens pulmonary surfactant protein D, promoter region and exon 1 | |
| 3453 8461 | 13488 | 4.36 | 3.4E-01 | AF106835.1 | NT | Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnak), and putative DnaJ (dnaj) genes, complete cds | |
| 3701 8705 | | 2.49 | 3.4E-01 | BF449010.1 | EST_HUMAN | 7n94e01_x1 NCI_CGAP_Ovrl8 Homo sapiens cDNA clone IMAGE:35722323' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1; | |
| 3939 8937 | | 1.48 | 3.4E-01 | AA584196.1 | EST_HUMAN | no11b0_51 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:11003473' | |
| 4509 9499 | 14478 | 1.77 | 3.4E-01 | BE069912.1 | EST_HUMAN | MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA qj85c05_x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:18672083' similar to contains Alu repetitive element, | |
| 4794 9778 | | 4.55 | 3.4E-01 | AI240973.1 | EST_HUMAN | Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene | |
| 14 5094 | 10078 | 16.57 | 3.3E-01 | X07990.1 | NT | Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene | |
| 106 5094 | 10078 | 4.08 | 3.3E-01 | X07990.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45 | |
| 445 5482 | 10500 | 0.92 | 3.3E-01 | AL161545.2 | NT | Homo sapiens KIAA1100 protein (KIAA1100), mRNA | |
| 627 5655 | 10660 | 1.67 | 3.3E-01 | 7662485 | NT | PROLINE-RICH PROTEIN LAS17 | |
| 1181 6183 | 11221 | 4.2 | 3.3E-01 | Q12446 | SWISSPROT | 6021B4016_1 NIH MGCG_42 Homo sapiens cDNA clone IMAGE:43002613' | |
| 1288 6287 | 11331 | 3.14 | 3.3E-01 | BFE68830.1 | EST_HUMAN | Mus musculus disintegrin 5 (Dign5), mRNA | |
| 1569 6366 | 11628 | 1.18 | 3.3E-01 | 6753685 | NT | | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1700 6695 | | | | 2.03 | AA332734.1 | EST_HUMAN | EST36722 Embryo, 8 week Homo sapiens cDNA 5' end |
| 1978 6953 | | | | 1.4 | 3.3E-01 AF031148.1 | NT | Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds |
| 2340 7314 | | | | 2.72 | 3.3E-01 | 4507834 NT | Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA |
| 2879 7898 | 12921 | | 1.79 | 3.3E-01 | AJ251805.1 | NT | Bacteriophage phi-YeO3-12 complete genome |
| 2947 7966 | | | 0.67 | 3.3E-01 | O02743 | SWISSPROT | INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 kDa) SUBUNIT (CLMF P35) |
| 2981 7999 | 13012 | | 1.05 | 3.3E-01 | AJ007932.2 | NT | Streptomyces argilaceus mithramycin biosynthetic genes |
| 3415 8424 | 13452 | | 1.05 | 3.3E-01 | AB012922.1 | NT | Homo sapiens MTA1-L1 gene, complete cds |
| 3720 8724 | 13724 | | 1.91 | 3.3E-01 | O84645 | SWISSPROT | EXODEOXYRIBONUCLEASE V BETA CHAIN |
| 3727 8731 | 13729 | | 1.01 | 3.3E-01 | P22802 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3] |
| 3858 8860 | 13866 | | 1.38 | 3.3E-01 | AL161498.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 3895 8895 | 13893 | | 1.71 | 3.3E-01 | AF200446.1 | NT | Hypoxylon fragiforme chitin synthase gene, partial cds |
| 4166 9161 | | | 2.36 | 3.3E-01 | 4759025 NT | NT | Homo sapiens RAS protein activator like 1 (GAP1 like) (RASA1) mRNA |
| 4242 9236 | | | 1.68 | 3.3E-01 | D31662.1 | NT | Rattus norvegicus DNA for regucalcin, partial cds |
| 4551 9539 | | | 1.7 | 3.3E-01 | AI539114.1 | EST_HUMAN | tp78512.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN); |
| 4690 9675 | 14658 | | 1.36 | 3.3E-01 | D64003.1 | NT | Synechocystis sp. PCC6803 complete genome, 2/27, 2755703-2868766 |
| 5071 10040 | 15007 | | 0.98 | 3.3E-01 | AI021992.1 | EST_HUMAN | ox04g09.x1 Scarce_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655392 3' similar to contains element MER4 repetitive element; |
| 454 5491 | | | 1.61 | 3.2E-01 | AF018281.1 | NT | Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds |
| 708 5732 | | | 0.78 | 3.2E-01 | AL161561.2 | NT | Arabidopsis thaliana DNA chromosome 4, config fragment No. 61 |
| 1144 6148 | 11180 | | 10.13 | 3.2E-01 | AF047013.1 | NT | Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds |
| 1263 6261 | 11304 | | 2.24 | 3.2E-01 | Z50202.1 | NT | P.vulgaris arc5-1 gene |
| 1367 6364 | 11413 | | 5.08 | 3.2E-01 | Q48624 | SWISSPROT | LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN) |
| 1737 6732 | 111809 | | 1.1 | 3.2E-01 | Z56041.1 | NT | S.cerevisiae chromosome II reading frame ORF YBR172c |
| 1746 6741 | 11820 | | 4.36 | 3.2E-01 | AW957794.1 | EST_HUMAN | EST369264 IMAGE sequences, MAGD Homo sapiens cDNA |
| 1746 6741 | 11821 | | 4.36 | 3.2E-01 | AW957794.1 | EST_HUMAN | EST369264 IMAGE sequences, MAGD Homo sapiens cDNA |
| 2096 7077 | 12191 | | 1.78 | 3.2E-01 | BF203817.1 | EST_HUMAN | 601868804 F1 NIH MG_C_17 Homo sapiens cDNA clone IMAGE:4111512 5' |
| 2470 7438 | | | 2.59 | 3.2E-01 | 7710079 NT | NT | Mus musculus Pbx/knotted 1 homeobox (Pbxknot1), mRNA |
| 2637 7597 | 12711 | | 1.11 | 3.2E-01 | AF060568.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 3045 8062 | 13070 | | 1.07 | 3.2E-01 | BF380745.1 | EST_HUMAN | IL2-UT0073-180900-161-H11 UT0073 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| | | | | | | | Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds |
| 4270 | 9263 | 14253 | 1.73 | 3.2E-01 | M18818.1 | NT | |
| 4369 | 9362 | 14342 | 1.43 | 3.2E-01 | Q10268 | SWISSPROT | HYPOTHETICAL_81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR |
| 4597 | 9585 | | | 7.8 | 3.2E-01 | BF693617.1 | EST_HUMAN |
| 5054 | 10025 | 14994 | 1.02 | 3.2E-01 | AL161514.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26 |
| 2680 | 7562 | 12680 | 2.32 | 3.1E-01 | R18051.1 | EST_HUMAN | ye00h06.1r Soares fetal liver spleen cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN); |
| 2625 | 7709 | 12696 | 2.72 | 3.1E-01 | 7661971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2785 | 7806 | 12697 | 2.72 | 3.1E-01 | 7661971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 3100 | 8116 | | | 1.27 | AW629036.1 | EST_HUMAN | hi46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3' |
| 3811 | 8814 | 13820 | 3.43 | 3.1E-01 | AB029066.1 | NT | Mus musculus gene for Ser/Thr kinase KI1AMRE, exon 6 |
| 4866 | 9790 | 14772 | 0.89 | 3.1E-01 | AJ251586.1 | NT | Daucus carota mRNA for transcription factor E2F (E2F gene) |
| 71 | 7689 | 10158 | 5.68 | 3.1E-01 | AE003984.1 | NT | Xylella fastidiosa, section 130 of 229 of the complete genome |
| 252 | 5312 | 10323 | 1.59 | 3.0E-01 | 67550083 | NT | Mus musculus protein kinase C, epsilon (Pkce), mRNA |
| 1204 | 6205 | 11242 | 9.02 | 3.0E-01 | AJ271755.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 1478 | 6475 | 11532 | 1.55 | 3.0E-01 | AW30040.1 | EST_HUMAN | xs63108.x1 NCI_CGAP Kid11 Homo sapiens cDNA clone IMAGE:2774343 3' |
| 1760 | 6752 | 11837 | 3.47 | 3.0E-01 | AJ006755.1 | NT | Balanoptera physalus gene encoding atrial natriuretic peptide |
| 3139 | 8155 | | | 3.0E-01 | X99082.1 | NT | A.immersus putative gene encoding Integrase, Mars2 (RP) |
| 3774 | 8777 | 13781 | 4.06 | 3.0E-01 | AB030481.1 | NT | Corynebacterium sp. ALV-1 alpPG gene for polygluturonate lyase, complete cds |
| 3867 | 8868 | 13871 | 1.61 | 3.0E-01 | AW817785.1 | EST_HUMAN | PM1-ST0262-261189-001-S01 ST0262 Homo sapiens cDNA |
| 4382 | 9373 | 14352 | 0.98 | 3.0E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 4589 | 9577 | | | 3.0E-01 | AJ006755.1 | NT | Balaenoptera physalus gene encoding atrial natriuretic peptide |
| 1973 | 6958 | 12063 | 0.99 | 3.0E-01 | AF157835.1 | NT | Bacteriophage APSE-1, complete genome |
| 3110 | 8126 | 13146 | 1.16 | 2.9E-01 | AE000736.1 | NT | Aquifex aeolicus section 68 of 109 of the complete genome |
| 3178 | 8194 | 13216 | 1.04 | 2.9E-01 | AF078111.1 | NT | Xenopus laevis Transcription factor E2F mRNA, complete cds |
| 3178 | 8194 | 13217 | 2.82 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0326-171299-001-H12 CT0326 Homo sapiens cDNA |
| 3178 | | | 2.82 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0326-171299-001-H12 CT0326 Homo sapiens cDNA |
| 3801 | 8804 | 13809 | 0.7 | 2.9E-01 | AI610836.1 | EST_HUMAN | tp21a11.x1 NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to qb:D15050 NII-2-A |
| 3959 | 8957 | 13946 | 12.27 | 2.9E-01 | AB016426.1 | NT | Zinc finger protein (HUMAN); contains element L1 repetitive element; |
| 4359 | 9350 | 14329 | 1.05 | 2.9E-01 | AA284468.1 | EST_HUMAN | z557d12.11 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element; |
| 4545 | 9534 | | 0.85 | 2.9E-01 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|---|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--|
| wa06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element; | | | | | | | |
| 4946 | 9923 | | | 1.33 | AI670899.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81 |
| 5020 | 9991 | | | 1.01 | AI_161585.2 | NT | Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds |
| 563 | 5597 | | | 2.11 | U67136.1 | NT | Prune dwarf virus movement protein, complete cds; coat protein, complete cds |
| 568 | 5601 | | | 0.7 | U28145.1 | NT | Guiria guira oocyte maturation factor Mos (c-mos) gene, partial cds |
| 1067 | 6075 | 11108 | | 2.54 | AF168060.1 | NT | 601148733F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1258 | 6256 | 11298 | | 0.98 | BE313442.1 | EST_HUMAN | 601148733F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1258 | 6256 | 11299 | | 0.98 | BE313442.1 | EST_HUMAN | 601148733F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1272 | 6270 | 11310 | | 0.92 | D86550.1 | NT | Human mRNA for serine/threonine protein kinase, complete cds |
| 1689 | 6685 | 11761 | | 2.03 | AW86020.1 | EST_HUMAN | QV1-CT0364-120200-065-b05 C7064 Homo sapiens cDNA clone DKFZp586I2321 |
| 1962 | 6948 | 12050 | | 1.44 | AL047620.1 | EST_HUMAN | DKFZp586I2321_r1 586 (synonym: Huie1) Homo sapiens cDNA clone IMAGE:2912333 3' |
| 2073 | 7055 | 12165 | | 1 | AW511195.1 | EST_HUMAN | hd44b03_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3' |
| 2401 | 7372 | 12493 | | 2.06 | 2.8E-01 AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2401 | 7372 | 12494 | | 2.06 | 2.8E-01 AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2476 | 7445 | | | 1.49 | 2.8E-01 AI_161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 2594 | 7557 | 12671 | | 1.4 | 2.8E-01 AB020975.1 | NT | Arabidopsis thaliana mRNA for lipoytransferase, complete cds |
| 2801 | 7920 | | | 1.35 | 2.8E-01 AF179480.1 | NT | Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds |
| 2902 | 7921 | 12941 | | 2.3 | 2.8E-01 Z14037.1 | NT | B.taurus microsatellite (ETH121) |
| 2902 | 7921 | 12942 | | 2.3 | 2.8E-01 Z14037.1 | NT | B.taurus microsatellite (ETH121) |
| 3294 | 8305 | 13330 | | 0.85 | 2.8E-01 AP000004.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (4/7) |
| 3890 | 8890 | 13888 | | 1.44 | 2.8E-01 AE001180.1 | NT | Borellia burgdorferi (section 66 of 70) of the complete genome |
| 4005 | 9001 | | | 0.91 | 2.8E-01 AE004450.1 | NT | Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome |
| 4075 | 9069 | | | 2.36 | 2.8E-01 AI090868.1 | EST_HUMAN | ov44g10_x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; |
| 4337 | 9328 | 14313 | | 2.15 | 2.8E-01 P13615 | SWISSPROT | RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN) |
| 4682 | 9867 | 14649 | | 2.85 | 2.8E-01 AF030154.1 | NT | Bovine adenovirus 3 complete genome |
| 4711 | 9896 | 14680 | | 1.28 | 2.8E-01 BF528188.1 | EST_HUMAN | 602042601F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5' |
| 4731 | 9716 | 14701 | | 2.3 | 2.8E-01 AI272669.1 | EST_HUMAN | qf59c11_x1 Soares_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element; |
| 5004 | 9975 | 14950 | | 1.68 | 2.8E-01 AA767084.1 | EST_HUMAN | oa41n01_s1 NCI CGBP Homo sapiens cDNA clone IMAGE:1307569 3' |
| 473 | 5509 | 10522 | | 2.82 | 2.7E-01 Y7324.1 | NT | Rattus norvegicus CDK104 mRNA |
| 609 | 5836 | 10637 | | 2.19 | 2.7E-01 AA450061.1 | EST_HUMAN | zx39b10_s1 Soares_total_fetus_Nb2HF8_sw Homo sapiens cDNA clone IMAGE:7388227 3' similar to contains Alu repetitive element |
| 1242 | 6240 | 11291 | | 1.57 | 2.7E-01 AB004906.1 | NT | Ipomoea purpurea transposable element Tlp100 gene for transposase, complete cds |

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| Probe Seq ID No: | Exon Seq ID No: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1582 | 6579 | | 1.3 | 2.7E-01 | X79875.1 | NT | Gambelia SP2 gene |
| 1691 | 6687 | 11762 | 2.21 | 2.7E-01 | W58067.1 | EST_HUMAN | zd22h10.11 Snaires_fetal_heart NbHH19W Homo sapiens cDNA clone IMAGE:341443 5' |
| 1739 | 6734 | 11811 | 1.16 | 2.7E-01 | P03341 | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2077 | 7762 | | 1.42 | 2.7E-01 | AF047575.1 | NT | Retinol nonvisual vesicular monoamine transporter type 2, promoter region and exon 1 |
| 2306 | 7281 | 12399 | 6.34 | 2.7E-01 | Y13868.1 | NT | Feline immunodeficiency virus env gene, isolate ITTO088P1U (M88), partial |
| 2386 | 7357 | 12479 | 2.78 | 2.7E-01 | AJ310858.1 | EST_HUMAN | ta43c11.22 NC1_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element; |
| 2915 | 7934 | | 0.72 | 2.7E-01 | BF088284.1 | EST_HUMAN | CM1-HTC0875-060900-385-e05 HT0875 Homo sapiens cDNA |
| 3904 | 8904 | 13902 | 1.98 | 2.7E-01 | AI928015.1 | EST_HUMAN | wc92e11.x1\CI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3' |
| 3918 | 8918 | 13911 | 2.26 | 2.7E-01 | L77569.1 | NT | Homo sapiens: DiGeorge syndrome critical region, telomeric end |
| 4739 | 9724 | 14709 | 1.14 | 2.7E-01 | L27516.1 | NT | Triticum aestivum (Wcs66) gene, complete cds |
| 4875 | 9854 | | 4.25 | 2.7E-01 | AW856131.1 | EST_HUMAN | RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA |
| 467 | 7721 | 10516 | 1.71 | 2.6E-01 | P78411 | SWISSPROT | IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2 |
| 477 | 5514 | | 1.08 | 2.6E-01 | D16459.1 | NT | Bos taurus mRNA for mb-1, complete cds |
| 1370 | 6367 | 11416 | 1.36 | 2.6E-01 | BE885087.1 | EST_HUMAN | 601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5' |
| 1410 | 6408 | 11466 | 0.92 | 2.6E-01 | AB013290.1 | NT | Glycine max pseudogene for Bd 30K |
| 1856 | 6845 | 11932 | 4.92 | 2.6E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| 1856 | 6845 | 11933 | 4.92 | 2.6E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| | | | | | | | bb04d10x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactin 3 protein gene (MOUSE); |
| 2037 | 7020 | | 7 | 2.6E-01 | AW733152.1 | EST_HUMAN | Human prelaminin gene, complete cds |
| 2092 | 7073 | 12187 | 1.04 | 2.6E-01 | M11844.1 | NT | B. maritimus rncL gene |
| 2402 | 7373 | | 3.5 | 2.6E-01 | Y12996.1 | NT | 601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:29900043 5' |
| 2475 | 7444 | | 5.05 | 2.6E-01 | BE272440.1 | EST_HUMAN | EST386635 MAGE sequences, MAGM Homo sapiens cDNA |
| 3018 | 8035 | | 1.09 | 2.6E-01 | AW974531.1 | EST_HUMAN | Homo sapiens: acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5 EST371580 MAGE sequences, MAGF Homo sapiens cDNA |
| 3558 | 8565 | 13572 | 2.15 | 2.6E-01 | AF229118.1 | NT | QV1-BT0830-040400-132-e03 BT0630 Homo sapiens cDNA |
| 3983 | 8981 | 13966 | 0.94 | 2.6E-01 | AW959510.1 | EST_HUMAN | Enterococcus faecium strain N97-330 vanD glycopptide resistance gene cluster, complete cds; and unknown genes aa89a07_r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5' |
| 4031 | 9027 | 14016 | 17.72 | 2.6E-01 | BE080598.1 | EST_HUMAN | Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3'1) mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--------------------|
| 4577 9565 | 14553 | 1.46 | 2.6E-01 | AF142703.1 | NT | Ophrestia reticulosa matruse-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product | |
| 4812 9796 | 14779 | 3.7 | 2.6E-01 | H04858.1 | EST_HUMAN | yf51e05.1r Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5' | |
| 4877 9856 | | 1.53 | 2.6E-01 | AA884625.1 | EST_HUMAN | am33b11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3' | |
| 5069 10038 | 15005 | 1.24 | 2.6E-01 | M37701.1 | NT | P.chrysosporium lignin peroxidase genes, complete cds | |
| 239 5301 | 10311 | 1.57 | 2.5E-01 | 4502296 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA | |
| 240 5301 | 10311 | 2.3 | 2.5E-01 | 4502296 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA | |
| 253 5313 | | 7.98 | 2.5E-01 | M26501.1 | NT | Starfish (<i>P. ochraceus</i>) cytoplasmic actin gene, complete cds | |
| 822 5842 | 10878 | 0.98 | 2.5E-01 | U09964.1 | NT | Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds | |
| 1043 6053 | | 0.73 | 2.5E-01 | AE002156.1 | NT | Ureaplasma urealyticum section 57 of 59 of the complete genome | |
| 1104 6111 | 11142 | 14.95 | 2.5E-01 | T89837.1 | EST_HUMAN | ye11g07.1r Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5' | |
| 1690 6686 | | 3.61 | 2.5E-01 | 4885406 | NT | Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA | |
| 1844 7757 | 11922 | 1.29 | 2.5E-01 | BE696604.1 | EST_HUMAN | PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA | |
| 1844 7757 | 11923 | 1.29 | 2.5E-01 | BE696604.1 | EST_HUMAN | PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA | |
| 2342 7316 | | 6.55 | 2.5E-01 | AE000675.1 | NT | Aquifex aeolicus section 7 of 109 of the complete genome | |
| 2565 7528 | 12646 | 1 | 2.5E-01 | X95310.1 | NT | B.taurus mRNA for D-spartate oxidase | |
| 3328 8338 | | 3.33 | 2.5E-01 | AW973471.1 | EST_HUMAN | EST385464 MAGE sequences, MAGM Homo sapiens cDNA | |
| 3457 8465 | 13492 | 1.12 | 2.5E-01 | AF233875.1 | NT | Danio rerio peptide YY precursor gene, complete cds | |
| 3473 8481 | 13500 | 6.31 | 2.5E-01 | AL161517.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29 | |
| 3757 8760 | 13759 | 1.55 | 2.5E-01 | AI741483.1 | EST_HUMAN | wg11c07.x1 Soares_NSE_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3' | |
| 3757 8760 | 13760 | 1.55 | 2.5E-01 | AI741483.1 | EST_HUMAN | wg11c07.x1 Soares_NSE_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3' | |
| 3895 8953 | | 1.09 | 2.5E-01 | P32323 | SWISSPROT | A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR | |
| 4181 9784 | | 0.91 | 2.5E-01 | Q03314 | SWISSPROT | RHIB PROTEIN | |
| 4606 9594 | | 1.31 | 2.5E-01 | Q27225 | SWISSPROT | MOLT-INHIBITING HORMONE PRECURSOR (MH) | |
| 4611 9597 | 14583 | 4.67 | 2.5E-01 | AF007768.1 | NT | Charitomys fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds | |
| 4637 9622 | 14614 | 2.24 | 2.5E-01 | AE004416.1 | NT | Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome | |
| 4658 9643 | | 3.61 | 2.5E-01 | AJ230113.1 | NT | Mus musculus annexin V gene, intron 4 segment containing 5'LTR and gag portion of MuERV-L (murine endogenous retrovirus) element | |
| 4722 9707 | 14694 | 0.8 | 2.5E-01 | UB3656.1 | NT | Rattus norvegicus NF-KB gene, promoter region | |
| 549 5583 | 10585 | 1.12 | 2.4E-01 | AA936316.1 | EST_HUMAN | on70dd4.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:11562023 3' | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 838 | 5857 | 10898 | 1.73 | 2.4E-01 | B576124.1 | EST_HUMAN | 602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5' |
| 1285 | 6284 | 11326 | 14.3 | 2.4E-01 | A1289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1285 | 6284 | 11327 | 14.3 | 2.4E-01 | A1289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1814 | 6804 | | 14.57 | 2.4E-01 | AF2677753.1 | NT | Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds |
| 1859 | 6848 | 11936 | 1.09 | 2.4E-01 | AF251708.1 | NT | Zeocys duoradius fructose-1,6-bisphosphatase mRNA, complete cds |
| 2104 | 7084 | | 1.04 | 2.4E-01 | P45384 | SWISSPROT | IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IgA1 PROTEASE) |
| 2200 | 7178 | 12301 | 1.86 | 2.4E-01 | AE000630.1 | NT | Aquifex aeolicus section 12 of 109 of the complete genome |
| 2320 | 7295 | 12415 | 131.89 | 2.4E-01 | BF002171.1 | EST_HUMAN | 7h23d04.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW.PRSB_XENLA O42586 26S PROTEASE REGULATORY SUBUNIT 6A ; |
| 2467 | 7436 | 12553 | 2.1 | 2.4E-01 | Z36534.1 | NT | D.diisodeum (A3-K) ponA gene |
| 2688 | 7646 | 12761 | 1.53 | 2.4E-01 | X71783.1 | NT | S.pombe swf5 gene |
| 2713 | 7670 | 12783 | 3.6 | 2.4E-01 | AF030154.1 | NT | Bovine adenovirus 3 complete genome |
| 3059 | 8076 | | 3.61 | 2.4E-01 | U72726.1 | NT | Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds |
| 3075 | 8091 | 13105 | 1.58 | 2.4E-01 | X74209.1 | NT | H.sapiens AGT gene, PstI fragment of intron 4 |
| 3675 | 8680 | 13683 | 0.71 | 2.4E-01 | AE000312.1 | NT | Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome |
| 3920 | 8920 | | 0.95 | 2.4E-01 | D28960.1 | NT | Rattus norvegicus mRNA for alphaB crystallin-related protein , complete cds |
| 4986 | 9960 | 14937 | 1.38 | 2.4E-01 | AF252302.1 | NT | Oncorhynchus mykiss shaker-related potassium channel Tsh2 gene, complete cds |
| 388 | 5426 | 10441 | 0.83 | 2.3E-01 | S75898.1 | NT | Poephila guttata-zebra finches, ovary mRNA, 3188 nt] |
| 631 | 5659 | | 4.7 | 2.3E-01 | U39713.1 | NT | Mycoplasma genitalium section 35 of 51 of the complete genome |
| 659 | 5686 | 10693 | 27.33 | 2.3E-01 | U67596.1 | NT | Methanococcus jannaschii section 138 of 150 of the complete genome |
| 921 | 5937 | 10968 | 3.41 | 2.3E-01 | BE311893.1 | EST_HUMAN | 601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5' |
| 1592 | 6588 | 11650 | 2.09 | 2.3E-01 | Y10887.2 | NT | Mus musculus cdh5 gene, exon 1, partial |
| 1994 | 6978 | | 1.08 | 2.3E-01 | AJ235353.1 | NT | Homo sapiens partial intron 3 of the wild type AF-4/FEL gene |
| 2378 | 7350 | 12470 | 1.58 | 2.3E-01 | BE297718.1 | EST_HUMAN | 601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5' |
| 2579 | 7542 | 12656 | 0.92 | 2.3E-01 | M11319.1 | NT | Human erythropoietin gene, complete cds |
| 2751 | 6362 | 11411 | 1.97 | 2.3E-01 | AB015033.1 | NT | Marinimillibia agarivorans gyB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957 |
| 2893 | 7912 | 12933 | 0.83 | 2.3E-01 | AA601379.1 | EST_HUMAN | no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element;contains element T-HR repetitive element; |
| 3010 | 8027 | | 6.01 | 2.3E-01 | R21732.1 | EST_HUMAN | yh21607.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3' |
| 3216 | 8231 | 13252 | 0.91 | 2.3E-01 | U65391.1 | NT | Lycopersicon esculentum PRF (Prf) gene, complete cds |
| 3288 | 8299 | 13326 | 1.23 | 2.3E-01 | H69836.1 | EST_HUMAN | yf97h10.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:213283 5' |
| 3832 | 8834 | | 5.25 | 2.3E-01 | 7662133 | NT | Homo sapiens KIAA0450 gene product (KIAA0450), mRNA |
| 4224 | 9218 | 14197 | 6.38 | 2.3E-01 | R82252.1 | EST_HUMAN | yf7f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1490175 |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 4277 9270 | | | 1.85 | 2.3E-01 | L78789.1 | NT | Mus musculus; renin (Ren-1c) gene, promoter region |
| 4329 9320 | 14305 | 0.87 | 2.3E-01 | D90899.1 | NT | Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859 | |
| 4360 9351 | 14330 | 2.08 | 2.3E-01 | AF082535.1 | NT | Homo sapiens; mitogen-activated protein kinase p38delta (PRK/M13) mRNA, complete cds | |
| 4422 9412 | 14400 | 5.79 | 2.3E-01 | 5031984 | NT | Homo sapiens; nuclear transport factor 2 (placental protein 15) (PP15) mRNA | |
| 4882 9861 | 14832 | 0.69 | 2.3E-01 | AB032400.1 | NT | Mus musculus tulip 1 mRNA, complete cds | |
| 88 5165 | 10176 | 0.8 | 2.2E-01 | A1052190.1 | EST_HUMAN | 0214a10_x1_Scares_fetal_liver_spleen_1NF1S_S1_Homo_sapiens cDNA clone IMAGE:1675280 3' similar to TR:Q13040 C13040 ATP-BINDING CASSETTE PROTEIN; | |
| 1532 6530 | 11590 | 2.42 | 2.2E-01 | AF187850.1 | NT | Homo sapiens; PPAR delta gene, promoter region | |
| 1969 6954 | | 1.16 | 2.2E-01 | AF171901.1 | NT | Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product | |
| 2035 7018 | 12128 | 1.86 | 2.2E-01 | M34640.1 | NT | Fresh-water sponge Emf1 alpha collagen (COLF1) gene | |
| 2339 7313 | 12434 | 4.2 | 2.2E-01 | BF677538.1 | EST_HUMAN | 60208560_8F1_NIH_MCC_83_Homo_sapiens cDNA clone IMAGE:4249969 5' | |
| 2512 7480 | 12595 | 1.38 | 2.2E-01 | BE618258.1 | EST_HUMAN | 6011462629F1_NIH_MCC_67_Homo_sapiens cDNA clone IMAGE:3866190 5' | |
| 2512 7480 | 12596 | 1.38 | 2.2E-01 | BE618258.1 | EST_HUMAN | 6011462629F1_NIH_MCC_67_Homo_sapiens cDNA clone IMAGE:3866190 5' | |
| 2812 7832 | 12848 | 5.48 | 2.2E-01 | BE155625.1 | EST_HUMAN | PM2-HT0353_2811299_303-812_H70353_Homo_sapiens cDNA | |
| 2812 7832 | 12849 | 5.48 | 2.2E-01 | BE155625.1 | EST_HUMAN | PM2-HT0353_2811299_303-812_H70353_Homo_sapiens cDNA | |
| 2850 7870 | | 1.44 | 2.2E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 | |
| 3308 8319 | | 2.3 | 2.2E-01 | AL161562.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62 | |
| 3667 8672 | 13676 | 1.51 | 2.2E-01 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 | |
| 3724 8728 | | 1.61 | 2.2E-01 | AF1585728.1 | NT | Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene | |
| 4091 9085 | | 1.09 | 2.2E-01 | AF119102.1 | NT | Drosophila melanogaster UNC-119 (unc-119) gene, complete cds | |
| 4098 9092 | 14078 | 6.31 | 2.2E-01 | AF155142.1 | NT | Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds | |
| 4141 9136 | 14119 | 2.24 | 2.2E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Makk1) mRNA, complete cds | |
| 4141 9136 | 14120 | 2.24 | 2.2E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Makk1) mRNA, complete cds | |
| 4230 9224 | 14206 | 1.24 | 2.2E-01 | U01307.1 | NT | Human sRNA (BC200 beta) pseudogene | |
| 4230 9224 | 14207 | 1.24 | 2.2E-01 | U01307.1 | NT | Human sRNA (BC200 beta) pseudogene | |
| 4679 9664 | | 1.4 | 2.2E-01 | D50604.1 | NT | Human beta- γ -tuboplasmic actin (ACTBP9) pseudogene | |
| 4684 9669 | 14651 | 2.15 | 2.2E-01 | AA211216.1 | EST_HUMAN | zo87cd5_r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:646968 5' | |
| 4878 9857 | | 1.24 | 2.2E-01 | L13289.1 | NT | Mus musculus vinculin gene, exon 3 | |
| 4961 9938 | 14915 | 0.91 | 2.2E-01 | H60548.1 | EST_HUMAN | yr42109_r1_Scares_fetal_liver_spleen_1NF1S_Homo_sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14116_m1 CD9 GLYCOPROTEIN PRECURSOR (HUMAN); | |
| 956 5972 | 11006 | 1.5 | 2.1E-01 | AA568289.1 | EST_HUMAN | nm31e11.s1 NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061804 | |
| 959 5974 | 11008 | 1.79 | 2.1E-01 | AL161504.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1107 | 6113 | | | 2.15 | 2.1E-01 AE002314.2 | NT | Chlamydia muridarum, section 45 of 85 of the complete genome |
| 1179 | 6181 | 11217 | | 1.22 | 2.1E-01 6754299 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA |
| 1179 | 6181 | 11218 | | 1.22 | 2.1E-01 6754299 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA |
| 1869 | 6858 | 11946 | | 1.52 | 2.1E-01 AA806824.1 | EST_HUMAN | ok73e02 s1 NCI_CGAP GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN); |
| 2094 | 7075 | 12189 | | 2.42 | 2.1E-01 BFG95073.1 | EST_HUMAN | 602053129f1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5' |
| 2854 | 7874 | 12889 | | 2.25 | 2.1E-01 6912445 | NT | Homo sapiens potassium voltage-gated channel, subfamily H (egg-related), member 4 (KCNH4), mRNA |
| 3718 | 8722 | | | 6.22 | 2.1E-01 9838361 | NT | Beta vulgaris mitochondrial, complete genome |
| 3940 | 8938 | 13930 | | 1.28 | 2.1E-01 P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 3940 | 8938 | 13931 | | 1.28 | 2.1E-01 P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 4128 | 9123 | | | 0.9 | 2.1E-01 AF124526.1 | NT | Orchestia cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds |
| 4251 | 9245 | | | 1.28 | 2.1E-01 AB033041.1 | NT | Homo sapiens mRNA for KIAA1215 protein, partial cds |
| 4443 | 9433 | 14416 | | 1.66 | 2.1E-01 AB010273.1 | NT | Homo sapiens hoxc1 proto-oncogene, exons 1 to 3 and hug-1 gene |
| 4719 | 9704 | 14690 | | 4 | 2.1E-01 AJ009794.1 | NT | Homo sapiens capsid protein C (core protein) (P22); ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35); ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21); PROTEASE/HELICASE NS3 (P70); NONSTRUCTURAL PROTEIN> |
| 5030 | 10001 | | | 0.92 | 2.1E-01 P26660 | SWISSPROT | Human surfactant protein-C (SP-C) gene, complete cds |
| 5067 | 10036 | 15003 | | 1 | 2.1E-01 U02948.1 | NT | Gallus gallus mRNA for avian, complete cds |
| 200 | 5264 | 10278 | | 2.64 | 2.0E-01 AB017437.1 | NT | Homo sapiens CG1-18 protein (LOC51008), mRNA |
| 5330 | 5865 | | | 2.17 | 2.0E-01 7705601 | NT | O.cuniculus germinal IgH heavy chain V-H pseudogene, allele type VH α 2 |
| 690 | 5714 | 10728 | | 1.32 | 2.0E-01 M77085.1 | NT | Mus musculus Major Histocompatibility Locus class II region |
| 801 | 5822 | 10852 | | 5.78 | 2.0E-01 AF027865.1 | NT | Synochocystis sp. PCC6803 complete genome, 7/27..781449-920915 |
| 996 | 6008 | 11038 | | 0.66 | 2.0E-01 D90905.1 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 1108 | 6114 | 11144 | | 2.91 | 2.0E-01 AL163213.2 | NT | Homo sapiens rac1 gene |
| 1235 | 6233 | 11277 | | 1.34 | 2.0E-01 AJ132695.5 | NT | PM1-HT0422-291299-002-006 HT0422 Homo sapiens cDNA |
| 1289 | 6288 | 11332 | | 1.08 | 2.0E-01 AW384937.1 | EST_HUMAN | Plum pox virus strain M, complete genome, isolate PS |
| 1332 | 6429 | | | 1.01 | 2.0E-01 AJ243957.1 | NT | Homo sapiens dystrobrevin, alpha (DTNA), mRNA |
| 1456 | 8453 | 11512 | | 7.19 | 2.0E-01 4503408 | NT | Homo sapiens chromosome 1 specific transcript KIAA0505 |
| 1520 | 6517 | 11574 | | 3.81 | 2.0E-01 AB007974.1 | NT | Homo sapiens sodium/nitride symporter mRNA, partial cds |
| 1526 | 6523 | 11580 | | 1.54 | 2.0E-01 AF260700.1 | NT | Human bradykinin B1 receptor (bradyb1) gene, complete cds |
| 1658 | 6654 | 11726 | | 1.48 | 2.0E-01 U22346.1 | NT | Homo sapiens Jagged2 gene, complete cds; and unknown gene |
| 1879 | 6679 | | | 1.48 | 2.0E-01 AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1720 | 6715 | | 3.96 | 2.0E-01 | U67525.1 | NT | Methanococcus jannaschii section 67 of 150 of the complete genome |
| 1853 | 6842 | 11930 | 0.93 | 2.0E-01 | 8922238 | NT | Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA |
| 2286 | 7282 | | 1.21 | 2.0E-01 | X82877.1 | NT | H. sapiens Na-D-glucose cotransport regulator gene |
| 3407 | 8416 | 13444 | 0.68 | 2.0E-01 | P46607 | SWISSPROT | HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (ATHB-10) |
| 3489 | 8497 | | 0.67 | 2.0E-01 | AW238005.1 | EST_HUMAN | xp15b02.x1 NC1_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element; |
| 3624 | 8631 | 13637 | 0.7 | 2.0E-01 | P34641 | SWISSPROT | CED-11 PROTEIN |
| 3919 | 8919 | 13912 | 0.77 | 2.0E-01 | X83997.1 | NT | C.parasitica espC gene |
| 4433 | 9423 | | 9.72 | 2.0E-01 | BE826165.1 | EST_HUMAN | QV4-EN032-190500-223-803 EN032 Homo sapiens cDNA |
| 4874 | 9853 | 14828 | 7.34 | 2.0E-01 | 8922080 | NT | Homo sapiens hypothetical protein ASH1 (ASH1), mRNA |
| 4931 | 9908 | 14885 | 0.93 | 2.0E-01 | Y19216.1 | NT | Homo sapiens putative pshHbD pseudogene for hair keratin, exons 1 to 9 |
| 4979 | 7840 | | 7.46 | 2.0E-01 | AF074990.1 | NT | Homo sapiens full length insert cDNA YH85A11 |
| 5045 | 10016 | 14985 | 1.19 | 2.0E-01 | AF197159.1 | NT | Mus musculus cubilin mRNA, partial cds |
| 5059 | 10029 | | 1.29 | 2.0E-01 | T47785.1 | EST_HUMAN | yb17a10.11 Strategene fetal spleen #937205 Homo sapiens cDNA clone IMAGE:71418 5' |
| 5182 | | 9.3 | 1.9E-01 | | 7549743 | NT | Rattus norvegicus AhR hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA |
| 350 | 5402 | 10412 | 5.34 | 1.9E-01 | AF004353.1 | NT | Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds |
| 648 | 5676 | 10682 | 24.68 | 1.9E-01 | U32581.2 | NT | Homo sapiens lambdoidota protein kinase C-interacting protein mRNA, complete cds |
| 648 | 5676 | 10683 | 24.68 | 1.9E-01 | U32581.2 | NT | Homo sapiens lambdoidota protein kinase C-interacting protein mRNA, complete cds |
| 655 | 5683 | 10690 | 6.04 | 1.9E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251199-01-001 BT0502 Homo sapiens cDNA |
| 656 | 5683 | 10690 | 5.32 | 1.9E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251199-01-001 BT0502 Homo sapiens cDNA |
| 971 | 5986 | | 0.96 | 1.9E-01 | 7305180 | NT | Mus musculus interleukin 2 receptor, gamma chain (lI2/g), mRNA |
| 1087 | 6094 | 11124 | 12.01 | 1.9E-01 | AA358813.1 | EST_HUMAN | EST67784 Fatal lung II Homo sapiens cDNA 5' end |
| 1353 | 6350 | 11400 | 3.22 | 1.9E-01 | AF061282.1 | NT | Sorghum bicolor 22 kDa kafirin cluster |
| 1409 | 6407 | | 2.64 | 1.9E-01 | AF184823.1 | NT | Plasmidium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds |
| 2319 | 7294 | 12414 | 2.22 | 1.9E-01 | 8922533 | NT | Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA |
| 2852 | 7872 | 12887 | 3.91 | 1.9E-01 | U66066.1 | NT | Sigmodon hispidus p53 gene, partial cds |
| 2868 | 7887 | | 5.5 | 1.9E-01 | J009222.1 | NT | Gallus gallus ovalbumin (Y) gene, complete cds |
| 3311 | 8322 | 13345 | 4.28 | 1.9E-01 | D13197.1 | NT | Mouse gene for immunoglobulin diversity region D1 |
| 3399 | 8408 | 13434 | 4.85 | 1.9E-01 | R16467.1 | EST_HUMAN | yf42f10.11 Suares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5' |
| 3716 | 8720 | 13721 | 0.77 | 1.9E-01 | AF264017.1 | NT | Rattus norvegicus arylacetamide deacetylase gene, complete cds |
| 3746 | 8750 | 13749 | 1 | 1.9E-01 | P39768 | SWISSPROT | PAIR-RULE PROTEIN ODD-PAIRED |
| 3886 | 8887 | 13886 | 3.37 | 1.9E-01 | AB006784.1 | NT | Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds |
| 3968 | 8967 | 13956 | 1.47 | 1.9E-01 | AW754106.1 | EST_HUMAN | CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 4110 9104 | 14090 | 1 | 1 | 1.9E-01 | BE834943.1 | EST_HUMAN | MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA |
| 4851 9833 | | 1.11 | 1.9E-01 | AF223642.1 | NT | Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds | |
| 32 5112 | 10098 | 1.73 | 1.8E-01 | U73200.1 | NT | Mus musculus p116Rip mRNA, complete cds | |
| 258 7717 | 10327 | 1.97 | 1.8E-01 | AB022090.1 | NT | Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds | |
| 369 5418 | 10433 | 1.48 | 1.8E-01 | 4 502532 | NT | Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products | |
| 737 5760 | 10783 | 1.61 | 1.8E-01 | AB021490.2 | NT | Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds | |
| 9677 5982 | 11014 | 0.75 | 1.8E-01 | AI912212.1 | EST_HUMAN | wd71102.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3' | |
| 1075 6082 | 11112 | 1.17 | 1.8E-01 | AF000580.1 | NT | Dictyostelium discoideum plasmid Ddp5, complete genome | |
| 1269 6267 | 11309 | 7.26 | 1.8E-01 | AL117189.1 | NT | Yersinia pestis plasmid pCD1 | |
| 1810 6800 | | 1.18 | 1.8E-01 | 4 505036 | NT | Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA | |
| 1829 6819 | | 1.34 | 1.8E-01 | AI733708.1 | EST_HUMAN | qg22d10.x5 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 O75936 GAMMA BUTYROBETANE HYDROXYLASE : | |
| 1871 6860 | 11948 | 1.42 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds | |
| 2620 7582 | | 1.63 | 1.8E-01 | AW935728.1 | EST_HUMAN | QV3-DT0018-181-289-036-g04 DT0018 Homo sapiens cDNA | |
| 2827 7848 | | 1.6 | 1.8E-01 | AF184589.1 | NT | Janopusodium bicorne LEAFY protein (LEAFY2) gene, partial cds | |
| 2833 7853 | 12873 | 1.28 | 1.8E-01 | AW182300.1 | EST_HUMAN | xJ41a03.x1 NC1 Soesies_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2659756 3' | |
| 3051 8068 | 13077 | 2.5 | 1.8E-01 | AW995178.1 | EST_HUMAN | QV0-BN0041-170300-147-c04 BN0041 Homo sapiens cDNA | |
| 3285 8296 | 13322 | 0.68 | 1.8E-01 | BF183582.1 | EST_HUMAN | 601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3' | |
| 3540 8546 | 13553 | 0.78 | 1.8E-01 | HO3369.1 | EST_HUMAN | yJ45e01.s1 Soesies_placenta_Nb2-hP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element; | |
| 3540 8546 | 13554 | 0.78 | 1.8E-01 | HO3369.1 | EST_HUMAN | yJ45e01.s1 Soesies_placenta_Nb2-hP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element; | |
| 4206 9199 | | 1.21 | 1.8E-01 | D37954.1 | NT | Bovine NB26 mRNA for MHC class II (BOLA-DQB), complete cds | |
| 4424 9414 | 14401 | 5.34 | 1.8E-01 | AL161556.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56 | |
| 4627 9612 | | 3.53 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya6 pseudogene, small inducible cytokine A5 precursor, complete cds | |
| 4661 9646 | | 1.89 | 1.8E-01 | X92179.1 | NT | S.tuberoseum mRNA for alcohol dehydrogenase | |
| 4880 9859 | 14830 | 2.79 | 1.8E-01 | AW814270.1 | EST_HUMAN | MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA | |
| 4924 9901 | 14877 | 6.38 | 1.8E-01 | AF181258.1 | NT | Mesocricetus auratus Na taurocholate cotransporting polypeptide mRNA, partial cds | |
| 4942 9919 | 14859 | 1.04 | 1.8E-01 | A1439881.1 | EST_HUMAN | ti57e04.x1 NC1 CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3' | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--------------------|
| 5061 10030 | 14997 | 0.93 | 1.8E-01 | X60206.1 | NT | Escherichia coli reverse transcriptase, rettron EC86 | |
| 5061 10030 | 14998 | 0.93 | 1.8E-01 | X60206.1 | NT | Escherichia coli reverse transcriptase, rettron EC86 | |
| 5605 572 | 10603 | 1.66 | 1.7E-01 | BE385164.1 | EST_HUMAN | 601274604F-1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5' | |
| 796 5817 | 10848 | 1.92 | 1.7E-01 | X53330.1 | NT | P_dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 | |
| 946 5963 | | 2 | 1.7E-01 | P35616 | SWISSPROT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) | |
| 1041 6051 | 11080 | 1.31 | 1.7E-01 | AF081810.1 | NT | Lymantria dispar nucleopolyhedrovirus, complete genome | |
| 1041 6051 | 11081 | 1.31 | 1.7E-01 | AF081810.1 | NT | Lymantria dispar nucleopolyhedrovirus, complete genome | |
| 1781 6773 | 11865 | 1.64 | 1.7E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 | |
| 1935 6921 | | 1.96 | 1.7E-01 | AF255056.1 | NT | Homo sapiens tRNIP3H (tRNIP3H) gene, complete cds; nuclear gene for mitochondrial product | |
| 2788 7809 | 12826 | 2.05 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL_VIBCO gene, partial cds | |
| 2788 7809 | 12827 | 2.05 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL_VIBCO gene, partial cds | |
| 2856 7876 | 12892 | 1.55 | 1.7E-01 | AA335890.1 | EST_HUMAN | EST41651 Endometrial tumor Homo sapiens cDNA 5' end | |
| 2928 7947 | 12964 | 1.1 | 1.7E-01 | AJ238736.1 | NT | Neja neja stra_1:k-1 gene, exons 1-3 | |
| 2928 7947 | 12965 | 1.1 | 1.7E-01 | AJ238736.1 | NT | Neja neja stra_1:k-1 gene, exons 1-3 | |
| 3032 8049 | 13058 | 1.45 | 1.7E-01 | AF081514.1 | NT | Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds | |
| 3363 8371 | 13391 | 1.56 | 1.7E-01 | AJ265505.1 | NT | Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene | |
| 3327 8553 | 13540 | 1.17 | 1.7E-01 | AJ224877.1 | NT | Homo sapiens hap1 gene, complete CDS | |
| 3835 8837 | 13843 | 6.17 | 1.7E-01 | AJ235377.1 | NT | Homo sapiens derivative 11 breakpoint fragment; partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/f-EL gene | |
| 4128 9418 | | 1.89 | 1.7E-01 | X52936.1 | NT | Schistocerca jamaicensis_alpha repetitive DNA qh57609_x1_Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to | |
| 4691 9676 | 14659 | 1.31 | 1.7E-01 | AI247635.1 | EST_HUMAN | contains OFR_b1 OFR repetitive element; | |
| 4932 9909 | 14886 | 8.76 | 1.7E-01 | AB007941.1 | NT | Homo sapiens mRNA for KIAA0472 protein, partial cds | |
| 126 5194 | 10208 | 1.54 | 1.6E-01 | AF217532.1 | NT | Homo sapiens mevalonate kinase gene, exon 6 and 7 | |
| 671 7696 | 10705 | 1.11 | 1.6E-01 | R3_497.1 | EST_HUMAN | yh75f12_r1 Soares placentae Nb2HP Homo sapiens cDNA clone IMAGE:135599 5' | |
| 1474 6471 | 11529 | 1.07 | 1.6E-01 | AA548863.1 | EST_HUMAN | nk28d12_s1 NCI CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3' | |
| 1490 6487 | 11542 | 2.68 | 1.6E-01 | AF298117.1 | NT | Homo sapiens homeobox protein OTX2 gene, complete cds | |
| 1883 6872 | 11961 | 1.19 | 1.6E-01 | P22063 | SWISSPROT | AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) | |
| 1938 6924 | | 1.08 | 1.6E-01 | U10334.1 | NT | Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2322 | 7768 | 12418 | 0.98 | 1.6E-01 | X94292.1 | NT | H. sapiens mRNA for novel T-cell activation protein |
| 2422 | 7393 | 12514 | 1.22 | 1.6E-01 | AB037729.1 | NT | Homo sapiens mRNA for KIAA1308 protein, partial cds |
| 2821 | 7842 | 12859 | 10.97 | 1.6E-01 | AF185589.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 2821 | 7842 | 12860 | 10.97 | 1.6E-01 | AF185589.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3548 | 8555 | 13562 | 1.16 | 1.6E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel AB13 gene |
| 3548 | 8555 | 13563 | 1.16 | 1.6E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobel AB13 gene |
| 3665 | 8689 | 13692 | 0.73 | 1.6E-01 | AE000962.1 | NT | Archaeoglobus fulgidus section 145 of 172 of the complete genome |
| 3854 | 8894 | | 2.51 | 1.6E-01 | AE004413.1 | NT | Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome |
| 4202 | 9195 | 14177 | 10.56 | 1.6E-01 | AF179680.1 | NT | Homo sapiens apelin gene, complete cds |
| 4334 | 9325 | | 2.61 | 1.6E-01 | AW968601.1 | EST_HUMAN | EST380677 MAGE sequences, MAGI Homo sapiens cDNA |
| 4340 | 9331 | | 3.9 | 1.6E-01 | 6753319 | NT | Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA |
| 4788 | 9772 | 14155 | 1.47 | 1.6E-01 | AA088343.1 | EST_HUMAN | ZB44h09_s1 Stratagene colon (#337204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR-E221955 |
| 4810 | 9794 | 14776 | 1.19 | 1.6E-01 | AJ006356.1 | NT | E221955_38.855 BP SEGMENT OF CHROMOSOME XIV. |
| 4810 | 9794 | 14777 | 1.19 | 1.6E-01 | AJ006356.1 | NT | Lycopersicon esculentum RsaI fragment 2, satellite region |
| 5029 | 10000 | 14973 | 1.21 | 1.6E-01 | P98158 | SWISSPROT | Lycopersicon esculentum RsaI fragment 2, satellite region |
| 246 | 5306 | 10316 | 1.38 | 1.5E-01 | BE710087.1 | EST_HUMAN | IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA |
| 246 | 5306 | 10317 | 1.38 | 1.5E-01 | BE710087.1 | EST_HUMAN | IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA |
| 582 | 7694 | | 2.11 | 1.5E-01 | AV711696 | DCA_HD06_5 | AV711696 DCA Homo sapiens cDNA clone DCA_HD06_5 |
| 774 | 5796 | 10824 | 1.39 | 1.5E-01 | AL163284.2 | NT | Human genes chromosome 21 segment HS21C084 |
| 1080 | 6087 | 11116 | 1.81 | 1.5E-01 | AJ251885.1 | NT | Human sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1 |
| 1096 | 6103 | | 2.69 | 1.5E-01 | L36125.1 | NT | Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end |
| 1197 | 6198 | 11234 | 0.7 | 1.5E-01 | AW195516.1 | EST_HUMAN | xn39d11_xr_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:26960865_3' |
| 1256 | 6254 | 11295 | 2.85 | 1.6E-01 | D26535.1 | NT | Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15) |
| 1256 | 6254 | 11296 | 2.85 | 1.6E-01 | D26535.1 | NT | Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15) |
| 1451 | 8448 | 11509 | 1.47 | 1.5E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds |
| 2839 | 7599 | 12713 | 1.34 | 1.5E-01 | BF695381.1 | EST_HUMAN | 60208326SF1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537_5' |
| 2843 | 7863 | | 1.06 | 1.5E-01 | AW572516.1 | EST_HUMAN | XW56e02_xr2_NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978_3' similar to gb:X556072_ma1 |
| 3274 | 8286 | 13310 | 4.64 | 1.5E-01 | AA935049.1 | EST_HUMAN | THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); 0068d05_s1 NCI_CGAP GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 |
| 3670 | 8675 | 13678 | 2.01 | 1.5E-01 | U09964.1 | NT | RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); Mus musculus ICRI/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3684 | 8688 | 13691 | 1.04 | 1.5E-01 | 7108358 | NT | Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDHK1), nuclear gene encoding mitochondrial protein, mRNA |
| 3775 | 8778 | 13782 | 2.39 | 1.5E-01 | AW665983.1 | EST_HUMAN | hj10f08x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29814113' |
| 3937 | 8936 | 13929 | 0.96 | 1.5E-01 | AW366569.1 | EST_HUMAN | RC2-HT049-191098-012-c09 HT0149 Homo sapiens cDNA |
| 4059 | 9053 | 14040 | 8.83 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4585 | 9573 | 14563 | 1.41 | 1.5E-01 | BF687665.1 | EST_HUMAN | 602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:40662235' |
| 4607 | 7599 | 12713 | 2.83 | 1.5E-01 | BF695381.1 | EST_HUMAN | 602063269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:42475375' |
| 4840 | 9824 | 14799 | 1.66 | 1.5E-01 | AL161560.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 297 | 5354 | | 1.51 | 1.4E-01 | AF009663.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region |
| 899 | 5917 | | 2.72 | 1.4E-01 | D78638.1 | NT | Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds |
| 1240 | 6238 | | 2.11 | 1.4E-01 | T91864.1 | EST_HUMAN | yd54c01.s1 Smares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1120323' |
| 1709 | 6704 | | 1.2 | 1.4E-01 | 6679980 | NT | Mus musculus growth differentiation factor 5 (Gdf5), mRNA |
| 1712 | 6707 | 11783 | 1.61 | 1.4E-01 | AE001710.1 | NT | Thermatoga maritima section 22 of 136 of the complete genome |
| 1939 | 6925 | | 8.74 | 1.4E-01 | AA720615.1 | EST_HUMAN | ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:12838213' |
| 2720 | 7677 | 12791 | 4.16 | 1.4E-01 | A1933496.1 | EST_HUMAN | wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:24146653' |
| 3464 | 8472 | | 1.55 | 1.4E-01 | BF341524.1 | EST_HUMAN | 602013527F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:41491265' |
| 3803 | 8806 | 13811 | 1.17 | 1.4E-01 | R59232.1 | EST_HUMAN | yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:414675' |
| 3803 | 8806 | 13812 | 1.17 | 1.4E-01 | R59232.1 | EST_HUMAN | yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:414675' |
| 4050 | 9046 | 14034 | 11.16 | 1.4E-01 | A1699094.1 | EST_HUMAN | tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:22735703' |
| 4050 | 9046 | 14035 | 11.16 | 1.4E-01 | A1699094.1 | EST_HUMAN | tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:22735703' |
| 4115 | 9109 | 14094 | 3.8 | 1.4E-01 | AE001710.1 | NT | Thermatoga maritima section 22 of 136 of the complete genome |
| 3220 | 5375 | 10384 | 2.28 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 3220 | 5375 | 10385 | 2.28 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 5225 | 5560 | 10563 | 1.88 | 1.3E-01 | AB013139.1 | NT | Homo sapiens gene for NBS1, complete cds |
| 630 | 5658 | 10663 | 1.51 | 1.3E-01 | AJ277606.1 | NT | Human calicivirus HUN/LV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUN/LV/Girlington/93/UK |
| 630 | 5658 | 10664 | 1.51 | 1.3E-01 | AJ277606.1 | NT | Human cell/civirus HUN/LV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUN/LV/Girlington/93/UK |
| 834 | 5853 | 10893 | 0.83 | 1.3E-01 | X53330.1 | NT | P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 883 | 5901 | 10942 | 1.49 | 1.3E-01 | AF139518.1 | NT | Rattus norvegicus A-Kinase anchor protein mRNA, complete cds |
| 1010 | 6020 | 11049 | 1.51 | 1.3E-01 | AL117078.1 | NT | Botrylloides clathratus strain 74 cDNA library under conditions of nitrogen deprivation |
| 1110 | 6116 | | 2.67 | 1.3E-01 | AL115265.1 | NT | Botrylloides clathratus strain 74 cDNA library under conditions of nitrogen deprivation |
| 1196 | 6197 | 11233 | 1.71 | 1.3E-01 | AV712467.1 | EST_HUMAN | AV712467D1CA Homo sapiens cDNA clone DCAAFF055' |
| 1418 | 6415 | | 0.91 | 1.3E-01 | AF146277.1 | NT | Homo sapiens adapter protein CMS mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|--|-----------------|----------------|-------------------|----------------------------------|-----------------------|---|--------------------|
| 1919 6905 11999 1.66 1.3E-01 AL117078.1 NT <i>Bacillus cereus</i> strain T4 cDNA library under conditions of nitrogen deprivation | | | | | | | |
| 2106 7086 | | | 0.97 | 1.3E-01 AJ243578.1 | NT | Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucC | genes and ORI:151 |
| 2228 7205 | | | 1.04 | 1.3E-01 AW812104.1 | EST_HUMAN | RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA | |
| 2318 7293 | | | 2.79 | 1.3E-01 AE001016.1 | NT | Archaeoglobus fulgidus section 91 of 172 of the complete genome | |
| 2510 7478 | 12593 | | 1.78 | 1.3E-01 M86918.1 | NT | Carassius auratus keratin type I mRNA, complete cds | |
| | | | | | | Homo sapiens transcription factor IGHM enhancer 3, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α2 | |
| 3278 8290 | 13315 | | 0.98 | 1.3E-01 AF196779.1 | NT | Bovine branched chain α-keto acid dihydrolyase mRNA, complete cds | |
| 3368 8376 | 13396 | | 1.03 | 1.3E-01 M21572.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287/000 nt, position (1/7) | |
| 3639 8645 | 13651 | | 0.81 | 1.3E-01 AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287/000 nt, position (1/7) | |
| 3639 8645 | 13652 | | 0.81 | 1.3E-01 AP000001.1 | NT | | |
| 3882 8883 | | | 1.37 | 1.3E-01 AL161581.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77 | |
| 3938 5658 | 10663 | | 1.73 | 1.3E-01 AJ277606.1 | NT | Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK | |
| 3938 5658 | 10664 | | 1.73 | 1.3E-01 AJ277606.1 | NT | Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK | |
| 4016 9012 | | | 0.82 | 1.3E-01 AF020713.1 | NT | Bacteriophage SPBc2 complete genome | |
| 4034 9030 | | | 4.19 | 1.3E-01 AW364341.1 | EST_HUMAN | QV3-DT0018-JB1289-036-ad3 D70018 Homo sapiens cDNA | |
| 4042 9038 | 14028 | | 1.79 | 1.3E-01 AF026805.1 | NT | Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds | |
| 4061 9055 | 14042 | | 18.31 | 1.3E-01 AW273741.1 | EST_HUMAN | xJ23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813985 3' | |
| 4187 9180 | | | 1.36 | 1.3E-01 AL163280.2 | NT | Human sapiens chromosome 21 segment HS21 C030 | |
| 4403 9394 | 14378 | | 2.77 | 1.3E-01 BE272339.1 | EST_HUMAN | 601260396F1 NIH MGIC_9 Homo sapiens cDNA clone IMAGE:2990063 5' | |
| 4940 9917 | 14897 | | 1.76 | 1.3E-01 AI432531.1 | EST_HUMAN | It38c10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3' | |
| 382 5457 | 10474 | | 9.01 | 1.2E-01 AI421744.1 | EST_HUMAN | Itf39b02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1 | |
| 421 5079 | | | 1.74 | 1.2E-01 U66912.1 | NT | Dictyostelium discoideum ORF DG1016 gene, partial cds | |
| 543 5577 | | | 2.9 | 1.2E-01 AF03942.1 | NT | Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds | |
| 1358 6355 | 11405 | | 2.5 | 1.2E-01 AU149146.1 | EST_HUMAN | AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001f691 3' | |
| 1358 6355 | 11406 | | 2.5 | 1.2E-01 AU149146.1 | EST_HUMAN | AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001f691 3' | |
| 1364 6361 | | | 3.56 | 1.2E-01 AV73529.1 | EST_HUMAN | AV735249 cda Homo sapiens cDNA clone cdAA-B11 5' | |
| 1477 6474 | | | 1.03 | 1.2E-01 AA897474.1 | EST_HUMAN | al48e09_s1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 | |
| | | | | | | O16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ; | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|---|---|---|
| 1591 | 6587 | 11649 | 1.16 | 1.2E-01 | Q14934 | SWISSPROT | NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFA13) (NF-ATC4) (NF-AT3) |
| 1611 | 6607 | 11671 | 2.24 | 1.2E-01 | AI285402.1 | EST_HUMAN | q163f09_x1_NCI_CGAP_Ese2 Homo sapiens cDNA clone IMAGE:1960533 3' |
| 1731 | 6726 | | 9.87 | 1.2E-01 | X89211.1 | NT | H sapiens DNA for endogenous retroviral like element |
| 1876 | 6885 | | 3.06 | 1.2E-01 | AW449368.1 | EST_HUMAN | U1-H-B13-akt1->10-0-U1_s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3' |
| 2118 | 7098 | 12211 | 2.31 | 1.2E-01 | BF248490.1 | EST_HUMAN | 6018215677F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5' |
| 2514 | 7482 | 12598 | 1.4 | 1.2E-01 | AW996556.1 | EST_HUMAN | QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA |
| 2769 | 7790 | 12812 | 1.4 | 1.2E-01 | U18018.1 | NT | Human E1A enhancer binding protein (E1A-F) mRNA, partial cds as80c9_x1 Barsteed colon HPLR7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:105095 |
| 2832 | 7852 | 12872 | 2.31 | 1.2E-01 | AI720470.1 | EST_HUMAN | 605_RIBOSOMAL PROTEIN L30 (HUMAN); |
| 2864 | 7884 | 12894 | 3.25 | 1.2E-01 | M16364.1 | NT | Human creatine kinase-B mRNA, complete cds |
| 2936 | 7955 | 12973 | 0.9 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3159 | 8175 | 13198 | 1.63 | 1.2E-01 | AW370668.1 | EST_HUMAN | QV1-BT0259-261098-021-d05 BT0259 Homo sapiens cDNA Methanococcus jannaschii section 142 of 150 of the complete genome |
| 3183 | 8199 | | 0.79 | 1.2E-01 | U67600.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3442 | 8450 | 13476 | 0.67 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3442 | 8450 | 13477 | 0.67 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3525 | 8407 | | 0.71 | 1.2E-01 | Z99118.1 | NT | Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540 |
| 4058 | 9052 | 14038 | 1.91 | 1.2E-01 | Z54255.1 | NT | P.clarkii mRNA; repeat region (ID 2mRT7) |
| 4058 | 9052 | 14039 | 1.91 | 1.2E-01 | Z54255.1 | NT | P.clarkii mRNA; repeat region (ID 2mRT7) |
| 4648 | 9633 | | 0.92 | 1.2E-01 | AF221633.1 | NT | Rana ridibunda pituitary adenylylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced |
| 4857 | 9838 | 14811 | 9.45 | 1.2E-01 | BF577357.1 | EST_HUMAN | 602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290165 5' |
| 4937 | 9914 | 14892 | 3.98 | 1.2E-01 | AI163227.2 | NT | Hom sapiens chromosome 21 segment HS21C027 |
| 4937 | 9914 | 14893 | 3.98 | 1.2E-01 | AI163227.2 | NT | Hom sapiens chromosome 21 segment HS21C027 |
| 5057 | 10027 | | 4.85 | 1.2E-01 | Q57599 | SWISSPROT | RIBONUCLEASE HII (RNASE HII) |
| 560 | 5594 | 10694 | 0.74 | 1.1E-01 | AI561003.1 | EST_HUMAN | In18a08_x1_NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3' |
| 611 | 5638 | 10640 | 6.71 | 1.1E-01 | AA569006.1 | EST_HUMAN | nm08g11_s1_NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:4286771 5' |
| 1037 | 6047 | 11077 | 1.16 | 1.1E-01 | BF5897308.1 | EST_HUMAN | HEME OXYGENASE 1 (HUMAN); |
| 1069 | 6077 | | 1.46 | 1.1E-01 | AI161560.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 1141 | 7740 | 11177 | 3.26 | 1.1E-01 | AW972158.1 | EST_T384142 MAGE resequences, MAGI_Homo sapiens cDNA | |
| 1230 | 6229 | 11274 | 1.76 | 1.1E-01 | D64004.1 | NT | Synechocystis sp. PCCE803 complete genome, 23/27, 2868767-3002965 |
| 1488 | 6485 | 11540 | 1.79 | 1.1E-01 | AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5' | AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5' | |
| 2250 | 7227 | | 2.31 | 1.1E-01 | 6755215 | NT | Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2468 | 7707 | | | 1.24 | 1.1E-01 | 6978676 NT | Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA |
| 2782 | 7803 | 12820 | | 1.07 | 1.1E-01 | S82418.1 NT | Interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5] |
| 2963 | 7981 | 12995 | | 0.83 | 1.1E-01 | F03265.1 EST HUMAN | HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf023' |
| 3267 | 8280 | | | 1.57 | 1.1E-01 | 6753231 NT | Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caenca1g), mRNA |
| 3336 | 8346 | 13364 | | 2.75 | 1.1E-01 | BE393186.1 EST HUMAN | Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caenca1g), mRNA |
| 3369 | 8377 | 13397 | | 1.5 | 1.1E-01 | X62135.1 NT | 601308679F1 NIH MGCG_44 Homo sapiens cDNA clone IMAGE:3627056 5' |
| 3411 | 8420 | 13449 | | 1.26 | 1.1E-01 | R96946.1 EST HUMAN | C.reinhardtii nuc ear gene on linkage group XIX |
| 3501 | 8509 | 13523 | | 0.8 | 1.1E-01 | Y07695.1 NT | yq62g08.s1 Socates fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:280414 3' similar to contains Alu repetitive element; |
| 3619 | 8626 | | | 0.84 | 1.1E-01 | P97384 SWISSPROT | A.immersus gene for transposase |
| 3627 | 8634 | 13639 | | 1.44 | 1.1E-01 | X52708.1 NT | ANXIN XI (CALCYCLIN-ASSOCIATED ANXEXIN 50) (CAP-50) |
| 3994 | 8991 | 13975 | | 1.01 | 1.1E-01 | AW819412.1 EST HUMAN | G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5 |
| 3994 | 8991 | 13976 | | 1.01 | 1.1E-01 | AW819412.1 EST HUMAN | MR3-ST0280-230100-025-907 ST0280 Homo sapiens cDNA |
| 4131 | 9126 | | | 9.98 | 1.1E-01 | AF157066.1 NT | MR3-ST0280-230100-025-907 ST0280 Homo sapiens cDNA |
| 4505 | 9495 | 14473 | | 0.96 | 1.1E-01 | S44957.1 NT | Drosophila melanogaster klaricht protein (klar) mRNA, complete cds |
| 4685 | 9670 | 14652 | | 1.09 | 1.1E-01 | Y07695.1 NT | Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7] |
| 4856 | 9837 | | | 0.86 | 1.1E-01 | AW026547.1 EST HUMAN | A.immersus gene for transposase |
| 5002 | 9973 | | | 1 | 1.1E-01 | 8923317 NT | wv4h02-X1 NC1 CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529555 3' |
| 1182 | 6184 | | | 3.86 | 1.0E-01 | O62855 SWISSPROT | Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA |
| 1253 | 6251 | 11292 | | 1.81 | 1.0E-01 | A198549.1 EST HUMAN | DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) |
| 1369 | 6366 | 11415 | | 1.69 | 1.0E-01 | AL161504.2 NT | ws8d01-X1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 |
| 3434 | 8442 | 13468 | | 0.99 | 1.0E-01 | BF033991.1 EST HUMAN | MER7 repetitive element; |
| 3657 | 8643 | 13649 | | 0.87 | 1.0E-01 | BF239818.1 EST HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 |
| 3848 | 8850 | 13858 | | 2.47 | 1.0E-01 | BF365703.1 EST HUMAN | 601456301F1 NIH MGCG_66 Homo sapiens cDNA clone IMAGE:3859849 5' |
| 4283 | 9275 | 14263 | | 1.88 | 1.0E-01 | AE002265.2 NT | 601906448F1 NIH MGCG_54 Homo sapiens cDNA clone IMAGE:4134071 5' |
| 4423 | 9413 | | | 1.85 | 1.0E-01 | AI792349.1 EST HUMAN | QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA |
| 45574 | 95627 | | | 1.74 | 1.0E-01 | U50450.1 NT | Chlamydophila pneumoniae AR39, section 91 of 94 of the complete genome |
| 4767 | 9751 | 14740 | | 2.04 | 1.0E-01 | AW952344.1 EST HUMAN | an32c04_Y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5' |
| 4967 | 9944 | 14921 | | 0.93 | 1.0E-01 | AL163247.2 NT | Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds |
| 5022 | 9993 | | | 3.42 | 1.0E-01 | BE881566.1 EST HUMAN | EST364414 MAGE sequences, MAGB Homo sapiens cDNA |
| 2714 | 7671 | 12784 | | 1.21 | 9.9E-02 | BE54554.1 EST HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 2714 | 7671 | 12785 | | 1.21 | 9.9E-02 | BE54554.1 EST HUMAN | 601490280F1 NIH MGCG_69 Homo sapiens cDNA clone IMAGE:3892842 5' |
| | | | | | | | 601070219F1 NIH MGCG_12 Homo sapiens cDNA clone IMAGE:3456365 5' |
| | | | | | | | 601070219F1 NIH MGCG_12 Homo sapiens cDNA clone IMAGE:3456365 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3192 | 8208 | 13229 | 1.36 | 9.9E-02 | AF099810.1 | NT | Homo sapiens naurexin III-alpha gene, partial cds |
| 559 | 5593 | | 1.41 | 9.8E-02 | X56388.1 | NT | O.sativa RAMy3C gene for alpha-amylase |
| 3072 | 8088 | 13101 | 4.03 | 9.8E-02 | AF184274.1 | NT | Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX-2 allele, complete cds |
| 4102 | 9096 | 14081 | 5.22 | 9.8E-02 | AF257329.1 | NT | Leptospira maculans beta-tubulin mRNA, complete cds |
| 4102 | 9096 | 14082 | 5.22 | 9.8E-02 | AF257329.1 | NT | Leptospira maculans beta-tubulin mRNA, complete cds |
| 1332 | 6330 | 11379 | 1.38 | 9.7E-02 | AB005680.1 | NT | Aloe arborescens mRNA for NADP-malic enzyme, complete cds |
| 1550 | 6547 | | 1.11 | 9.7E-02 | 4503710 | NT | Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 2199 | 7177 | 12300 | 1.44 | 9.7E-02 | BE168660.1 | EST_HUMAN | QV1-HT0516-07_0300-095-804 HT0516 Homo sapiens cDNA |
| 3875 | 8876 | | 3.83 | 9.7E-02 | Q99795 | SWISSPROT | CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33) |
| 1966 | 6951 | 12054 | 0.92 | 9.6E-02 | AI080721.1 | EST_HUMAN | ox247d11x1 Soares_NIHIMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3' |
| 1966 | 6951 | 12055 | 0.92 | 9.6E-02 | AI080721.1 | EST_HUMAN | ox247d11x1 Soares_NIHIMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3' |
| 4219 | 9212 | 14191 | 5.54 | 9.6E-02 | Z32986.2 | NT | Proteus mirabilis fimbrial operon, strain HI4320 |
| 4842 | 9825 | 14800 | 1.16 | 9.6E-02 | AW966230.1 | EST_HUMAN | EST3/8303 MAGE resequences, MAGI Homo sapiens cDNA |
| 4972 | 9948 | 14926 | 0.97 | 9.6E-02 | BE061729.1 | EST_HUMAN | RC5-BT0254-03_1099-011-a03 BT0254 Homo sapiens cDNA |
| 3985 | 8983 | 13969 | 2.27 | 9.5E-02 | AW992395.1 | EST_HUMAN | CM2-BN0023/05/200-087-f12 BN0023 Homo sapiens cDNA |
| 4947 | 9924 | 14902 | 0.93 | 9.5E-02 | U633174.1 | NT | Lycopersicon esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds |
| 1797 | 6788 | 11877 | 2.69 | 9.4E-02 | BF671063.1 | EST_HUMAN | 1G02150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5' |
| 3788 | 8791 | 13796 | 5.14 | 9.4E-02 | Z33059.1 | NT | M.capricolum DNA for CONTIG MC073 |
| 2920 | 7939 | | 1.7 | 9.3E-02 | 4809280 | NT | Homo sapiens BA11-associated protein 3 (BA1AP3) mRNA |
| 2959 | 7978 | | 6.91 | 9.3E-02 | 6912525 | NT | Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA |
| 3182 | 8198 | 13222 | 2.33 | 9.3E-02 | BF75511.1 | EST_HUMAN | 602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5' |
| 4029 | 9025 | 14012 | 3.03 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5' |
| 4029 | 9025 | 14013 | 3.03 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5' |
| 4595 | 9583 | | 2.31 | 9.3E-02 | AV732224.1 | EST_HUMAN | AV732224 HTT: Homo sapiens cDNA clone HTFAUA06 5' |
| 228 | 5291 | 10297 | 7.76 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 228 | 5291 | 10298 | 7.76 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 228 | 5291 | 10299 | 7.76 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 2166 | 7145 | | 3.57 | 9.2E-02 | R54156.1 | EST_HUMAN | 9g8f07.1 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:41618 5' |
| 3106 | 8122 | 13140 | 3.95 | 9.2E-02 | Q28631 | SWISSPROT | MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20) |
| 3233 | 8248 | 13269 | 0.82 | 9.2E-02 | AA534354.1 | EST_HUMAN | nt79e01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:926136 3' |
| 3505 | 8513 | | 1.06 | 9.2E-02 | 6755215 | NT | Mus musculus pre T-cell antigen receptor alpha (Itcra), mRNA |
| 4116 | 9110 | | 0.98 | 9.2E-02 | U92048.1 | NT | Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region |
| 4181 | 9174 | | 0.72 | 9.2E-02 | BE299722.1 | EST_HUMAN | 6009443655F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980776 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4504 | 9494 | 14472 | 1.99 | 9.2E-02 | X96402.1 | NT | G. gallus Mta-Ck gene |
| 420 | 5078 | 10063 | 6.08 | 9.1E-02 | X77665.1 | NT | O. cuniculus K12 keratin gene |
| 3585 | 8592 | | 0.93 | 9.1E-02 | AW372559.1 | EST_HUMAN | PM2-BT039-161239-001-f02 BT0349 Homo sapiens cDNA |
| 4357 | 9348 | 14328 | 1.84 | 9.1E-02 | AL161554.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54 |
| | | | | | | | FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MO/18) (KB CELLS FBP) |
| 735 | 5758 | 10780 | 4.53 | 9.0E-02 | P15328 | SWISSPROT | Inv39g10.X1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element, |
| 1594 | 6590 | 11651 | 5.3 | 9.0E-02 | BE220482.1 | EST_HUMAN | HIV-1 p8c095-16 from USA envelope glycoprotein (env) gene, partial cds |
| 2731 | 7688 | 12802 | 2.97 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c095-16 from USA envelope glycoprotein (env) gene, partial cds |
| 2731 | 7688 | 12803 | 2.97 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c095-16 from USA envelope glycoprotein (env) gene, partial cds |
| 3262 | 8275 | 13299 | 0.76 | 9.0E-02 | AF279135.1 | NT | Dichotostellum discoideum spore coat structural protein SP85 (cotE) gene, complete cds |
| 4175 | 9169 | 14157 | 0.87 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt] |
| 4175 | 9169 | 14158 | 0.87 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Salmin sciurus=squirrel monkeys, liver, mRNA, 1474 nt] |
| 4294 | 9286 | 14274 | 0.91 | 9.0E-02 | P55268 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) |
| 4533 | 9523 | 14510 | 2.08 | 9.0E-02 | X65740.2 | NT | Plasmidium falciparum P-type ATPase 3 gene |
| 5028 | 9999 | 14972 | 1.01 | 9.0E-02 | Q24597 | SWISSPROT | REGULATOR PROTEIN ZESTE |
| 1411 | 6409 | 11467 | 1.4 | 8.9E-02 | BF701593.1 | EST_HUMAN | 6021290301F2 NIH_MCG_56 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 1411 | 6409 | 11468 | 1.4 | 8.9E-02 | BF701593.1 | EST_HUMAN | 6021290301F2 NIH_MCG_56 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 4076 | 9070 | | 2.28 | 8.9E-02 | AF286055.1 | NT | Atrichum argutatum AtranFlc2 protein (AtranFlc2) gene, partial cds |
| 1355 | 6352 | 11402 | 1.5 | 8.8E-02 | Q27474 | SWISSPROT | PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATPI]) |
| 3807 | 8810 | 13816 | 1.16 | 8.8E-02 | AA289128.1 | EST_HUMAN | EST11595 Uterus Homo sapiens cDNA 5' end |
| 3924 | 8924 | | 3.83 | 8.8E-02 | O00268 | SWISSPROT | TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII-130) |
| 1608 | 6604 | 11667 | 1.11 | 8.7E-02 | AI167281.1 | EST_HUMAN | ox65b01.s1_Scares_NhiIMPu_S1 Homo sapiens cDNA clone IMAGE:1661161 3' |
| 3610 | 8617 | 13626 | 4.63 | 8.7E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ280RF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 3610 | 8617 | 13627 | 4.63 | 8.7E-02 | U82695.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ280RF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 4568 | 9556 | 14544 | 1.24 | 8.7E-02 | AF178636.1 | NT | Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds |
| 4929 | 9908 | | 1.08 | 8.7E-02 | AE000895.1 | NT | Methanobacterium thermophilicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome |

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Table 4

Single Exon Probes Expressed in TBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1233 | 6231 | 11275 | 6.22 | 8.6E-02 | AJ271736.1 | NT | Homo sapiens X1 pseudoeukaryosomal region; segment 2/2 |
| 2182 | 7161 | 12281 | 1.3 | 8.6E-02 | BE408667.1 | EST_HUMAN | G013040167-1 NIH MGIC_21 Homo sapiens cDNA clone IMAGE:3638643 5' |
| 3114 | 8130 | 13149 | 3.35 | 8.6E-02 | LO5468.1 | NT | Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds |
| 3559 | 8566 | | 3.97 | 8.6E-02 | AF153362.1 | NT | Dichotomium discolatum adenylyl cyclase (acrA) gene, complete cds |
| 2333 | 7307 | 12428 | 1.85 | 8.5E-02 | AE000652.1 | NT | Helicobacter pylori 26695 section 130 of 134 of the complete genome |
| 2596 | 7776 | 12674 | 3.69 | 8.4E-02 | W69330.1 | EST_HUMAN | Zd44e11.1r1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:343532 5' |
| 4228 | 9222 | 14202 | 0.99 | 8.4E-02 | AF257213.1 | NT | Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds |
| 4228 | 9222 | 14203 | 0.99 | 8.4E-02 | AF257213.1 | NT | Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds |
| 3512 | 8520 | 13532 | 5.85 | 8.3E-02 | P75334 | SWISSPROT | HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR |
| 4559 | 9547 | 14532 | 0.83 | 8.3E-02 | AB039490.1 | NT | Homo sapiens gene for fululin, complete cds |
| 1360 | 6357 | | 6.17 | 8.2E-02 | Y08170.2 | NT | Gallicus gallus mRNA for OBCAM protein gamma isoform |
| 1465 | 6462 | 11521 | 2.51 | 8.2E-02 | AF167077.2 | NT | Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds |
| 3000 | 8018 | | 2.44 | 8.2E-02 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 3713 | 8717 | | 1.37 | 8.2E-02 | AL161498.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 3901 | 8901 | 13899 | 1.16 | 8.2E-02 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 4161 | 9156 | 14139 | 5.75 | 8.2E-02 | P48960 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4161 | 9156 | 14140 | 5.75 | 8.2E-02 | P48960 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4161 | 9156 | 14141 | 5.75 | 8.2E-02 | P48960 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4909 | 9888 | 14861 | 3.34 | 8.2E-02 | U76009.1 | NT | Mus musculus zinc transporter (ZnT-3) gene, complete cds |
| 5027 | 9998 | 14971 | 1.29 | 8.2E-02 | AU119830.1 | EST_HUMAN | AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5' |
| 1464 | 6461 | 11520 | 1.06 | 8.1E-02 | AB017138.1 | NT | Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdCH, mdCL and mdCM genes), complete cds |
| 5062 | 10031 | 14999 | 1.05 | 8.1E-02 | AE004673.1 | NT | Pseudomonas aeruginosa PA01, section 234 of 529 of the complete genome |
| 6 | 7711 | 10072 | 4.12 | 8.0E-02 | AW954653.1 | EST_HUMAN | EST366723 MAGE resequences, MGAC Homo sapiens cDNA |
| 1659 | 7752 | 11728 | 9.29 | 8.0E-02 | D26535.1 | NT | Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15) |
| 1659 | 7752 | 11729 | 9.29 | 8.0E-02 | D26535.1 | NT | Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15) |
| 1862 | 6851 | 11939 | 2.81 | 8.0E-02 | BE067219.1 | EST_HUMAN | PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA |
| 2400 | 7371 | | 2.75 | 8.0E-02 | BF246744.1 | EST_HUMAN | 601855548F1 NIH MGIC_57 Homo sapiens cDNA clone IMAGE:4075619 5' |
| 2830 | 7850 | 12869 | 0.67 | 8.0E-02 | AL445067.1 | NT | Thermoplasma acidophilum complete genome; segment 5/5 |
| 3726 | 8730 | 13728 | 0.73 | 8.0E-02 | AW966118.1 | EST_HUMAN | EST378191 MAGE resequences, MAGI Homo sapiens cDNA |
| 3958 | 8956 | | 0.76 | 8.0E-02 | 4503034 | NT | Homo sapiens cAMP responsive element binding protein-like 2 (CREBBL2) mRNA |
| 4631 | 9616 | 14607 | 1.25 | 8.0E-02 | AJ434202.1 | EST_HUMAN | I31g12,X1 NC CGAP Gαs4 Homo sapiens cDNA clone IMAGE:2132114 3' |
| 4669 | 9654 | | 7.08 | 8.0E-02 | X72794.1 | NT | M.musculus gene for gelatinase B |
| 5060 | 5939 | 10971 | 0.67 | 8.0E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 2109 | 7089 | 12203 | 2.54 | 7.9E-02 | BE250008.1 | EST_HUMAN | 600943191F NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5' arg98c08_x1 Bertrand colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173648 3' similar to gb:7226876 |
| 2910 | 7929 | 12948 | 11.99 | 7.9E-02 | AI582029.1 | EST_HUMAN | 605 RIBOSOMAL PROTEIN L38 (HUMAN); |
| 3760 | 8763 | 131763 | 5.05 | 7.9E-02 | 6681044 NT | Mus musculus colony stimulating factor 1 receptor (Csf1), mRNA | |
| 3760 | 8763 | 13764 | 5.05 | 7.9E-02 | 6681044 NT | Mus musculus colony stimulating factor 1 receptor (Csf1), mRNA | |
| 4666 | 9651 | | 1.4 | 7.9E-02 | AB008019.1 | NT | Arabidopsis thaliana RXW24L mRNA, partial cds |
| 1191 | 6192 | 11228 | 1.59 | 7.8E-02 | AI793275.1 | EST_HUMAN | oc59d02_v5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.3 L1 repetitive element; |
| 1191 | 6192 | 11229 | 1.59 | 7.8E-02 | AI793275.1 | EST_HUMAN | oc59d02_v5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.3 L1 repetitive element; |
| 2332 | 7306 | 12426 | 1 | 7.8E-02 | AF221942.1 | NT | Sus scrofa telomerase RNA pseudogene |
| 2332 | 7306 | 12427 | 1 | 7.8E-02 | AF221942.1 | NT | Sus scrofa telomerase RNA pseudogene |
| 3663 | 8668 | | 1.25 | 7.8E-02 | BE250048.1 | EST_HUMAN | 600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5' |
| 4914 | 8668 | | 3.15 | 7.8E-02 | BE250048.1 | EST_HUMAN | 600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5' |
| 5066 | 10035 | 15002 | 1.02 | 7.8E-02 | AI148520.1 | EST_HUMAN | tg48g12x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.1S MEF10 repetitive element; |
| 3506 | 8514 | | 2.61 | 7.7E-02 | AJ238093.1 | NT | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| 3303 | 8314 | 13340 | 2.57 | 7.6E-02 | BE514432.1 | EST_HUMAN | 601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5' |
| 3324 | 8334 | 13354 | 0.82 | 7.6E-02 | AA286447.1 | EST_HUMAN | EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43 |
| 776 | 5798 | 10826 | 1.86 | 7.5E-02 | 5902093 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA |
| 776 | 5798 | 10827 | 1.86 | 7.5E-02 | 5902093 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA |
| 1877 | 6866 | 11954 | 1.15 | 7.5E-02 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 4377 | 9368 | 14348 | 0.92 | 7.5E-02 | AB015961.1 | NT | Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2 |
| 474 | 5510 | 10523 | 1.1 | 7.4E-02 | AW838547.1 | EST_HUMAN | RC5_LT0054-260100-011-H09_LT0054 Homo sapiens cDNA |
| 3514 | 8622 | 13533 | 0.77 | 7.4E-02 | AI807885.1 | EST_HUMAN | wf43n01_X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358885 3' |
| 4566 | 9554 | 14541 | 1.18 | 7.4E-02 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 4650 | 9635 | 14628 | 2.97 | 7.4E-02 | 6978442 | NT | Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA |
| 4784 | 9768 | 14752 | 1.75 | 7.4E-02 | 6678492 | NT | Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchtp), mRNA |
| 466 | 5503 | 10514 | 1.23 | 7.3E-02 | BE94961.2 | EST_HUMAN | 601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888209 3' |
| 466 | 5503 | 10515 | 1.23 | 7.3E-02 | BE964961.2 | EST_HUMAN | 601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888209 3' |
| 676 | 5701 | 10709 | 3.86 | 7.3E-02 | AE001789.1 | NT | Thermatoga maritima section 101 of 138 of the complete genome |
| 1450 | 7748 | 11508 | 2.33 | 7.3E-02 | AW900281.1 | EST_HUMAN | CN0-NN1004-130300-284-q08 NN1004 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 1808 | 7756 | | | 11.5 | 7.3E-02 AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 4838 | 9822 | | | 1.14 | 7.3E-02 U12283.1 | NT | Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds |
| 120 | 5190 | 10202 | 1.2 | 7.2E-02 AE000882.1 | NT | Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome | |
| 120 | 5190 | 10203 | 1.2 | 7.2E-02 AE000882.1 | NT | Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome | |
| 1446 | 6443 | 11501 | 1.67 | 7.2E-02 AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 | |
| 1446 | 6443 | 11502 | 1.67 | 7.2E-02 AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 | |
| 2478 | 7447 | | | 1.86 | 7.2E-02 U14794.1 | NT | Human immunodeficiency virus type 1 Isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds |
| 3791 | 8794 | 13759 | 1.62 | 7.2E-02 AW298322.1 | EST_HUMAN | U1-H-BW0- gj-4-0-U1..s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3' | |
| 4220 | 9213 | 14192 | 5.17 | 7.2E-02 BF572307.1 | EST_HUMAN | 602077737F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5' | |
| 1863 | 6852 | 11940 | 1.58 | 7.1E-02 L02290.1 | NT | Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds | |
| 2225 | 7202 | | 1.06 | 7.1E-02 AE004890.1 | NT | Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome | |
| 2230 | 7207 | 12322 | 5.78 | 7.1E-02 BF208802.1 | EST_HUMAN | 6018722BF1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:2823921 5' similar to gb:X52851_ma1 | |
| | | | | | | ba10b05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823921 5' similar to gb:X52803 Mouse mRNA for cyclophilin PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); gb:X52803 Mouse mRNA for cyclophilin (MOUSE); | |
| 4997 | 9969 | 14946 | 1.09 | 7.1E-02 BE208576.1 | EST_HUMAN | COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR | |
| 524 | 5559 | 10562 | 1.16 | 7.0E-02 Q07092 | SWISSPROT | M.artellia Milt-1 gene | |
| 1470 | 6467 | | 0.92 | 7.0E-02 X96677.1 | NT | Z166104.s1 Stratogene colon (#837204) Homo sapiens cDNA clone IMAGE:509599 3' | |
| 1724 | 6719 | 11797 | 1.17 | 7.0E-02 AA056342.1 | EST_HUMAN | U1-H-B11- acy-1-07-0-U1..s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S | |
| 2960 | 7979 | 12983 | 2.25 | 7.0E-02 AW138152.1 | EST_HUMAN | al66a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S | |
| 3802 | 8805 | 13810 | 0.82 | 7.0E-02 AA815438.1 | EST_HUMAN | RIBOSOMAL PROTEIN L32 (HUMAN); | |
| 3931 | 8931 | 13922 | 1.07 | 7.0E-02 BE070264.1 | EST_HUMAN | QV4-BT0407-280100-09-010_B10407 Homo sapiens cDNA CM0-LJM001-060300-270- e12 UM0001 Homo sapiens cDNA | |
| 4017 | 9013 | | 0.96 | 7.0E-02 AW792962.1 | EST_HUMAN | CM0-LJM001-060300-270- e12 UM0001 Homo sapiens cDNA CM0-LJM001-060300-270- e12 UM0001 Homo sapiens cDNA | |
| 4093 | 9087 | 14076 | 1.2 | 7.0E-02 AF077821.1 | NT | Canis familiaris Inducible nitric oxide synthase mRNA, complete cds | |
| 4773 | 9757 | 14745 | 7.8 | 7.0E-02 BF381987.1 | EST_HUMAN | 601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5' | |
| 510 | 5545 | 10548 | 17.58 | 6.9E-02 AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 | |
| 510 | 5545 | 10549 | 17.58 | 6.9E-02 AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 | |
| 1313 | 6310 | | 1.29 | 6.9E-02 4507968 | NT | Homo sapiens regulator of G _z -selective protein signalling (ZGAP1) mRNA, and translated products | |
| 3703 | 8707 | 13709 | 1.03 | 6.9E-02 Q06364 | SWISSPROT | 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) | |

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Table 4

Single Exon Probes Expressed In HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3703 | 8707 | 13710 | 1.03 | 6.9E-02 | Q06384 | SWISSPROT | 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) aa30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 |
| 1843 | 6833 | 119220 | 1.06 | 6.8E-02 | AA496759.1 | EST_HUMAN | MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); aa30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 |
| 1843 | 6833 | 11921 | 1.06 | 6.8E-02 | AA496759.1 | EST_HUMAN | MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds |
| 1865 | 6854 | 11942 | 3.07 | 6.8E-02 | AF156673.1 | NT | Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds |
| 3027 | 8044 | 13053 | 1.01 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a06.s1 Soares testis NT Homo sapiens cDNA clone 1376626 3' |
| 3027 | 8044 | 13054 | 1.01 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a06.s1 Soares testis NT Homo sapiens cDNA clone 1376626 3' |
| 3027 | 8044 | 13055 | 1.01 | 6.8E-02 | AA781996.1 | EST_HUMAN | ai75a06.s1 Soares testis NT Homo sapiens cDNA clone 1376626 3' |
| 1497 | 6495 | | 1.66 | 6.7E-02 | AF115536.1 | NT | Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP101 allele, complete cds |
| 1854 | 6843 | 11931 | 1.32 | 6.7E-02 | A1220285.1 | EST_HUMAN | qq79e04.x1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3' |
| 3635 | 8641 | 13646 | 4.56 | 6.7E-02 | P17278 | SWISSPROT | HOMEobox PROTEIN HOX-D4 (CHO-X-A) |
| 1330 | 6328 | 11376 | 1.14 | 6.6E-02 | A1735509.1 | EST_HUMAN | at12e9.x1 Barsleid aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SWI:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG ; |
| 1352 | 6349 | 11399 | 0.98 | 6.6E-02 | AF245116.1 | NT | Drosophila melanogaster cactin mRNA, complete cds |
| 2117 | 7097 | 12210 | 1.74 | 6.6E-02 | A1289241.1 | NT | Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts |
| 3382 | 8390 | 13413 | 9.7 | 6.6E-02 | R64306.1 | EST_HUMAN | yifBb10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3' |
| 3398 | 8406 | 13432 | 2.63 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 3398 | 8406 | 13433 | 2.63 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 3965 | 8963 | 13653 | 1.53 | 6.6E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 4819 | 9803 | 14783 | 9.95 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-1-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 4819 | 9803 | 14784 | 9.95 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-1-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 577 | 5609 | 10608 | 2 | 6.5E-02 | BFG027639.1 | EST_HUMAN | 601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5' |
| 972 | 5988 | 11022 | 3.15 | 6.5E-02 | 7706068 | NT | Homo sapiens E2F-like protein (LOC51270), mRNA |
| 1368 | 6365 | 11414 | 2.48 | 6.5E-02 | U47624.1 | NT | Xenopus laevis: alpha(E)-catenin mRNA, complete cds |
| 1697 | 6692 | 11768 | 1.65 | 6.5E-02 | AE000764.1 | NT | Aequifex aeolicus section 96 of 109 of the complete genome |
| 570 | 5603 | 10601 | 1.52 | 6.4E-02 | X84549.1 | NT | A carterae precursor of peridinin-chlorophyll-a-protein (PCP) gene |
| 1695 | 6650 | 11765 | 0.96 | 6.4E-02 | AE001777.1 | NT | Thermologos maritima section 89 of 136 of the complete genome |
| 1695 | 6650 | 11766 | 0.96 | 6.4E-02 | AE001777.1 | NT | Thermologos maritima section 89 of 136 of the complete genome |
| 2946 | 7985 | 12984 | 1.88 | 6.4E-02 | 6996923 | NT | Mus musculus histone deacetylase 5 (Hdac5), mRNA |
| 4928 | 9805 | 14883 | 1.21 | 6.4E-02 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 1716 | 6711 | 11788 | 2.39 | 6.3E-02 | AF109905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |

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 Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3523 | 8530 | | 2.55 | 6.3E-02 | P37092 | SWISSPROT | HEAT SHOCK PROTEIN 70 HOMOLOG |
| 4129 | 9124 | 14108 | 3.54 | 6.2E-02 | AL161572.2 | NT | Arabidopsis thaliana DNA chromosome 4 contig fragment No. 68 |
| 4212 | 9205 | | 1 | 6.2E-02 | AF271235.1 | NT | Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds |
| 4450 | 9440 | | 5.98 | 6.2E-02 | Q62191 | SWISSPROT | 52 KD ROPROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO52) |
| 5016 | 9987 | 14963 | 1.58 | 6.2E-02 | R59526.1 | EST_HUMAN | ys97a12.s1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41477 3' similar to gb:Y57198_cds1 |
| 254 | 5314 | 10324 | 3.36 | 6.1E-02 | D16471.1 | NT | TRANSCRIPTION ELONGATION FACTOR S-II (HUMAN); Human mRNA, Xq terminal portion |
| 3895 | 8886 | | 2.17 | 6.1E-02 | U73325.1 | NT | Arabidopsis thaliana K+ inward rectifying channel protein (AKCC1) gene, complete cds |
| 5000 | 9971 | 14947 | 0.92 | 6.1E-02 | Y12803.1 | NT | S.scofa mRNA for Man9-mannosidase |
| 5018 | 9998 | | 1.37 | 6.1E-02 | A1220330.1 | EST_HUMAN | qgg90e08.X1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842470 3' |
| 1243 | 6241 | 11282 | 0.88 | 6.0E-02 | AE001777.1 | NT | Thermotoga maritima section 89 of 136 of the complete genome |
| 2700 | 7657 | | 2.19 | 6.0E-02 | AB031289.1 | NT | Mesocestidae: corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2 |
| 2866 | 5173 | 10183 | 0.91 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04..11 Stralagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5' |
| 2866 | 5173 | 10184 | 0.91 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04..11 Stralagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5' |
| 3158 | 8174 | 13196 | 1.62 | 6.0E-02 | AA317237.1 | EST_HUMAN | EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3158 | 8174 | 13197 | 1.62 | 6.0E-02 | AA317237.1 | EST_HUMAN | EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3549 | 8556 | | 2.87 | 6.0E-02 | BE964443.2 | EST_HUMAN | 601658150R1 NIH MGIC_88 Homo sapiens cDNA clone IMAGE:3876060 3' |
| 229 | 5292 | 10300 | 6.97 | 5.9E-02 | AW934719.1 | EST_HUMAN | RC1-DT0001-280100-012-e10 DT0001 Homo sapiens cDNA |
| 2914 | 7933 | 12952 | 2.79 | 5.9E-02 | AF190269.1 | NT | Mus musculus: p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced |
| 920 | 5936 | | 3.97 | 5.8E-02 | D90110.1 | NT | Thiobacillus ferrooxidans merC, merA genes and URF-1 |
| 1620 | 6617 | 11683 | 2.52 | 5.8E-02 | Q61768 | SWISSPROT | KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) |
| 2789 | 7810 | | 0.94 | 5.8E-02 | AJ223621.1 | NT | Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5 |
| 3579 | 8586 | 13591 | 1.8 | 5.8E-02 | AE001775.1 | NT | Thermotoga maritima section 87 of 136 of the complete genome |
| 4229 | 9223 | 14204 | 5.55 | 5.8E-02 | AW051927.1 | EST_HUMAN | wx24c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| 4229 | 9223 | 14205 | 5.55 | 5.8E-02 | AW051927.1 | EST_HUMAN | qh56f01.x1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); qh56f01.x1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to |
| 4416 | 9408 | 14392 | 4.67 | 5.8E-02 | A1247505.1 | EST_HUMAN | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |
| 4416 | 9408 | 14393 | 4.67 | 5.8E-02 | A1247505.1 | EST_HUMAN | gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| 4441 | 9431 | | 2.28 | 5.8E-02 | AF086264.1 | NT | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |
| 4892 | 9984 | 14842 | 4.11 | 5.8E-02 | 7657006 | NT | Homo sapiens dual adaptor of phosphotyrosine and 3'-phosphoinositides (DAPP1), mRNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2983 | 8001 | 13013 | 1.08 | 5.7E-02 | AJ081644.1 | EST_HUMAN | out63b05.s1 NC1 CGAP_B1/2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 |
| 2988 | 8016 | 13029 | 1.11 | 5.7E-02 | AF119117.1 | NT | Homo sapiens clozapine transporter (SLC6A3) gene, complete cds |
| 3625 | 8632 | | | 1.02 | 5.7E-02 | AF001292.1 | Chironomus thummi thummi globin VIIa.1 (ctt-7A.1), globin 8.1 (ctt-8.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-3RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds |
| 3712 | 8716 | 13718 | 2.21 | 5.7E-02 | AW966791.1 | EST_HUMAN | EST378865 MAGE resequences, MAGI Homo sapiens cDNA |
| 4546 | 9535 | | | 1.05 | 5.7E-02 | M95099.1 | Bos taurus lysozyme gene (cow 3), complete cds |
| 1495 | 6493 | 11548 | 1.7 | 5.6E-02 | AF094455.1 | NT | Hydrocotyle rotundifolia ribosomal protein L16 (rp116) gene, Intron; chloroplast product |
| 2226 | 7203 | | | 1.01 | 5.6E-02 | BE904308.1 | EST_HUMAN |
| 4506 | 9496 | 14474 | 1.56 | 5.6E-02 | AB013100.1 | NT | Lycopersicon esculentum LE-AC56 mRNA for 1-aminoacyclopropane-1-carboxylate synthase, complete cds |
| 4557 | 9545 | 14530 | 0.84 | 5.6E-02 | AA290599.1 | EST_HUMAN | zg45c01.s1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416.3 |
| 2583 | 7546 | 12660 | 4.77 | 5.5E-02 | X97869.1 | NT | H.sapiens gene encoding La autoantigen |
| 3143 | 8159 | 13181 | 3.85 | 5.5E-02 | 8755501 | NT | Mus musculus SH3 domain protein FB (Sh3d1B), mRNA |
| 4095 | 9089 | 14077 | 1.04 | 5.5E-02 | L41561.1 | NT | Gallid herpesvirus mRNA fragment |
| 1270 | 6268 | | | 0.75 | 5.4E-02 | AF157623.1 | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |
| 2953 | 7972 | | | 0.93 | 5.4E-02 | AJ277468.1 | Oryza sativa ribb3-1 gene for putative Bowman Birky trypsin inhibitor |
| 3337 | 10056 | | | 6.65 | 5.4E-02 | BE073468.1 | RC5-BT0589-/40200-012-C03 BT0559 Homo sapiens cDNA |
| 1036 | 6046 | 11075 | 1.48 | 5.3E-02 | AW391248.1 | EST_HUMAN | QV0-ST0213-i021299-062-a09 ST0213 Homo sapiens cDNA |
| 1036 | 6046 | 11076 | 1.48 | 5.3E-02 | AW391248.1 | EST_HUMAN | QV0-ST0213-i021299-062-a09 ST0213 Homo sapiens cDNA |
| 1476 | 6473 | 11531 | 7.24 | 5.3E-02 | T94759.1 | EST_HUMAN | ye37f12.1 Stratogene lung (#937210) Homo sapiens cDNA clone IMAGE:119851 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DP(1) ALPHA CHAIN (HUMAN); |
| 2124 | 7395 | 12516 | 1.9 | 5.3E-02 | AJ276408.1 | NT | Pseudomonas putida ttgS gene |
| 2872 | 7891 | 12913 | 0.82 | 5.3E-02 | M58417.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 2872 | 7891 | 12914 | 0.82 | 5.3E-02 | M58417.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 3079 | 8095 | 13109 | 4.71 | 5.3E-02 | AJ276408.1 | NT | Pseudomonas putida ttgS gene |
| 4916 | 9894 | 14868 | 9.18 | 5.3E-02 | M80463.1 | NT | Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds |
| 2221 | 7198 | | | 56.99 | 5.2E-02 | 5031908 | Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEPA1) mRNA |
| 3040 | 8057 | 13065 | 2.21 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 3040 | 8057 | 13066 | 2.21 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 4156 | 9151 | 14133 | 3.13 | 5.2E-02 | U07132.1 | NT | Human steroid hormone receptor Nef-1 mRNA, complete cds |
| 2303 | 7278 | | | 0.96 | 5.1E-02 | AL134071.1 | DKFZp547D073_1 547 (synonym: hifr1) Homo sapiens cDNA clone DKFZp547D073_5' |
| 4845 | 9827 | | | 0.91 | 5.1E-02 | AB031740.1 | Homo sapiens PBL gene for salivary proline-rich protein P-B, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 479 | 5516 | 10526 | 1.87 | 5.0E-02 | AF098004.1 | NT | Mus musculus fatty acid amide hydrolase gene, exon 10 |
| 1185 | 6186 | 11223 | 12.26 | 5.0E-02 | Z99104.1 | NT | Bacillus subtilis complete genome (section 1 of 21) from 1 to 213080 |
| 1944 | 6930 | 12029 | 2.86 | 5.0E-02 | P02810 | SWISSPROT | SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR OR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C] |
| 2746 | 5987 | 11021 | 1.3 | 5.0E-02 | U72742.1 | NT | Oncotilagus curicus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds |
| 3263 | 8276 | | 1.24 | 5.0E-02 | 7305610 | NT | Mus musculus Unc-51 like kinase 2 (C. elegans) (ULK2), mRNA |
| 3515 | 8523 | | 1.04 | 5.0E-02 | U32782.1 | NT | Haemophilus influenzae Rd section 97 of 163 of the complete genome |
| 3600 | 8607 | 13615 | 7.06 | 5.0E-02 | U12769.2 | NT | Antheraea pernisi period clock protein homolog mRNA, complete cds |
| 223 | 5285 | | 30.11 | 4.9E-02 | M14230.1 | NT | Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds |
| 368 | 5417 | 10431 | 2.47 | 4.9E-02 | AF275948.1 | NT | Hom sapiens ABCA1 (ABCA1) gene, complete cds |
| 368 | 5417 | 10432 | 2.47 | 4.9E-02 | AF275948.1 | NT | Hom sapiens ABCA1 (ABCA1) gene, complete cds |
| 2803 | 7823 | 12838 | 0.89 | 4.9E-02 | U32636.1 | NT | Zea mays phytene synthase (Y1) gene, complete cds |
| 3217 | 8232 | 13253 | 1.52 | 4.9E-02 | P54258 | SWISSPROT | ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN) |
| 3480 | 8498 | | 2.64 | 4.9E-02 | AA188940.1 | EST_HUMAN | zeta48a12_s1 Strategene hNT neuron (#37233) Homo sapiens cDNA clone IMAGE:6329263' similar to zeta48a12_s1 Strategene hNT neuron (#37233) Homo sapiens cDNA clone IMAGE:6329263' similar to |
| 3511 | 8519 | 13530 | 0.71 | 4.9E-02 | AA400914.1 | EST_HUMAN | contains Alu repetitive element; contains element M8R1 repetitive element; contains Alu repetitive element; contains element M8R1 repetitive element; Zf78a03_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428_3' |
| 3511 | 8519 | 13531 | 0.71 | 4.9E-02 | AA400914.1 | EST_HUMAN | Zf78a03_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428_3' |
| 4692 | 9677 | 14660 | 2.02 | 4.9E-02 | AW167821.1 | EST_HUMAN | xg56g10_x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:26323386_3' |
| 4692 | 9677 | 14661 | 2.02 | 4.9E-02 | AW167821.1 | EST_HUMAN | xg56g10_x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:26323386_3' |
| 3283 | 5381 | 10390 | 1.13 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 329 | 5381 | 10390 | 2.65 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 485 | 5522 | 10531 | 8.84 | 4.8E-02 | AF003100.1 | NT | Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds |
| 2211 | 7188 | 12309 | 1.27 | 4.8E-02 | W51983.1 | EST_HUMAN | zc49b02_s1 Soares, senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611_3' similar to |
| 3136 | 8152 | 13175 | 2.05 | 4.8E-02 | X17144.1 | NT | gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN); Tetrahymena rostrata histone H3II and histone H4II intergenic DNA |
| 268 | 5327 | 10338 | 1.22 | 4.6E-02 | BE153583.1 | EST_HUMAN | PM0-HT0339-251199-003-q05 HT0339 Homo sapiens cDNA |
| 730 | 5753 | 10774 | 2.86 | 4.6E-02 | AE000445.1 | NT | Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome |
| 1273 | 6271 | | 0.71 | 4.6E-02 | AI014255.1 | EST_HUMAN | am50d02_s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979_3' similar to TR:R80533 |
| 1342 | 6339 | 11390 | 2.41 | 4.6E-02 | AV727059.1 | EST_HUMAN | P90533 LIMA; contains element LTR1 repetitive element; AV727059 HTC Homo sapiens cDNA clone HTCBW0015' |
| 2418 | 7389 | 12509 | 2.09 | 4.6E-02 | AW236023.1 | EST_HUMAN | xn24f03_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653_3' similar to SW:GRF1_HUMAN |
| 2736 | 5327 | 10338 | 2.38 | 4.6E-02 | BE153583.1 | EST_HUMAN | Q12849 G-RICH SEQUENCE FACTOR-1; PM0-HT0339-251199-003-q05 HT0339 Homo sapiens cDNA |
| 3416 | 7958 | 12976 | 0.76 | 4.6E-02 | BE153583.1 | EST_HUMAN | PM0-HT0339-251199-003-q05 HT0339 Homo sapiens cDNA |

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 Table 4
 Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4004 | 9000 | | | 0.86 | 4.6E-02 AF220365.1 | NT | Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds |
| 444 | 5481 | 10499 | | 1.67 | 4.5E-02 P22448 | SWISSPROT | RETINOIC ACID RECEPTOR BETA (RAR-BETA) |
| 1199 | 6200 | 11236 | | 0.81 | 4.5E-02 AF005730.1 | NT | Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 1199 | 6200 | 11237 | | 0.81 | 4.5E-02 AF005730.1 | NT | Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 1769 | 6760 | 11847 | | 4.15 | 4.5E-02 P32182 | SWISSPROT | HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B) |
| 2051 | 7033 | 12145 | | 2.17 | 4.5E-02 AE03964.1 | NT | Xylella fastidiosa, section 110 of 229 of the complete genome |
| 3640 | 8646 | 13653 | | 3.82 | 4.5E-02 AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 219 | 5282 | | | 3.85 | 4.4E-02 BE97273.1 | EST_HUMAN | 601652154F1_NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5' |
| 2039 | 7022 | | | 3.33 | 4.4E-02 P31568 | SWISSPROT | HYPOTHETICAL PROTEIN (ORF 2280) |
| 2419 | 7390 | 12510 | | 1.11 | 4.4E-02 AW875475.1 | EST_HUMAN | QY2-P10012-010300-070-902 PT0012_Homo sapiens cDNA |
| 3555 | 8562 | 13568 | | 1.81 | 4.4E-02 AF159160.1 | NT | Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds |
| 4493 | 9483 | 14461 | | 0.99 | 4.4E-02 AF109907.1 | NT | Homo sapiens i3164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 4493 | 9483 | 14462 | | 0.99 | 4.4E-02 AF109907.1 | NT | Homo sapiens i3164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 772 | 5794 | 10522 | | 6.82 | 4.3E-02 AF003249.1 | NT | Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 3345 | 8354 | 13372 | | 8.44 | 4.3E-02 AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3575 | 8582 | | | 1.23 | 4.3E-02 AF0650568.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 812 | 5833 | 10866 | | 1.73 | 4.2E-02 AU123327.1 | EST_HUMAN | AU123327 NT:2RM2_Homo sapiens cDNA clone N2RM2/2000020 5' |
| 855 | 5874 | | | 1.9 | 4.2E-02 AU123327.1 | EST_HUMAN | AU123327 NT:2RM2_Homo sapiens cDNA clone N2RM2/2000020 5' |
| 885 | 5903 | 10944 | | 1.49 | 4.2E-02 AW003645.1 | EST_HUMAN | wx34g01.x1 NCL CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 |
| 1682 | 6678 | | | 2.39 | 4.2E-02 AL445066.1 | NT | L1 RETROPOSON ORF2 mRNA, contains L1.13 L1.1 repetitive element; Thermoplasma acidophilum complete genome; segment 4/5 |
| 3580 | 8587 | 13592 | | 1.51 | 4.2E-02 P23091 | SWISSPROT | TRANSFORMING PROTEIN MAF |
| 4600 | 9588 | 14575 | | 3.38 | 4.2E-02 BF342995.1 | EST_HUMAN | 602017105F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5' |
| 2605 | 7567 | 12682 | | 1.08 | 4.1E-02 AE002330.2 | NT | Chlamydia muridarum, section 60 of 85 of the complete genome |
| 4347 | 9338 | | | 8.04 | 4.1E-02 AW893484.1 | EST_HUMAN | QV1-NN0012-180400-164-106 NN0012_Homo sapiens cDNA |
| 4954 | 9931 | | | 0.67 | 4.1E-02 X85880.1 | NT | L monocytogenes type 3 partial lyp gene (strain 443) |
| 1603 | 6599 | 11660 | | 0.9 | 4.0E-02 AI675392.1 | EST_HUMAN | wb98h01.x1 NCL CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2313745.3' |
| 3170 | 8186 | 13207 | | 3.01 | 4.0E-02 AB040904.1 | NT | Homo sapiens mRNA for KIAA1471 protein, partial cds |
| 1103 | 6110 | 11141 | | 3.41 | 3.9E-02 BF516149.1 | EST_HUMAN | U1-H-BW1-mac-rH-08-0-U1_s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3' |
| 1326 | 6324 | 11371 | | 1.9 | 3.9E-02 P41047 | SWISSPROT | FAS ANTIGEN LIGAND |
| 1921 | 6907 | 12001 | | 1.85 | 3.9E-02 AJ403386.1 | NT | M.musculus DNA for desmin binding fragment DesD7 |

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Table 4

Single Exon Probes Expressed In HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| | | | | | | | Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA |
| 2632 | 7592 | | | 1.51 | 3.9E-02 | 4506862 NT | LAMININ ALPH _A -1 CHAIN PRECURSOR (LAMININ A CHAIN) mRNA |
| 977 | 5992 | 11025 | 5.31 | 3.7E-02 | P19137 | SWISSPROT EST_HUMAN | wr85e08_x1 NC_ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3' |
| 2175 | 7154 | 12274 | 5.07 | 3.7E-02 | AI984806.1 | NT | Homo sapiens mRNA for KIAA0718 protein, partial cds |
| 2502 | 7470 | 12586 | 1.04 | 3.7E-02 | AB018261.1 | NT | EOMESODERMIN |
| 2976 | 7994 | 13008 | 1.04 | 3.7E-02 | P79944 | SWISSPROT EST_HUMAN | 601896233TF1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5' |
| 2978 | 7996 | 13009 | 3.76 | 3.7E-02 | BF312963.1 | EST_HUMAN | Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA |
| 3372 | 8380 | | | 1.16 | 3.7E-02 | 68080541 NT | Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt, position (37) |
| 3115 | 8131 | 13150 | 43.98 | 3.6E-02 | AP000003.1 | NT | H vulgaris Sst1 gene for sucrose synthase |
| 3570 | 8577 | 13583 | 0.8 | 3.6E-02 | X73221.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens |
| 3578 | 8585 | 13590 | 0.73 | 3.6E-02 | AL096806.1 | NT | Drosophila melanogaster tiggrin mRNA, complete cds |
| 884 | 5902 | 10943 | 1.6 | 3.5E-02 | U09506.1 | NT | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |
| 993 | 6006 | 11037 | 1.11 | 3.5E-02 | AF253447.1 | NT | 602085136F11 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 1531 | 6529 | 11568 | 1.01 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F11 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 1531 | 6529 | 11569 | 1.01 | 3.5E-02 | BF678085.1 | EST_HUMAN | Thermotoga maritima section 85 of the complete genome |
| 4092 | 9086 | 14075 | 3.28 | 3.5E-02 | AE001773.1 | NT | |
| 4189 | 9182 | 14165 | 1.13 | 3.5E-02 | P53780 | SWISSPROT | CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) |
| 573 | 5606 | 10604 | 1.18 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 573 | 5606 | 10605 | 1.18 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 574 | 5606 | 10604 | 4.61 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 574 | 5606 | 10605 | 4.61 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 1034 | 6044 | 11073 | 3.13 | 3.4E-02 | AW274020.1 | EST_HUMAN | xv26d07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW_C211_HUMAN P5301 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR : |
| 1187 | 6188 | | 9.31 | 3.4E-02 | 11345459 NT | NT | Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA |
| | | | | | | | yc2ne6f_1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER28 repetitive element |
| 2328 | 7302 | 12422 | 1.86 | 3.4E-02 | T57160.1 | EST_HUMAN | |
| 3346 | 8355 | 13373 | 1.39 | 3.4E-02 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 3688 | 8692 | 13694 | 0.7 | 3.4E-02 | BE-83951.4 | EST_HUMAN | RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA |
| 3821 | 8823 | 13830 | 3.3 | 3.4E-02 | AW794952.1 | EST_HUMAN | RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA |
| 4467 | 9457 | 14437 | 3.07 | 3.4E-02 | X59799.1 | NT | M.musculus S-antigen gene promoter region |
| 4892 | 9871 | | 2.79 | 3.4E-02 | Q28457 | SWISSPROT | LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG) |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 4906 | 98895 | 14856 | 1.61 | 3.4E-02 | AJ012469.1 | NT | Caenorhabditis elegans mRNA for DYS-1 protein, partial |
| 3711 | 5420 | | | 15.62 | 3.3E-02 | AA398735.1 | EST_HUMAN z75e08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3' |
| 1149 | 6153 | 11185 | 14.2 | 3.3E-02 | AB035867.1 | NT | Cricketus griseus CTP2A17 mRNA for cytochrome P450 2A17, complete cds |
| 1599 | 6595 | 11656 | 1.34 | 3.3E-02 | AF110763.1 | NT | Homo sapiens skeletal muscle LM-protein 1 (FHL1) gene, complete cds |
| 2031 | 7014 | | | 1.55 | 3.3E-02 | R08112.1 | EST_HUMAN yf25c09.r1 Soares fetal liver spleen 1NF-S Homo sapiens cDNA clone IMAGE:127988 5' |
| 4053 | 6595 | 11656 | 2.72 | 3.3E-02 | AF110763.1 | NT | Homo sapiens skeletal muscle LM-protein 1 (FHL1) gene, complete cds |
| 4343 | 9334 | 14318 | 2.06 | 3.3E-02 | 6755862 | NT | Mus musculus tumor rejection antigen gp96 (Tr1), mRNA |
| 1322 | 5198 | 10214 | 2.52 | 3.2E-02 | AJ002005.1 | NT | Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter |
| 1109 | 6115 | 11145 | 14.14 | 3.2E-02 | AF096275.1 | NT | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 allele, complete cds |
| 1109 | 6115 | 11146 | 14.14 | 3.2E-02 | AF096275.1 | NT | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 allele, complete cds |
| 2060 | 7042 | | | 8.6 | 3.2E-02 | P28955 | SWISSPROT LARGE TEGMENT PROTEIN |
| 3061 | 8078 | 13091 | 13.22 | 3.2E-02 | BE867353.1 | EST_HUMAN 601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5' | |
| 3632 | 86358 | 13644 | 1.3 | 3.2E-02 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C033 |
| 3854 | 8856 | 13861 | 0.88 | 3.2E-02 | Z74103.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL055c |
| 3854 | 8856 | 13862 | 0.88 | 3.2E-02 | Z74103.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL055c |
| 4097 | 9091 | | | 17.68 | 3.2E-02 | X94768.1 | NT |
| 4622 | 9607 | 14595 | 3.39 | 3.2E-02 | AF114182.1 | NT | Saxifraga nitidula maturease (matK) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 4681 | 9666 | 14648 | 2.57 | 3.2E-02 | AF067083.1 | NT | Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Tip repressor binding protein gene, partial cds; and unknown genes |
| 1241 | 62239 | | | 1.62 | 3.1E-02 | 4503416 | NT |
| 1286 | 62285 | 11328 | 1.44 | 3.1E-02 | P18845 | SWISSPROT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3) | |
| 1852 | 6841 | 11929 | 0.95 | 3.1E-02 | 6671564 | NT | Mus musculus adrioplatin-related protein complex AF-3, delta subunit (Ap3d), mRNA |
| 4998 | 9117 | | | 12.58 | 3.1E-02 | AU119006.1 | EST_HUMAN AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5' |
| 5072 | 10041 | | | 5.51 | 3.1E-02 | 6730074 | NT |
| 1584 | 6581 | | | 11.29 | 3.0E-02 | AF187125.1 | NT |
| 2509 | 7477 | 12592 | 0.99 | 3.0E-02 | AA402242.1 | EST_HUMAN z65j03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:7227253 5' | |
| 3486 | 8484 | 13511 | 0.95 | 3.0E-02 | M94176.1 | NT | |
| 3569 | 8576 | 13582 | 2.92 | 3.0E-02 | AF247644.1 | NT | |
| 3660 | 8665 | | | 0.72 | 3.0E-02 | AW820223.1 | EST_HUMAN QV2-ST0296-150200-040-009 ST0296 Homo sapiens cDNA |
| 4885 | 9884 | 14834 | 7.12 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropillin 2 (NRP2) gene, complete cds, alternatively spliced |
| 4885 | 9884 | 14835 | 7.12 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropillin 2 (NRP2) gene, complete cds, alternatively spliced |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|---|
| 2368 | 7769 | 12459 | 1.06 | 2.9E-02 | AF228703.1 | NT | Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced |
| 3827 | 8829 | 13836 | 1.37 | 2.9E-02 | H72805.1 | EST_HUMAN | yy07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5' |
| 3877 | 8878 | 13881 | 0.73 | 2.9E-02 | O15440 | SWISSPROT | MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-C) (PABC11) (SMRP) |
| 4858 | 9839 | 14812 | 1.81 | 2.9E-02 | X65137.1 | NT | S. vulgaris pepC gene for PEP carboxylase |
| 4858 | 9839 | 14813 | 1.81 | 2.9E-02 | X65137.1 | NT | S. vulgaris pepC gene for PEP carboxylase |
| 2406 | 7377 | | 1 | 2.8E-02 | AA782516.1 | EST_HUMAN | ai55c09.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1360912 3' |
| 3286 | 8297 | 13323 | 1.1 | 2.8E-02 | AF086063.1 | NT | Homo sapiens retinal fascin (FSCN2) gene, exon 2 |
| 3286 | 8297 | 13324 | 1.1 | 2.8E-02 | AF086063.1 | NT | Homo sapiens retinal fascin (FSCN2) gene, exon 2 |
| 4185 | 9178 | | 0.8 | 2.8E-02 | 8393751 | NT | Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA |
| | | | | | | | Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1F, TCRBV22S1A2N1T, TCRBV9S1A1N2T, TCRBV7S1A1N1T, TCRBV13S3, TCRBV6SP, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S> |
| 1457 | 6454 | 11513 | 1.09 | 2.7E-02 | U66059.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 3347 | 8356 | 13374 | 1.84 | 2.7E-02 | AL161494.2 | NT | yy86h12.r1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5' |
| 4079 | 9073 | 14060 | 2.12 | 2.7E-02 | NA47258.1 | EST_HUMAN | yy86h12.r1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5' |
| 4079 | 9073 | 14061 | 2.12 | 2.7E-02 | NA47258.1 | EST_HUMAN | yy39f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120127 3' similar to contains Alu repetitive element |
| 5040 | 10011 | 14980 | 1.04 | 2.7E-02 | T95073.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C0B2 |
| 566 | 5599 | 10598 | 0.98 | 2.6E-02 | AL163282.2 | NT | IL3-CT0219-230100-062-C09 CT0219 Homo sapiens cDNA ab02b02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3' |
| 1350 | 6347 | 0.93 | 2.6E-02 | AW850515.1 | EST_HUMAN | Mus musculus histidine rich calcium binding protein (Hrc), mRNA | |
| 2305 | 7280 | 12398 | 1.97 | 2.6E-02 | AA490021.1 | EST_HUMAN | Mus musculus histidine rich calcium binding protein (Hrc), mRNA |
| 2307 | 7282 | 12400 | 1.98 | 2.6E-02 | 6754241 | NT | Mus musculus histidine rich calcium binding protein (Hrc), mRNA |
| 2307 | 7282 | 12401 | 1.98 | 2.6E-02 | 6754241 | NT | Mus musculus MHC class III region RD gene, partial cds; Bf, C22, G9A, NG22, G9, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes |
| 2845 | 7865 | | 1.39 | 2.6E-02 | AF109906.1 | NT | Deinococcus radiodurans R1 section 161 of 229 of the complete chromosome 1 |
| 4749 | 9754 | 14720 | 3.57 | 2.6E-02 | L12032.1 | NT | Chicken dorsalin-1 mRNA, complete cds |
| 4759 | 9743 | 14728 | 1.27 | 2.6E-02 | AJ403239.1 | NT | M.musculus DNA for vimentin-binding fragment VimE7 |
| 4759 | 9743 | 14729 | 1.27 | 2.6E-02 | AJ403239.1 | NT | M.musculus DNA for vimentin-binding fragment VimE7 |
| 4897 | 9876 | 14844 | 1.74 | 2.6E-02 | AE002014.1 | NT | Q15041 HYPOTHETICAL PROTEIN KIAA0069 ; |
| 4921 | 9899 | 14874 | 2.61 | 2.6E-02 | AW241154.1 | EST_HUMAN | Q126f06.y5.NC1_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |
| 528 | 5563 | 10565 | 1.4 | 2.5E-02 | AI783130.1 | EST_HUMAN | Q126f06.y5.NC1_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 528 | 5563 | 10567 | 1.4 | 2.5E-02 | A1793130.1 | EST_HUMAN | on26106_y5_NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |
| 800 | 5821 | 10851 | 12.78 | 2.5E-02 | BE974314.1 | EST_HUMAN | 601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3' |
| 858 | 5877 | 10918 | 4.21 | 2.5E-02 | BE974314.1 | EST_HUMAN | 601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850665 3' |
| 2689 | 7847 | | 1.83 | 2.5E-02 | U12571.1 | NT | Rattus norvegicus rabbphilin-3A mRNA, complete cds |
| 2885 | 7904 | 12924 | 3.25 | 2.5E-02 | X98697.1 | NT | H_carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 |
| 2885 | 7904 | 12925 | 3.25 | 2.5E-02 | X98697.1 | NT | H_carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 |
| 3932 | 10049 | 13923 | 0.85 | 2.5E-02 | BE701165.1 | EST_HUMAN | PM2_NN0128-080700-001-a12 NN0128 Homo sapiens cDNA clone IMAGE:2934015 3' |
| 3932 | 10049 | 13924 | 0.85 | 2.5E-02 | BE701165.1 | EST_HUMAN | PM2_NN0128-080700-001-a12 NN0128 Homo sapiens cDNA clone IMAGE:2934015 3' |
| 4083 | 9077 | 14065 | 5.51 | 2.5E-02 | AW592114.1 | EST_HUMAN | h36n08_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2070156 3' |
| 173 | 5237 | 10249 | 0.68 | 2.4E-02 | A1378582.1 | EST_HUMAN | tc72c07_x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1561149 5' |
| 1563 | 6560 | 11622 | 1.86 | 2.4E-02 | H65884.1 | EST_HUMAN | y75f11_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5' |
| 1993 | 7760 | 12082 | 1.31 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 1993 | 7760 | 12083 | 1.31 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4243 | 9237 | 14220 | 1.46 | 2.4E-02 | J05110.1 | NT | T_thermophilus calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds |
| 4390 | 9381 | 14362 | 1.56 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4390 | 9381 | 14363 | 1.56 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 1834 | 6824 | | 3.68 | 2.3E-02 | W05340.1 | EST_HUMAN | zab4g08.11 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289294 5' |
| 1848 | 6837 | | 5.18 | 2.3E-02 | U94165.1 | NT | 4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4 |
| 2289 | 7264 | 12382 | 1.88 | 2.3E-02 | Z74293.1 | NT | S_cerevisiae chromosome IV reading frame ORF YDL245c |
| 3598 | 8605 | 13613 | 5.37 | 2.3E-02 | Z20377.1 | EST_HUMAN | HSAAACADH_P_Human_fetal_Brain Whole tissue Homo sapiens cDNA |
| 4026 | 9022 | 14009 | 0.76 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4026 | 9022 | 14010 | 0.76 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4296 | 9288 | 14275 | 1.14 | 2.3E-02 | AW889107.1 | EST_HUMAN | CMA4_NN0080-280400-180-d04 NN0080 Homo sapiens cDNA |
| 4327 | 9319 | 14301 | 0.85 | 2.3E-02 | BE935225.1 | EST_HUMAN | CMV3-MT0118-010900-318-907 M10118 Homo sapiens cDNA |
| 4327 | 9319 | 14302 | 0.85 | 2.3E-02 | BE935225.1 | EST_HUMAN | CMV3-MT0118-010900-318-907 M10118 Homo sapiens cDNA |
| 4328 | 10051 | 14303 | 0.82 | 2.3E-02 | AW5931693.1 | EST_HUMAN | xs25608_x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4328 | 10051 | 14304 | 0.82 | 2.3E-02 | AW5931693.1 | EST_HUMAN | xs25608_x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4463 | 9453 | 14434 | 2.76 | 2.3E-02 | BF026487.1 | EST_HUMAN | 601672279f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5' |
| 4463 | 9453 | 14435 | 2.76 | 2.3E-02 | BF026487.1 | EST_HUMAN | 601672279f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5' |
| 4860 | 9841 | | 0.95 | 2.3E-02 | 7662173 | NT | Homo sapiens KIAA0547 gene product (KIAA0547), mRNA |
| 4977 | 9953 | 14931 | 0.77 | 2.3E-02 | AF257110.1 | NT | Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds |
| 4977 | 9953 | 14932 | 0.77 | 2.3E-02 | AF257110.1 | NT | Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds |
| 728 | 5751 | 10772 | 2.95 | 2.2E-02 | AF018267.1 | NT | Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 1708 | 6703 | | | 1.21 | 2.2E-02 | 4557448 NT | <i>Homo sapiens</i> chromodomain helicase DNA binding protein 2 (CHD2) mRNA |
| 1723 | 6718 | 11795 | 0.97 | 2.2E-02 | P07313 | SWISSPROT | <i>MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)</i> |
| 1723 | 6718 | 11796 | 0.97 | 2.2E-02 | P07313 | SWISSPROT | <i>MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)</i> |
| 1965 | 6950 | 12053 | 1.43 | 2.2E-02 | 2B2001.1 | NT | <i>S. pneumoniae</i> psPA gene and open reading frames |
| 3350 | 8359 | | 1.88 | 2.2E-02 | AA577785.1 | EST_HUMAN | <i>mn24a4.s1 NCI CGAP Gas1</i> <i>Homo sapiens</i> cDNA clone IMAGE:1084782 3' |
| 3561 | 8568 | | 3.57 | 2.2E-02 | Af083094.1 | NT | Infectious burst disease virus segment B strain IL 4 VP1 gene, complete cds |
| 3763 | 8766 | 13769 | 1.18 | 2.2E-02 | AW601317.1 | EST_HUMAN | PM0-BT0340-170100-004-b03 BT0340 <i>Homo sapiens</i> cDNA |
| 3820 | 8822 | 13829 | 0.68 | 2.2E-02 | Z74293.1 | NT | <i>S. cerevisiae</i> chromosome IV reading frame ORF YDL245c |
| 416 | 5453 | | 4.33 | 2.1E-02 | AV761502.1 | EST_HUMAN | AV761502 MD5 <i>Homo sapiens</i> cDNA clone MDSADG01 5' |
| 446 | 5483 | | 7.77 | 2.1E-02 | Af029726.1 | NT | Dicytostellum discoidin histidine kinase C (dhkC) mRNA, complete cds |
| 1244 | 6242 | 11283 | 7.23 | 2.1E-02 | U72073.1 | NT | Bacillus subtilis codKLM cluster, CodK (codK), CodL (codL), and spore coat protein CodM (codM) genes, complete cds |
| 1744 | 6739 | 11816 | 1.17 | 2.1E-02 | P02438 | SWISSPROT | KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A |
| 1744 | 6739 | 11817 | 1.17 | 2.1E-02 | P02438 | SWISSPROT | KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A |
| 1744 | 6739 | 11818 | 1.17 | 2.1E-02 | P02438 | SWISSPROT | KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A |
| 2744 | 5792 | 10820 | 3.7 | 2.1E-02 | N29286.1 | EST_HUMAN | y43h07.11 Soares melanocyte 2NbHM <i>Homo sapiens</i> cDNA clone IMAGE:264541 5' |
| 3502 | 8510 | 13524 | 0.94 | 2.1E-02 | AA461271.1 | EST_HUMAN | zg3b09.11 Soares total fetus Nb2HF8 9w <i>Homo sapiens</i> cDNA clone IMAGE:786121 5' |
| 4009 | 9005 | 13993 | 0.67 | 2.1E-02 | Z74293.1 | NT | <i>S. cerevisiae</i> chromosome IV reading frame ORF YDL245c |
| 4182 | 9175 | 14159 | 0.8 | 2.1E-02 | BF343655.1 | EST_HUMAN | 6020153005f1 NCI CGAP_Bm64 <i>Homo sapiens</i> cDNA clone IMAGE:4161161 5' |
| 4322 | 9314 | 14297 | 1.92 | 2.1E-02 | U44914.1 | NT | Borelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes |
| 4333 | 9324 | 14310 | 1.35 | 2.1E-02 | AI768127.1 | EST_HUMAN | wg81d11.X1 Soares_NSF_F8_9W_OT_PA_P_S1 <i>Homo sapiens</i> cDNA clone IMAGE:2371509 3' |
| 4540 | 9358 | | 0.68 | 2.1E-02 | Y19213.1 | NT | <i>Homo sapiens</i> putative pishhBbA pseudogene for hair keratin, exons 2 to 7 |
| 4572 | 9560 | 14549 | 5.38 | 2.1E-02 | Y08501.1 | NT | <i>A. thaliana</i> mitochondrial genome, part A |
| 4591 | 9579 | 14569 | 0.76 | 2.1E-02 | AA665737.1 | EST_HUMAN | sq55g12.s1 Gessert Wilms tumor <i>Homo sapiens</i> cDNA clone IMAGE:1126918 3' |
| 1 | 5097 | 10080 | 1.78 | 2.0E-02 | BF002932.1 | EST_HUMAN | MER1 repetitive element; |
| 1 | 5098 | 10081 | 9.9 | 2.0E-02 | AW895565.1 | EST_HUMAN | QV4-NN0038-270400-1B7-h05 NN0038 <i>Homo sapiens</i> cDNA |
| 257 | 5317 | 10326 | 2.81 | 2.0E-02 | 6753635 NT | Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA | |
| 293 | 5350 | 10363 | 1.85 | 2.0E-02 | AA456538.1 | EST_HUMAN | aa15b10.r1 Soares_NhIMPu_S1 <i>Homo sapiens</i> cDNA clone IMAGE:813307 5' |
| 790 | 5811 | 10841 | 1.4 | 2.0E-02 | 6753635 NT | Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA | |
| 1071 | 6079 | 11110 | 1 | 2.0E-02 | AL096805.1 | NT | <i>Homo sapiens</i> genomic region containing hypervariable minisatellites chromosome [11p36.33] of Homo sapiens |
| 1180 | 6182 | 11219 | 1.31 | 2.0E-02 | 8922391 NT | <i>Homo sapiens</i> hypothetical protein FLJ10379 (FLJ10379), mRNA | |
| 1180 | 6182 | 11220 | 1.31 | 2.0E-02 | 8922391 NT | <i>Homo sapiens</i> hypothetical protein FLJ10379 (FLJ10379), mRNA | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1835 | 6825 | 11912 | 1.69 | 2.0E-02 | 8922453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 1835 | 6825 | 11913 | 1.69 | 2.0E-02 | 8922453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 2726 | 7683 | | 1.8 | 2.0E-02 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 3005 | 5097 | 10080 | 1.66 | 2.0E-02 | BF002932.1 | EST_HUMAN | 7951c08_x1 NC1 CGAP_Pt28 Homo sapiens cDNA clone IMAGE:33099898 3' similar to contains MER1;3 MER1 repetitive element; |
| 3071 | 8087 | | 2.21 | 2.0E-02 | 7305474 | NT | Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA |
| 3156 | 8172 | | 1.54 | 2.0E-02 | AF095588.1 | NT | Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds |
| 3900 | 8900 | 13893 | 1.61 | 2.0E-02 | MI8095.1 | NT | P vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end |
| 4943 | 8920 | | 0.84 | 2.0E-02 | AI271985.1 | EST_HUMAN | q83e03_x1 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866076 3' |
| 684 | 5708 | 10720 | 1.76 | 1.9E-02 | AA572764.1 | EST_HUMAN | mf19a07_s1 NC1 CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.H1_L1 repetitive element; |
| 1983 | 6973 | 12077 | 2.16 | 1.9E-02 | AL162303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 1983 | 6973 | 12078 | 2.16 | 1.9E-02 | AL162303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2434 | 7405 | 12523 | 1.18 | 1.9E-02 | AL161550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 2835 | 7855 | 12874 | 7.79 | 1.9E-02 | AA713856.1 | EST_HUMAN | nw_04105_s1 NC1 CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3' |
| 2881 | 7900 | 12922 | 1.67 | 1.9E-02 | AV648669.1 | EST_HUMAN | AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3' |
| 3185 | 8201 | | 0.75 | 1.9E-02 | AB033611.1 | NT | Urothicus talpoides mitochondrial gene for cytochrome b, complete cds |
| 3530 | 8536 | | 0.91 | 1.9E-02 | N52250.1 | EST_HUMAN | yZ28b02_s1 Soares_multiple_sclerosts_2NbHMSP Homo sapiens cDNA clone IMAGE:3839564 5' |
| 3622 | 8629 | | 8.78 | 1.9E-02 | BE738088.1 | EST_HUMAN | 601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5' |
| 3633 | 8639 | 13645 | 0.74 | 1.9E-02 | AI301183.1 | EST_HUMAN | qn04c07_x1 NC1 CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element; |
| 3934 | 8933 | 13926 | 1.5 | 1.9E-02 | AF141940.1 | NT | Mycoplasma irritans ViHA1 precursor (ViHA1) and ViHA2 precursor (ViHA2) genes, partial cds |
| 4070 | 9064 | 14053 | 1.75 | 1.9E-02 | PP09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4070 | 9064 | 14054 | 1.75 | 1.9E-02 | PP09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4410 | 9400 | 14385 | 2.81 | 1.9E-02 | AI452999.1 | EST_HUMAN | qj6dd0_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element; |
| 4852 | 7405 | 12523 | 3.15 | 1.9E-02 | AL161550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 344 | 5396 | 10403 | 1.36 | 1.8E-02 | AW771104.1 | EST_HUMAN | mf52c06_x1 NC1 CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element; |
| 1142 | 6146 | 11178 | 1.42 | 1.8E-02 | X17664.1 | NT | H.francisci mRNA for myelin basic protein (MBP) |
| 2607 | 7569 | 12684 | 1.45 | 1.8E-02 | AE004544.1 | NT | Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome |
| 3138 | 8154 | | 0.69 | 1.8E-02 | AI805629.1 | EST_HUMAN | te52a09_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3' |
| 3793 | 8796 | 13801 | 0.91 | 1.8E-02 | AW879122.1 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed In HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 3793 | 8796 | 13902 | 0.91 | 1.8E-02 | AW879122.1 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA al24f04_s1_Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3' |
| 3970 | 8969 | | 1.08 | 1.8E-02 | AA861446.1 | EST_HUMAN | al24f04_s1_Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3' |
| 4306 | 9298 | 14284 | 1.59 | 1.8E-02 | AW936363.1 | EST_HUMAN | QV4-DT0021-501289-071-b11 DT0021 Homo sapiens cDNA SWISSPROT HYPOTHETICAL PROTEIN DJ845024.2 |
| 4798 | 9782 | 14765 | 0.95 | 1.8E-02 | O60810 | EST_HUMAN | 601310626F11 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5' |
| 895 | 5913 | 10952 | 1.21 | 1.7E-02 | BE394869.1 | EST_HUMAN | hf34aa03_x1_Soares_cDNA clone IMAGE:2933740 3' similar to contains hf34aa03_x1_Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' |
| 1753 | 6747 | 11828 | 2.15 | 1.7E-02 | AW573183.1 | EST_HUMAN | L1.t1 L1 repetitive element; hf34aa03_x1_Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element; |
| 1753 | 6747 | 11829 | 2.15 | 1.7E-02 | AW573183.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C004 |
| 1833 | 6823 | | 2.15 | 1.7E-02 | AL168204.2 | NT | Oryctolagus cuniculus mRNA for mitogenin[29], complete cds |
| 2054 | 7036 | | 7.25 | 1.7E-02 | AB004816.1 | NT | Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA |
| 2569 | 7532 | | 1.47 | 1.7E-02 | 7657495 | NT | qb22a08_x1_Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696932 3' |
| 2929 | 7948 | 12966 | 1.09 | 1.7E-02 | AI147615.1 | EST_HUMAN | qb22a04_x1_NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains hm45a04_x1_NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19_b1 MER19 repetitive element; |
| 3433 | 8441 | | 4.78 | 1.7E-02 | AW827368.1 | EST_HUMAN | act18f04_s1_Strategene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element; |
| 4045 | 9041 | | 1.04 | 1.7E-02 | AA669618.1 | EST_HUMAN | ye86f08_x1_Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:124647 5' |
| 4077 | 9071 | | 1.86 | 1.7E-02 | R02506.1 | EST_HUMAN | qm08g07_x1_NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to qb22a03_x1_Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains FINGER PROTEIN 30 (HUMAN); |
| 4332 | 9323 | 14309 | 1.34 | 1.7E-02 | AI305279.1 | EST_HUMAN | hf34aa03_x1_Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element; |
| 4398 | 9387 | 14370 | 1.47 | 1.7E-02 | AW573183.1 | EST_HUMAN | Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatosatin II |
| 4576 | 9564 | 14552 | 1.82 | 1.7E-02 | Y00641.1 | NT | ow51602_s1_Soares_cDNA clone IMAGE:1640858 3' |
| 4668 | 9653 | | 6.38 | 1.7E-02 | AI015076.1 | EST_HUMAN | Mycobacterium tuberculosis H37RV complete genome; segment 13/162 |
| 5077 | 5542 | | 1.83 | 1.6E-02 | AL021928.1 | NT | Treponema malophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue |
| 1616 | 6613 | 11680 | 1.13 | 1.6E-02 | Y18889.1 | NT | 2187 7166 12285 1.01 1.6E-02 Q64176 SWISSPROT LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASTYN) (ESTERASE-22) |
| 2187 | 7166 | 12285 | 1.01 | 1.6E-02 | Q64176 | SWISSPROT LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASTYN) (ESTERASE-22) | |
| 2187 | 7166 | 12286 | 1.01 | 1.6E-02 | Q64176 | neq1d06_s1_NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667 | |
| 2572 | 7535 | 12652 | 1.12 | 1.6E-02 | AA484872.1 | EST_HUMAN | Homo sapiens: mRNA for KIAA0634 protein, partial cds |
| 2622 | 7584 | | 0.95 | 1.6E-02 | AB014534.1 | NT | Lassea sp. Isolate Bd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product |
| 2951 | 7970 | 12987 | 0.73 | 1.6E-02 | AF112282.1 | NT | IL3-Ct0219-160200-063-C07 CT0219 Homo sapiens cDNA |
| 3447 | 8455 | 13481 | 5.11 | 1.6E-02 | AW850652.1 | EST_HUMAN | IL3-Ct0219-160200-063-C07 CT0219 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3758 | 8761 | 13761 | 1.1 | 1.6E-02 | AL163301.2 | NT | Homo sapiens: chromosome 21 segment HS21C101 |
| 4051 | 9047 | | 1.82 | 1.6E-02 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RatGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 742 | 5765 | | 23.96 | 1.5E-02 | 8923734 | NT | Homo sapiens: transcription factor (HSA130884), mRNA |
| 2081 | 7062 | 12171 | 2.42 | 1.5E-02 | N39521.1 | EST_HUMAN | y27b07_s1_Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3' |
| 2110 | 7090 | 12204 | 1.29 | 1.5E-02 | AL161894.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |
| 2987 | 8005 | 13017 | 1.24 | 1.5E-02 | AJ006216.1 | NT | Homo sapiens: CACNA1F gene, exons 1 to 48 |
| 2987 | 8005 | 13018 | 1.24 | 1.5E-02 | AJ006216.1 | NT | Homo sapiens: CACNA1F gene, exons 1 to 48 |
| 3641 | 8647 | 13654 | 0.88 | 1.5E-02 | BF092942.1 | EST_HUMAN | MR4-TN0115_080900-201-b12 TN0115 Homo sapiens cDNA |
| 5006 | 9977 | 14952 | 0.97 | 1.5E-02 | 4503534 | NT | Homo sapiens eukaryotic translation initiation factor 4E (EIF4E) mRNA |
| 414 | 5451 | | 1.25 | 1.4E-02 | AE002230.2 | NT | Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome |
| 1101 | 6108 | 11138 | 3.55 | 1.4E-02 | 7705980 | NT | Homo sapiens NESH protein (LOC51225), mRNA |
| 1237 | 6235 | | 1.37 | 1.4E-02 | U32800.1 | NT | Haemophilus influenzae Rd section 115 of 163 of the complete genome |
| 1279 | 6278 | | 2.38 | 1.4E-02 | UG67779.1 | NT | Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds |
| 1486 | 6483 | | 0.96 | 1.4E-02 | AV723785.1 | EST_HUMAN | AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5' |
| 2926 | 7945 | 12962 | 0.87 | 1.4E-02 | 7657040 | NT | Homo sapiens down-regulated in metastasis (DRM), mRNA |
| | | | | | | | Bifidobacterium longum Na+-H+ antiporter (nhbB), cytosine deaminase, and alpha-galactosidase (egI) |
| 3140 | 8156 | 13177 | 2.22 | 1.4E-02 | AF160969.2 | NT | genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/nxr) gene, partial cds |
| 3314 | 8325 | 13347 | 0.73 | 1.4E-02 | AW074212.1 | EST_HUMAN | xb09d09_x1_NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3' |
| 3404 | 8413 | 13439 | 6.12 | 1.4E-02 | AL161566.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3404 | 8413 | 13440 | 6.12 | 1.4E-02 | AL161566.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3572 | 8579 | 13585 | 10.27 | 1.4E-02 | 6996918 | NT | Mus musculus: histocompatibility 2, complement component factor B (H2-Bf), mRNA |
| 4361 | 9352 | 14331 | 7.06 | 1.4E-02 | AW962688.1 | EST_HUMAN | EST374761 IMAGE sequences, MAGG Homo sapiens cDNA |
| 4361 | 9352 | 14332 | 7.06 | 1.4E-02 | AW962688.1 | EST_HUMAN | EST374761 IMAGE sequences, MAGG Homo sapiens cDNA |
| 4726 | 9711 | 14695 | 6.63 | 1.4E-02 | BE73142.1 | EST_HUMAN | 601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5' |
| 4726 | 9711 | 14696 | 6.63 | 1.4E-02 | BE73142.1 | EST_HUMAN | 601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5' |
| 1828 | 6818 | | 1.4 | 1.3E-02 | BE739263.1 | EST_HUMAN | 601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5' |
| 1915 | 6901 | 11994 | 1.7 | 1.3E-02 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 2934 | 7953 | 12970 | 0.87 | 1.3E-02 | M81725.1 | NT | Oenothera berteroana NADH dehydrogenase subunit 2 (nad2) gene, exons 1-2 |
| 3141 | 8157 | 13178 | 1.9 | 1.3E-02 | BFE97081.1 | EST_HUMAN | 602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:42886203 5' |
| 3141 | 8157 | 13179 | 1.9 | 1.3E-02 | BFE97081.1 | EST_HUMAN | 602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:42886203 5' |
| 3862 | 8864 | | 1.18 | 1.3E-02 | AF169288.1 | NT | Mus musculus: beta-sacroglycan gene, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| | | | | | | | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,> zf65g01.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element: |
| 4771 | 9755 | 14742 | 1.07 | 1.3E-02 | U66061.1 | NT | zf65g01.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element: |
| 353 | 5404 | 10414 | 4.04 | 1.2E-02 | AA059299.1 | EST_HUMAN | HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3REGION |
| 450 | 5487 | 10502 | 1.52 | 1.2E-02 | P38898 | SWISSPROT | qd68e12.x1 Soares_nestis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element: |
| 729 | 5752 | 10773 | 5.89 | 1.2E-02 | AI1835922.1 | EST_HUMAN | qd68e12.x1 Soares_nestis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element: |
| 2112 | 7092 | 12206 | 1.27 | 1.2E-02 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2115 | 7095 | 12209 | 1.07 | 1.2E-02 | AV731704.1 | EST_HUMAN | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 2375 | 7347 | 12468 | 1.15 | 1.2E-02 | AW172350.1 | EST_HUMAN | xJ37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 2564 | 7347 | 12468 | 1.16 | 1.2E-02 | AW172350.1 | EST_HUMAN | xJ37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 3028 | 8045 | 8230 | 6.93 | 1.2E-02 | AA075418.1 | EST_HUMAN | zm88e03.r1 Stratagene ovarian cancer (#337219) Homo sapiens cDNA clone IMAGE:5452020 5' |
| 3215 | 8230 | 13251 | 1.97 | 1.2E-02 | R62805.1 | EST_HUMAN | y11508.s1 Soares placenta NB214P Homo sapiens cDNA clone IMAGE:138803 3' |
| 4729 | 9714 | 14639 | 0.95 | 1.2E-02 | 6754367 | NT | Mus musculus Interferon regulatory factor 5 (Ifi5), mRNA |
| | | | | | | | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatos (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 4761 | 9745 | 14731 | 3.66 | 1.2E-02 | U91328.1 | NT | Cynops pyrrhogaster Cyplobigt mRNA, partial cds |
| 4876 | 9855 | | 1.51 | 1.2E-02 | AB019786.1 | NT | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 4912 | 9891 | 14865 | 2.45 | 1.2E-02 | AV731704.1 | EST_HUMAN | Mus musculus POZ/zinc finger transcription factor ODA-8 mRNA, complete cds |
| 5025 | 9996 | 14969 | 1.29 | 1.2E-02 | AF185576.1 | NT | zm96e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3' |
| 1250 | 6248 | 11289 | 1.26 | 1.1E-02 | AA070364.1 | EST_HUMAN | H.sapiens LPA gene, exon 4 |
| 1668 | 6664 | 11739 | 1.43 | 1.1E-02 | X75491.1 | NT | H.sapiens LPA gene, exon 4 |
| 1668 | 6664 | 11740 | 1.43 | 1.1E-02 | X75491.1 | NT | 6020180377I NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4163808 5' |
| 1987 | 6972 | 12076 | 3.37 | 1.1E-02 | BF345283.1 | EST_HUMAN | Iq93b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW_XPF_HUMAN |
| 2808 | 7828 | | 4.07 | 1.1E-02 | N99523.1 | EST_HUMAN | Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ; |
| 3444 | 8452 | 13479 | 3.11 | 1.1E-02 | AI653508.1 | EST_HUMAN | RC3-ST0197-120200-015-q11 ST0197 Homo sapiens cDNA |
| 3990 | 8988 | | 0.69 | 1.1E-02 | AW813796.1 | EST_HUMAN | DKE7p586E0124_s1_586 (synonym: huet1) Homo sapiens cDNA |
| 4683 | 9668 | 14650 | 2.3 | 1.1E-02 | AL048383.2 | EST_HUMAN | MR3-CT0176-111089-003-e10 CT0176 Homo sapiens cDNA |
| 7 | 5087 | 10073 | 8.28 | 1.0E-02 | AW846120.1 | EST_HUMAN | cc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1360495 3' |
| 2497 | 7465 | | 0.95 | 1.0E-02 | AA806389.1 | EST_HUMAN | RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA |
| 3016 | 8033 | 13044 | 2.95 | 1.0E-02 | BE835556.1 | EST_HUMAN | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 3188 | 8204 | 13226 | 0.98 | 1.0E-02 | BE968999.1 | EST_HUMAN | 601649867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:35933689 3' |
| 4632 | 9617 | 14608 | 4.68 | 1.0E-02 | 6753521 NT | Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA | |
| 4697 | 9682 | 14665 | 3.4 | 1.0E-02 | R96567.1 | EST_HUMAN | yp54h01_r1 Soares fetal liver spleen 1NTFLS Homo sapiens cDNA clone IMAGE:199633 5' |
| 4835 | 9836 | 14810 | 1.72 | 1.0E-02 | L05632.1 | NT | Human glycoprotein hormone alpha-subunit (GCA) gene, 5' flank |
| | | | | | | | wh42f09_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MEF22 repetitive element; |
| 882 | 5900 | 10941 | 2.15 | 9.0E-03 | AT796126.1 | EST_HUMAN | 601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5' |
| 1245 | 6243 | | 1.46 | 9.0E-03 | BE781889.1 | EST_HUMAN | 601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5' |
| 2331 | 7305 | 12425 | 1.79 | 9.0E-03 | AL161559.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59 |
| 4828 | 9812 | 14793 | 1.02 | 9.0E-03 | BE047849.1 | EST_HUMAN | t244e10_y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291466 5' |
| 5026 | 9997 | 14970 | 0.98 | 9.0E-03 | 6753521 NT | Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA | |
| 498 | 5534 | | 2.78 | 8.0E-03 | AA723007.1 | EST_HUMAN | zh30e03_s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413595 3' similar to contains Alu repetitive element; |
| 974 | 5990 | 11023 | 52.19 | 8.0E-03 | AF106656.1 | NT | Homo sapiens adenylosuccinate lyase gene, complete cds |
| 2095 | 7076 | 12190 | 1.39 | 8.0E-03 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3280 | 8292 | 13317 | 0.68 | 8.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 3591 | 8598 | 13603 | 1.23 | 8.0E-03 | P32644 | SWISSPROT | HYPOTHETICAL 127.0 kD PROTEIN IN RAD24-BMH1 INTERGENIC REGION |
| 3591 | 8598 | 13604 | 1.23 | 8.0E-03 | P32644 | SWISSPROT | HYPOTHETICAL 127.0 kD PROTEIN IN RAD24-BMH1 INTERGENIC REGION |
| 4134 | 9129 | 14112 | 0.95 | 8.0E-03 | BE840049.1 | EST_HUMAN | Q0V-FN0181-140700-304-910 FN0181 Homo sapiens cDNA CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA |
| 4258 | 9252 | 14239 | 5.95 | 8.0E-03 | BF563327.1 | EST_HUMAN | Cryptosporidium parvum HC-10 gene, complete cds |
| 685 | 5709 | 10721 | 11.47 | 7.0E-03 | AF097183.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 685 | 5709 | 10722 | 11.47 | 7.0E-03 | AF097183.1 | NT | Glycine max glutathione S-transferase GST 21 mRNA, partial cds |
| 962 | 5977 | 11011 | 11.8 | 7.0E-03 | AF243376.1 | NT | AV731712 H1 F Homo sapiens cDNA clone HTFAZF10 5' |
| 1099 | 6106 | 11136 | 2.63 | 7.0E-03 | AV731712.1 | EST_HUMAN | ab79b09_s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853145 3' |
| 1372 | 6369 | 11418 | 2.08 | 7.0E-03 | AA668298.1 | EST_HUMAN | x121602_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3' |
| 1473 | 6470 | 11528 | 4.65 | 7.0E-03 | AW303599.1 | EST_HUMAN | SWISSPROT HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 2196 | 7765 | 12297 | 1.36 | 7.0E-03 | P04929 | EST_HUMAN | |
| 3680 | 8685 | 13687 | 0.92 | 7.0E-03 | AW444463.1 | EST_HUMAN | Ui-H-Bi3-erb-c-10-0-U1s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733591 3' |
| 3722 | 8726 | 13726 | 0.78 | 7.0E-03 | AF196344.1 | NT | Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds |
| 4213 | 9206 | | 1.05 | 7.0E-03 | U60086.1 | NT | Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagc) mRNA, complete cds |
| 4404 | 9395 | | 1.12 | 7.0E-03 | AW117711.1 | EST_HUMAN | x634f09_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 |
| 4468 | 9458 | | 1.1 | 7.0E-03 | AW630888.1 | EST_HUMAN | ACIDIC B2 KDA PROTEIN ; hh89a05_y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869936 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4830 | 9814 | | 2.67 | 7.0E-03 | AL163278.2 | NT | Homo sapiens; chromosome 21 segment HS21C078 |
| 1221 | 6221 | 11263 | 9.46 | 6.0E-03 | AW511148.1 | EST_HUMAN | hd22e05_x1_Scares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW_PXR_HUMAN_O75469_ORPHAN_NUCLEAR_RECEPTOR_PXR ; |
| 1221 | 6221 | 11264 | 9.46 | 6.0E-03 | AW511148.1 | EST_HUMAN | hd22e05_x1_Scares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW_PXR_HUMAN_O75469_ORPHAN_NUCLEAR_RECEPTOR_PXR ; |
| 2699 | 7656 | 12770 | 1.02 | 6.0E-03 | AF112374.1 | NT | Danio rerio odont receptor gene cluster |
| 2820 | 7841 | 12857 | 4.19 | 6.0E-03 | AA759135.1 | EST_HUMAN | ah78e11_s1_Scares_testis_NHT_Homo sapiens cDNA clone 1321772 3' |
| 2820 | 7841 | 12858 | 4.19 | 6.0E-03 | AA759135.1 | EST_HUMAN | ah78e11_s1_Scares_testis_NHT_Homo sapiens cDNA clone 1321772 3' |
| 3173 | 8189 | | 2.51 | 6.0E-03 | H75690.1 | EST_HUMAN | y77h04_r1_Scares fetal liver spleen tNFLS_Homo sapiens cDNA clone IMAGE:211351 5' |
| 3232 | 8247 | | 0.85 | 6.0E-03 | AF190338.1 | NT | Notoncus sp.: cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product |
| 3298 | 8309 | 13335 | 1.31 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds |
| 3298 | 8309 | 13336 | 1.31 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds |
| 3470 | 8478 | | 1.13 | 6.0E-03 | W37985.1 | EST_HUMAN | zc13a1.11_Scares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:3221172 5' |
| 3576 | 8583 | 13588 | 5.07 | 6.0E-03 | BF510986.1 | EST_HUMAN | U-H-BI4-apm-c-06-0-U1_s1_NCI_CGAP_Sub8_Homo sapiens cDNA clone IMAGE:3087754 3' |
| 3611 | 8618 | 13628 | 1.29 | 6.0E-03 | BE077356.1 | EST_HUMAN | RC1-BT0606-260400-014-807_B10606_Homo sapiens cDNA |
| 3690 | 8694 | 13696 | 1.18 | 6.0E-03 | 6754029 | NT | Mus musculus glucosaminyl-6-phosphate deaminase (Gnpl), mRNA |
| 3850 | 8852 | | 0.86 | 6.0E-03 | BE250108.1 | EST_HUMAN | 600942904_F1_NIH_MGC_15_Homo sapiens cDNA clone IMAGE:2956513 5' |
| 4199 | 9192 | | 1.31 | 6.0E-03 | N58946.1 | EST_HUMAN | yy62h10_s1_Scares_multiple_sclerosis_2NbH-MSP_Homo sapiens cDNA clone IMAGE:278179 3' |
| 4239 | 9233 | | 1.27 | 6.0E-03 | A016833.1 | EST_HUMAN | ov33c11_x1_Scares_testis_NHT_Homo sapiens cDNA clone IMAGE:1639124 3' |
| 4556 | 9544 | 14529 | 6.94 | 6.0E-03 | AA324242.1 | EST_HUMAN | EST27116_Cat esophagus II_Homo sapiens cDNA 5' end similar to EST containing Aliu repeat |
| 4950 | 9927 | | 0.98 | 6.0E-03 | L34170.1 | NT | Human germiline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22 |
| 661 | 5688 | 10696 | 1.81 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 661 | 5688 | 10697 | 1.81 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 662 | 5688 | 10696 | 2.2 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 662 | 5888 | 10697 | 2.2 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds |
| 1095 | 6102 | 11132 | 1.24 | 5.0E-03 | AJ010457.1 | NT | Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3 |
| 2610 | 7572 | 12686 | 2.3 | 5.0E-03 | AB033006.1 | NT | Homo sapiens mRNA for KIAA1180 protein, partial cds |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|--------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2865 | 7885 | 12905 | 0.69 | 5.0E-03 | BE266057.1 | EST_HUMAN | 601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5' |
| 3063 | 8080 | 13094 | 3.89 | 5.0E-03 | T87623.1 | EST_HUMAN | yc8ff09.s1 Scare infant brain TNB Homo sapiens cDNA clone IMAGE:22395 3' |
| 3081 | 8097 | | 2.71 | 5.0E-03 | AL181491.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3 |
| 3093 | 8109 | 13126 | 1.36 | 5.0E-03 | R71784.1 | EST_HUMAN | y86g02.s1 Scare breast 2NIBHs1 Homo sapiens cDNA clone IMAGE:155666 3' |
| 3204 | 8219 | | 0.75 | 5.0E-03 | AJ297357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 3616 | 8623 | 13631 | 3.67 | 5.0E-03 | AF147449.2 | NT | Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds |
| 3673 | 8678 | 13681 | 0.67 | 5.0E-03 | U38914.1 | NT | Citrus sinensis seed storage protein citrin mRNA, complete cds |
| 3864 | 8866 | | 1.7 | 5.0E-03 | AA298657.1 | EST_HUMAN | EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end |
| 4119 | 8678 | 13681 | 0.68 | 5.0E-03 | U38914.1 | NT | Citrus sinensis seed storage protein citrin mRNA, complete cds |
| 4476 | 9466 | 14445 | 0.78 | 5.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 4580 | 9568 | 14557 | 1.55 | 5.0E-03 | AI752367.1 | EST_HUMAN | cm15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm15c02 random |
| 232 | 5295 | 10304 | 2.13 | 4.0E-03 | AW500196.1 | EST_HUMAN | UI-HF-BN0-ak-c-h-04-0-U_1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:30768315' |
| 319 | 5374 | 10383 | 1.88 | 4.0E-03 | R46482.1 | EST_HUMAN | y951e04.s1 Scare infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3' |
| 440 | 5477 | 10485 | 0.67 | 4.0E-03 | P54675 | SWISSPROT | PHOSPHATIDYLINOSITOL 3-KINASE (PTDINS-3-KINASE) (P13K) |
| 598 | 5629 | 10628 | 3.1 | 4.0E-03 | AA939339.1 | EST_HUMAN | ont75g12.s1 Scare NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15625666 3' |
| 886 | 5884 | 10927 | 1.7 | 4.0E-03 | R46482.1 | EST_HUMAN | y951e04.s1 Scare infant brain TNB Homo sapiens cDNA clone IMAGE:35988 3' |
| 900 | 5918 | | 2.96 | 4.0E-03 | AW749101.1 | EST_HUMAN | RC3-BT0333-110100-012-f01_B10333 Homo sapiens cDNA |
| 1133 | 6138 | 11169 | 24.08 | 4.0E-03 | AA058977.1 | EST_HUMAN | z871a08.r1 Strategene colon #937204 Homo sapiens cDNA clone IMAGE:510998 5' |
| 1151 | 6155 | 11188 | 1.42 | 4.0E-03 | AW794740.1 | EST_HUMAN | RC6-LM0014-170400-023-G01 UM0014 Homo sapiens cDNA |
| 1284 | 6283 | 11325 | 1.02 | 4.0E-03 | AA284374.1 | EST_HUMAN | z559a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5' |
| 1551 | 6548 | | 1.29 | 4.0E-03 | AV708305.1 | EST_HUMAN | AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5' |
| 1704 | 6699 | 11775 | 1.99 | 4.0E-03 | U33472.1 | NT | Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds |
| 1968 | 6953 | 12058 | 7.06 | 4.0E-03 | AA059777.1 | EST_HUMAN | z871a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5' |
| 2186 | 7165 | | 1.43 | 4.0E-03 | BE410556.1 | EST_HUMAN | 601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3538510 5' |
| 2215 | 7192 | 12314 | 1.14 | 4.0E-03 | AW794740.1 | EST_HUMAN | RC6-LM0014-170400-023-G01 UM0014 Homo sapiens cDNA |
| 2498 | 7466 | 12580 | 1.56 | 4.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (FPL1Ba), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 2619 | 7581 | 12691 | 2.52 | 4.0E-03 | AJ277365.1 | NT | Homo sapiens polyglutamine-containing C14orf4 gene |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2619 | 7581 | 12692 | 2.52 | 4.0E-03 | AJ277365.1 | NT | Homo sapiens polyglutamine-containing C14ORF4 gene |
| 2624 | 7585 | 12695 | 1.04 | 4.0E-03 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3154 | 8170 | 13191 | 1.06 | 4.0E-03 | BE154134.1 | EST_HUMAN | PM1-HT0340_151289-003-n08 HT0340 Homo sapiens cDNA |
| 3154 | 8170 | 13192 | 1.06 | 4.0E-03 | BE154134.1 | EST_HUMAN | PM1-HT0340_151289-003-n08 HT0340 Homo sapiens cDNA |
| 3452 | 8460 | 13486 | 0.92 | 4.0E-03 | AW188426.1 | EST_HUMAN | X98f04_X1_NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279'3' |
| 3452 | 8460 | 13487 | 0.92 | 4.0E-03 | AW188426.1 | EST_HUMAN | X98f04_X1_NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279'3' |
| 3815 | 8548 | 13556 | 1.02 | 4.0E-03 | Q13606 | SWISSPROT | OLFFACTORY RECEPTOR 51 (OLFFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 3889 | 8889 | | 1.73 | 4.0E-03 | AJ011712.1 | NT | Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS) |
| 4480 | 9470 | 14451 | 1.08 | 4.0E-03 | AI732754.1 | EST_HUMAN | ab18a08_x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142'3' similar to contains Alu repetitive element |
| 370 | 5419 | 10434 | 2.62 | 3.0E-03 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 868 | 5886 | 10928 | 5.77 | 3.0E-03 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 1621 | 6618 | 11684 | 2.72 | 3.0E-03 | AA468110.1 | EST_HUMAN | nc73c05_s1_NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:7829B4 similar to contains Alu repetitive element; |
| 2231 | 7208 | | 7.09 | 3.0E-03 | Z32521.1 | NT | S.cereale (cv. Halo) mRNA for triosephosphate isomerase |
| 2232 | 7209 | 12323 | 0.92 | 3.0E-03 | U46858.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| 2232 | 7209 | 12324 | 0.92 | 3.0E-03 | U46858.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| 2923 | 7942 | | 0.93 | 3.0E-03 | Y09006.1 | NT | Arabidopsis thaliana rpl17 gene |
| 3009 | 8026 | 13038 | 4.49 | 3.0E-03 | BE37926.1 | EST_HUMAN | 601237982f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608933 5' |
| 3078 | 8094 | 13108 | 3.09 | 3.0E-03 | AW802687.1 | EST_HUMAN | IL2-LJM0076-240300-056-D03 UM0076 Homo sapiens cDNA |
| 3333 | 8343 | 13361 | 2.06 | 3.0E-03 | U34606.1 | NT | Mus musculus alpha-1(XVII) collagen (COL1BA1) gene, exon 1 and 2 |
| 3342 | 8351 | | 7.49 | 3.0E-03 | Y12500.1 | NT | C.elegans strand gene |
| 3870 | 8871 | 13876 | 7.05 | 3.0E-03 | AV762392.1 | EST_HUMAN | AV762392 MDS Homo sapiens cDNA clone MDSESG01 5' |
| 3870 | 8871 | 13877 | 7.05 | 3.0E-03 | AV762392.1 | EST_HUMAN | AV762392 MDS Homo sapiens cDNA clone MDSESG01 5' |
| 3925 | 8925 | 13915 | 1.6 | 3.0E-03 | AI792278.1 | EST_HUMAN | eh04fd9_5f Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155639 5' |
| 4027 | 9023 | | 1.04 | 3.0E-03 | Z32521.1 | NT | S.cereale (cv. Halo) mRNA for triosephosphate isomerase |
| 4271 | 9264 | 14254 | 4.26 | 3.0E-03 | AJ011432.1 | NT | Rattus norvegicus gdf1 gene |
| 4338 | 9329 | | 0.68 | 3.0E-03 | BE348739.1 | EST_HUMAN | hf68g08_X1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3' |
| 4387 | 9378 | 14359 | 5.15 | 3.0E-03 | AI536141.1 | EST_HUMAN | xu8.P10.H3 econorm Homo sapiens cDNA |
| 4686 | 9671 | 14653 | 2.19 | 3.0E-03 | AJ732754.1 | EST_HUMAN | ab18a08_x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142'3' similar to contains Alu repetitive element |
| 4705 | 9690 | 14673 | 6.19 | 3.0E-03 | BE787945.1 | EST_HUMAN | 60148271f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3888483 5' |
| 4968 | 9945 | 14922 | 0.92 | 3.0E-03 | 4506414 | NT | Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA |
| 4968 | 9945 | 14923 | 0.92 | 3.0E-03 | 4506414 | NT | Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 5014 | 9885 | 14961 | 0.98 | 3.0E-03 | SG2213.1 | NT | CD11b-leukocyte integrin alpha chain [human, Genomic, 104 nt, segment 23 of 31] |
| 511 | 5546 | 10550 | 0.69 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 511 | 5546 | 10551 | 0.69 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 777 | 7731 | | | 10.87 | T70874.1 | EST_HUMAN | Yd15n03_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5' |
| 1346 | 6343 | 11394 | 1.92 | 2.0E-03 | M20783.1 | NT | Human alpha-2-plasmin inhibitor gene, exons 6 and 7 |
| 1348 | 6345 | 11396 | 1.98 | 2.0E-03 | AA661605.1 | EST_HUMAN | nu86f01_s1 NCI_CGAP AlVi Homo sapiens cDNA clone IMAGE:1217593 |
| 1357 | 6354 | 11404 | 8.74 | 2.0E-03 | AF284446.1 | NT | Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds |
| 1458 | 6455 | 11514 | 4.39 | 2.0E-03 | P48509 | SWISSPROT | PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA3) (GP27) MEMBRANE GLYCOPROTEIN (SFA-1) (CD151 ANTIGEN) |
| 1485 | 6482 | 116337 | 1.7 | 2.0E-03 | 4557836 | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA |
| 1485 | 6482 | 115338 | 1.7 | 2.0E-03 | 4557836 | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA |
| 1556 | 6553 | | | 4.37 | 2.0E-03 | P29400 | COLLAGEN ALPHA 5(V) CHAIN PRECURSOR |
| 1734 | 6729 | 11806 | 1.16 | 2.0E-03 | AA450138.1 | EST_HUMAN | z242a10.1 Soares_total fetus_Nb21If8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 1949 | 6935 | 12036 | 1.19 | 2.0E-03 | AF302691.1 | NT | Mus musculus myelin expression factor-3-like protein gene, partial cds |
| 2188 | 7167 | 12287 | 1.03 | 2.0E-03 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 2504 | 7472 | | | 3.15 | 2.0E-03 | AW137782.1 | EST_HUMAN |
| 3332 | 8342 | 13380 | 5.57 | 2.0E-03 | AA450138.1 | EST_HUMAN | zr242a10.1 Soares_total fetus_Nb21If8_9w Homo sapiens cDNA clone IMAGE:2717010 3' |
| 3338 | 8347 | 13365 | 0.86 | 2.0E-03 | BF568955.1 | EST_HUMAN | 602183965011 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 31 |
| 3582 | 8589 | 13593 | 5.61 | 2.0E-03 | X87344.1 | NT | H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DCB2 and RING8, 9, 13 and 14 genes |
| 3997 | 8993 | 13980 | 2.35 | 2.0E-03 | P03374 | SWISSPROT | ENV POLYPROTEIN (CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36) |
| 4099 | 9093 | | 8.68 | 2.0E-03 | U68491.1 | NT | Rattus norvegicus 5-hydroxytryptamine receptor gene, partial cds |
| 4303 | 9295 | | | 1.17 | 2.0E-03 | AW297380.1 | EST_HUMAN |
| 4307 | 9299 | 14285 | 0.92 | 2.0E-03 | AI064748.1 | EST_HUMAN | UI-H-BW0-sfrg-03-0-U1_s1 NCI_CGAP_Sub6 Homo sapiens cDNA library Homo sapiens cDNA HA0507 Human fetal liver cDNA library Homo sapiens cDNA |
| 4415 | 9405 | 14390 | 2.22 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds |
| 4415 | 9405 | 14391 | 2.22 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds |
| 4573 | 9561 | | 1.9 | 2.0E-03 | R87773.1 | EST_HUMAN | y045e02_s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3' |
| 4861 | 9842 | 14814 | 0.94 | 2.0E-03 | AF003528.1 | NT | Homo sapiens X-linked arthridistic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 436 | 5474 | 10490 | 1.26 | 1.0E-03 | H96471.1 | EST_HUMAN | yf88c08_r1 Soares_pineal gland N3HPG Homo sapiens cDNA clone IMAGE:232334 5' |
| 819 | 5839 | 10876 | 1.31 | 1.0E-03 | AI720263.1 | EST_HUMAN | es70b08_x1 Bertrand colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE; |

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Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 819 | 5839 | 10877 | 1.31 | 1.0E-03 | AI720263.1 | EST_HUMAN | as7/0b08_x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR.Q13825 |
| 1078 | 6085 | 11114 | 3.35 | 1.0E-03 | AI865788.1 | EST_HUMAN | wk86a06_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' |
| 1098 | 6105 | 11135 | 1.17 | 1.0E-03 | AI954572.1 | EST_HUMAN | wk83e10_x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3' |
| 1148 | 6152 | 11184 | 4.08 | 1.0E-03 | AI692616.1 | EST_HUMAN | wdb6a01_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element |
| 1977 | 6962 | 12069 | 2.86 | 1.0E-03 | P47808 | SWISSPROT | HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI) |
| 2093 | 7074 | 12188 | 4.54 | 1.0E-03 | AJ131016.1 | NT | Homo sapiens mRNA for KIAA1291 protein, partial cds |
| 2911 | 7930 | 12549 | 1.8 | 1.0E-03 | AB033117.1 | NT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) |
| 3118 | 8134 | 13153 | 2.17 | 1.0E-03 | P18915 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (SALIVARY CARBONIC ANHYDRASE) |
| 3118 | 8134 | 13154 | 2.17 | 1.0E-03 | P18915 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) |
| 3228 | 8243 | 13265 | 0.75 | 1.0E-03 | P08547 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (SALIVARY CARBONIC ANHYDRASE) |
| 3466 | 8474 | 13498 | 0.78 | 1.0E-03 | U68061.1 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3466 | 8474 | 13499 | 0.76 | 1.0E-03 | U68061.1 | NT | Human MUC2 gene, promoter region |
| 3581 | 8598 | | 1.51 | 1.0E-03 | AB044400.1 | NT | Human MUC2 gene, promoter region |
| 3831 | 8833 | 13840 | 0.76 | 1.0E-03 | Z49849.1 | NT | Homo sapiens: SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 |
| 4312 | 9304 | 14288 | 5.29 | 1.0E-03 | BE989162.1 | EST_HUMAN | S.cerevisiae chromosome X reading frame ORF YJR149w |
| 4349 | 9340 | 14321 | 4.94 | 1.0E-03 | BE246536.1 | EST_HUMAN | RC1-TN0128-160800-021-001 TN0128 Homo sapiens cDNA TCBAP1D919 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA_Homo sapiens cDNA clone TCBAP4909 |
| 4538 | 9518 | 14505 | 0.91 | 1.0E-03 | U29449.1 | NT | Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes |
| 4677 | 9662 | 14644 | 1.69 | 1.0E-03 | AI073485.1 | EST_HUMAN | ai45604_x1_Sparres_tests_NHT Homo sapiens cDNA clone IMAGE:1640282 3' |
| 4677 | 9662 | 14645 | 1.69 | 1.0E-03 | AI073485.1 | EST_HUMAN | ai45c04_x1_Sparres_tests_NHT Homo sapiens cDNA clone IMAGE:1640282 3' |
| 4678 | 9663 | | 5.57 | 1.0E-03 | BE154067.1 | EST_HUMAN | PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA |
| 4905 | 9884 | 14855 | 8.4 | 1.0E-03 | O46409 | SWISSPROT | APOLIOPROTEIN A-IV PRECURSOR (APO-IV) |
| 4866 | 9875 | 14843 | 1.32 | 9.0E-04 | AA815400.1 | EST_HUMAN | ai61c12_s1_Sparres_tests_NHT Homo sapiens cDNA clone 1375318 3' similar to SW.AATC_CHICK P00504 |
| 4056 | 9050 | | 4.35 | 8.0E-04 | P08547 | SWISSPROT | ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ; LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 4619 | 9604 | 14592 | 2.42 | 8.0E-04 | U29185.1 | NT | Homo sapiens: prion protein (PrP) gene, complete cds |
| 2325 | 7309 | 12430 | 1.75 | 7.0E-04 | U29185.1 | NT | Homo sapiens: prion protein (PrP) gene, complete cds |
| 2642 | 7602 | 12715 | 1.09 | 7.0E-04 | AL163210.2 | NT | Homo sapiens: chromosome 21 segment HS21 C2010 |
| 3207 | 82222 | 13244 | 1.03 | 7.0E-04 | 4885170 | NT | Homo sapiens: chromosome X open reading frame 6 (CXorf6) mRNA |
| 3853 | 8855 | 13860 | 1.51 | 6.0E-04 | AI862525.1 | EST_HUMAN | wj15a11_x1_NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4060 | 9054 | 14041 | 3.01 | 6.0E-04 | U45983_1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 643 | 5671 | 10675 | 10.72 | 5.0E-04 | O10341 | SWISSPROT | HYPOTHETICAL 29.3 KD PROTEIN (ORF92) |
| 1472 | 6469 | | 1.4 | 5.0E-04 | AW851844_1 | EST_HUMAN | QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Aliu |
| 3329 | 8339 | 13357 | 1.21 | 5.0E-04 | AA548931_1 | EST_HUMAN | nl27611.s1 NCLCGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Aliu repetitive element; |
| 665 | 5691 | 10700 | 1.07 | 4.0E-04 | U32748_1 | NT | Haemophilus influenzae Rd section 63 of 163 of the complete genome |
| 837 | 5856 | 10896 | 1.34 | 4.0E-04 | AI720263_1 | EST_HUMAN | as70b08_x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 837 | 5856 | 10897 | 1.34 | 4.0E-04 | AI720263_1 | EST_HUMAN | Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ; |
| 1437 | 6434 | 11491 | 2.18 | 4.0E-04 | AW753356_1 | EST_HUMAN | as70b08_x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 2030 | 7013 | 12122 | 1.19 | 4.0E-04 | AL163278_2 | NT | Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ; |
| 2075 | 7057 | | 0.94 | 4.0E-04 | AL046704_1 | EST_HUMAN | RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA clone DKFZp434D059 5' |
| 2554 | 7519 | 12636 | 2.01 | 4.0E-04 | O96615 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C078 |
| 3091 | 8107 | 13123 | 3.3 | 4.0E-04 | AF281074_1 | NT | DKFZp434D059 r1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434D059 5' |
| 3776 | 8779 | | 1.12 | 4.0E-04 | AL163267_2 | NT | SERINC2 (SILK GUM PROTEIN 2) |
| 4196 | 9189 | 14169 | 2.79 | 4.0E-04 | AA576331_1 | EST_HUMAN | Homo sapiens neurophilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 4196 | 9189 | 14170 | 2.79 | 4.0E-04 | AA576331_1 | EST_HUMAN | Hom sapiens chromosome 21 segment HS21C067 |
| 4407 | 9398 | 14382 | 2.39 | 4.0E-04 | AA086324_1 | EST_HUMAN | Hom sapiens chromosome 21 segment HS21C067 |
| 4915 | 9893 | 14867 | 3.42 | 4.0E-04 | BE560680_1 | EST_HUMAN | nh10a10 s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC FRANTES PROTEIN PRECURSOR (HUMAN); |
| 5019 | 9890 | 14965 | 1.02 | 4.0E-04 | NA4831_1 | EST_HUMAN | nh10a10 s1 NCL CGAP Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC FRANTES PROTEIN PRECURSOR (HUMAN); |
| 155 | 5221 | 10233 | 2.94 | 3.0E-04 | AL119426_1 | EST_HUMAN | DKFZp761j221_1761 (synonym: hany2) Homo sapiens cDNA clone DKFZp761j221 5' |
| 195 | 5259 | 10272 | 1.5 | 3.0E-04 | P49259 | SWISSPROT | 180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R) |
| 869 | 5887 | 10929 | 2.14 | 3.0E-04 | U83891_1 | NT | Human short chain acyl CoA dehydrogenase gene, exons 1 and 2 |
| 1803 | 6794 | 111884 | 1.68 | 3.0E-04 | AI262100_1 | EST_HUMAN | q228d03_y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5' |
| 1817 | 6807 | | 2.03 | 3.0E-04 | AI399674_1 | EST_HUMAN | th23a02_x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2116082 3' |
| 3236 | 8250 | 13271 | 4.06 | 3.0E-04 | P25147 | SWISSPROT | INTERNALIN B PRECURSOR |
| 3857 | 8859 | 13865 | 3.31 | 3.0E-04 | P49448 | SWISSPROT | GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH) |
| 3942 | 8940 | | 1.31 | 3.0E-04 | AJ271735_1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 3946 | 8974 | | 1.09 | 3.0E-04 | BE140609_1 | EST_HUMAN | RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA |
| 4671 | 9656 | | 5.1 | 3.0E-04 | BE153778_1 | EST_HUMAN | PM0-HT039-190200-007-312 HT039 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| | | | | | | | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M6B, and ADP-ribosylation factor related protein 1 (ARFIP1) genes, complete cds |
| 175 | 5239 | 10250 | 1.52 | 2.0E-04 | Af217786.1 | NT | AU146707 HEMBB1 Homo sapiens cDNA clone IMAGE:1001253 3' |
| 475 | 5511 | 10524 | 5.11 | 2.0E-04 | AU146707.1 | EST_HUMAN | Human dystrophin gene |
| 896 | 5914 | 10953 | 6.36 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 896 | 5914 | 10954 | 6.36 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 1160 | 6164 | | 3.63 | 2.0E-04 | AI286021.1 | EST_HUMAN | q98e11_x1 Soesres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3_b2 MER3 repetitive element; |
| 1167 | 6170 | | 2.07 | 2.0E-04 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C0033 |
| 1796 | 6787 | | 0.97 | 2.0E-04 | AF224268.1 | NT | Mus musculus 5' flanking region of Pib3 gene |
| 2120 | 7100 | | 1.21 | 2.0E-04 | AA478980.1 | EST_HUMAN | z13gb05_s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Au repetitive element; |
| | | | | | | | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV17S1A1T, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB_relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TCRBJ1S1, TCRBJ1S2, am5gc09_x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3' |
| 2500 | 7468 | 12583 | 3.15 | 2.0E-04 | U66061.1 | NT | QV2-BT0636-C70500-194-b07 BT0636 Homo sapiens cDNA |
| 2918 | 7937 | 12954 | 1.18 | 2.0E-04 | A1124529.1 | EST_HUMAN | Human tyrosine kinase TXX (tak) gene, exons 9 and 10 |
| 3260 | 8273 | 13296 | 1.1 | 2.0E-04 | 5174736 | NT | EST390550 IMAGE resequences, MAGP Homo sapiens cDNA |
| 3351 | 8360 | 13376 | 2.67 | 2.0E-04 | BE082317.1 | EST_HUMAN | Phaeocystis vulgaris nitrate reductase (PVNR2) gene, complete cds |
| 3381 | 8389 | 13412 | 0.91 | 2.0E-04 | U34374.1 | NT | jud1le11_r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5' |
| 3816 | 8818 | 13825 | 1.04 | 2.0E-04 | AW978441.1 | EST_HUMAN | jud1le11_r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5' |
| 4020 | 9016 | | 5.76 | 2.0E-04 | U01029.1 | NT | Galus gallus proteasome 28 kDa subunit homolog mRNA, complete cds |
| 4534 | 9524 | 14511 | 1.51 | 2.0E-04 | H96265.1 | EST_HUMAN | Danio rerio haicromo gene, exons 1 to 6, partial cds |
| 4534 | 9524 | 14512 | 1.51 | 2.0E-04 | H96265.1 | EST_HUMAN | yc28e09_s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element; |
| 4651 | 8636 | | 1.39 | 2.0E-04 | U09226.1 | NT | RETRORVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 4891 | 9870 | 14838 | 1.87 | 2.0E-04 | AB037997.1 | NT | U1-H-B10-aeb-9-0-U:s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 758 | 5779 | 10806 | 1.09 | 1.0E-04 | H99646.1 | EST_HUMAN | U1-H-B10-aeb-9-0-U:s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1058 | 6067 | 11097 | 1.86 | 1.0E-04 | P11369 | SWISSPROT | U1-H-B10-aeb-9-0-U:s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1097 | 6104 | 11133 | 3.05 | 1.0E-04 | AW013847.1 | EST_HUMAN | U1-H-B10-aeb-9-0-U:s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1097 | 6104 | 11134 | 3.05 | 1.0E-04 | AW013847.1 | EST_HUMAN | Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds |
| 1312 | 6309 | | 3.3 | 1.0E-04 | U62918.1 | NT | |

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Table 4
Single Exon Probes Expressed in H1BL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit No. | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|---------------|-----------------------|-------------------------|--|
| | | | | | | | | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycaminidine synthase, and LAMP (LAMP) genes, complete cds |
| 1588 | 6585 | 11646 | 3.97 | 1.0E-04 | AF148805.1 | NT | | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycaminidine synthase, and LAMP (LAMP) genes, complete cds |
| 1588 | 6585 | 11647 | 3.97 | 1.0E-04 | AF148805.1 | NT | | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycaminidine synthase, and LAMP (LAMP) genes, complete cds |
| 1824 | 6814 | 11908 | 1.7 | 1.0E-04 | AB048342.1 | NT | | Equus caballus DNA, chromosome 24q14, microsatellite TKY36 |
| 3211 | 8226 | 13248 | 0.96 | 1.0E-04 | Q62203 | | SWISSPROT | SPliceosome ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66) |
| 3651 | 8657 | 13663 | 0.72 | 1.0E-04 | AI440282.1 | EST_HUMAN | | [p]01f11_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element |
| 3948 | 8946 | 13936 | 1.86 | 1.0E-04 | M14042.1 | NT | | Mouse alpha 1 type-IV collagen mRNA |
| 3967 | 8966 | 13955 | 1.09 | 1.0E-04 | AV647727.1 | EST_HUMAN | | AV647727 GLC Homo sapiens cDNA clone GLCBBD04 3' |
| 4925 | 8902 | 14878 | 1.64 | 1.0E-04 | 7662015 | NT | | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |
| 4925 | 8902 | 14879 | 1.84 | 1.0E-04 | 7662015 | NT | | Homo sapiens KIAA0237 gene product (KIAA0237), mRNA |
| 689 | 5713 | 10727 | 1.84 | 9.0E-05 | AA718933.1 | EST_HUMAN | | ah45c11.1st Scares testis NHT Homo sapiens cDNA clone 1292468 3' |
| 811 | 5832 | 10865 | 1.19 | 9.0E-05 | AJ251646.1 | NT | | Pisum sativum mRNA for beta-1,3 glucanase (grn2 gene) |
| 853 | 5872 | | | 12.78 | 8.0E-05 | AJ251646.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (grn2 gene) |
| 4353 | 9344 | 14323 | 0.67 | 8.0E-05 | AW044605.1 | EST_HUMAN | | wy78a04_x1 Scares_NSF_F8_9W_OT_PA_P_S1_Homo sapiens cDNA clone IMAGE:2556463B 3' |
| 345 | 5397 | 10404 | 11.8 | 7.0E-05 | AW847445.1 | EST_HUMAN | | RC3-C10208-2-20899-01-1-E04 C10208 Homo sapiens cDNA |
| 345 | 5397 | 10405 | 11.8 | 7.0E-05 | AW847445.1 | EST_HUMAN | | RC3-C10208-2-20899-01-1-E04 C10208 Homo sapiens cDNA |
| 562 | 5596 | 10595 | 1.24 | 7.0E-05 | L49075.1 | EST_HUMAN | | HUM072014F Human foetal cDNA Homo sapiens cDNA clone EST_HFD072014 |
| 562 | 5596 | 10596 | 1.24 | 7.0E-05 | L49075.1 | EST_HUMAN | | HUM072014F Human foetal cDNA Homo sapiens cDNA clone EST_HFD072014 |
| 1038 | 6048 | 11078 | 1.43 | 7.0E-05 | Q22949 | | SWISSPROT | PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT) |
| 2646 | 7606 | 12718 | 2.46 | 7.0E-05 | AL163278.2 | NT | | Homo sapiens chromosome 21 segment HS21C078 |
| 3085 | 8101 | 13116 | 4.38 | 7.0E-05 | AB009080.1 | NT | | Dictyostelium discoideum gene for TRFA, complete cds |
| 3617 | 8624 | | 1.24 | 7.0E-05 | AI432413.1 | EST_HUMAN | | tg73c09_x1 Scares_NhHMPPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3' |
| 3943 | 8941 | | | 0.72 | 7.0E-05 | AF111167.2 | NT | Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 4247 | 8241 | 14225 | 1.61 | 7.0E-05 | AL163201.2 | NT | | Homo sapiens chromosome 21 segment HS21C01 |
| 4769 | 9753 | 14741 | 0.66 | 7.0E-05 | 9845300 | NT | | Rat cytomegalovirus Maastricht, complete genome |
| 1976 | 6961 | 12067 | 1.6 | 6.0E-05 | 4885170 | NT | | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 1976 | 6961 | 12068 | 1.6 | 6.0E-05 | 4885170 | NT | | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| | | | | | | | wb54n06_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gbi:J03250 DNA |
| 2513 | 7481 | 12597 | 1.15 | 6.0E-05 | AI655241.1 | EST_HUMAN | TOPOISOMERASE I (HUMAN) |
| 2742 | 5696 | 10704 | 2.86 | 6.0E-05 | AF053630.1 | NT | Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds |
| 1379 | 6376 | 11424 | 65.3 | 5.0E-05 | AW392086.1 | EST_HUMAN | QV4-ST0234-241189-040t-h11 ST0234 Homo sapiens cDNA |
| 1826 | 6816 | | 2.39 | 5.0E-05 | 8923891 | NT | Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA |
| 2790 | 7811 | 12828 | 0.67 | 5.0E-05 | AI251058.1 | NT | Homo sapiens MEP1A gene, promoter region and exon 1 |
| 3872 | 8873 | 13878 | 4.04 | 5.0E-05 | AI251884.1 | NT | Homo sapiens partial SLC22a13 gene for extraneuronal monoamine transporter (EMT), exon 1 |
| 2735 | 5289 | | 3.87 | 4.0E-05 | U12821.1 | NT | Human renin (R.E.N.) gene, 5' flanking region |
| 4355 | 9346 | 14325 | 0.92 | 4.0E-05 | P49193 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 4355 | 9346 | 14326 | 0.92 | 4.0E-05 | P49193 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 4725 | 9710 | | 0.99 | 4.0E-05 | AI164488.1 | NT | Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds |
| 672 | 5697 | 10706 | 0.69 | 3.0E-05 | AI248061.1 | EST_HUMAN | contains Alu repetitive element; contains element KER repetitive element; |
| 1042 | 6052 | 11082 | 1.01 | 3.0E-05 | AW2723851.1 | EST_HUMAN | x22403_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3' |
| 1114 | 6120 | 11148 | 1.64 | 3.0E-05 | BF037898.1 | EST_HUMAN | 601461463F11 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:38651142 5' |
| 1114 | 6120 | 11149 | 1.64 | 3.0E-05 | BF037899.1 | EST_HUMAN | 601461463F11 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:38651142 5' |
| 2648 | 7608 | 12720 | 0.92 | 3.0E-05 | Q62234 | SWISSPROT | SKELMIN |
| 4257 | 9251 | 14237 | 9.42 | 3.0E-05 | BE165211.1 | EST_HUMAN | PM1-HT0521-1-20200-001-010 HT0521 Homo sapiens cDNA |
| 4257 | 9251 | 14238 | 9.42 | 3.0E-05 | BE169211.1 | EST_HUMAN | PM1-HT0521-1-20200-001-010 HT0521 Homo sapiens cDNA |
| 4342 | 9333 | 14316 | 0.94 | 3.0E-05 | AA368679.1 | EST_HUMAN | EST78986 Flakenta I Homo sapiens cDNA similar to p53-associated protein |
| 4342 | 9333 | 14317 | 0.94 | 3.0E-05 | AA368679.1 | EST_HUMAN | EST78986 Flakenta I Homo sapiens cDNA similar to p53-associated protein |
| 4486 | 9476 | 14456 | 0.76 | 3.0E-05 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 4695 | 9680 | 14663 | 0.93 | 3.0E-05 | AU125721.1 | EST_HUMAN | AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM402075 5' |
| 2262 | 7239 | 12356 | 1.33 | 2.0E-05 | AI286021.1 | EST_HUMAN | qh88e11_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contents MER3.b2 MER3 repetitive element; |
| 2506 | 7474 | 12589 | 1.85 | 2.0E-05 | M13792.1 | NT | Human adenosine deaminase (ADA) gene, complete cds |
| 2641 | 7601 | | | 5.26 | 2.0E-05 | AA160562.1 | EST_HUMAN |
| 3064 | 8081 | 13095 | | 1.66 | 2.0E-05 | BE066036.1 | EST_HUMAN |
| 3272 | 8284 | 13307 | | 0.85 | 2.0E-05 | AF18461.1 | NT |
| 328 | 8288 | 13325 | | 1.06 | 2.0E-05 | X89211.1 | NT |
| 3414 | 8423 | | | 0.69 | 2.0E-05 | X95465.1 | NT |
| 2623 | 7777 | 12694 | | 1.66 | 1.0E-05 | AL163282.2 | NT |
| 3565 | 8572 | 13578 | | 2.01 | 1.0E-05 | AF088273.1 | NT |

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 Table 4
 Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| | | | | | | | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 3723 | 8727 | | | 1.18 | 1.0E-05 AF223391.1 | NT SWISSPROT | MOSAIC PROTEIN LGN |
| 3860 | 8862 | 13867 | | 10.08 | 1.0E-05 P81274 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4049 | 9045 | 14033 | | 1.04 | 1.0E-05 AL163203.2 | | Homo sapiens chromosome 21 segment HS21C003 |
| 4155 | 9150 | 14132 | | 1.76 | 1.0E-05 AA431119.1 | EST_HUMAN | Zw69g04.11 Soares_testis_NHt Homo sapiens cDNA clone IMAGE:2856548 3' |
| 4703 | 9688 | 14671 | | 1.9 | 1.0E-05 AW419134.1 | EST_HUMAN | Xy49g1.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2246386 3' |
| 2601 | 7563 | 12981 | | 2.89 | 9.0E-06 A1583811.1 | EST_HUMAN | Itf73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3' |
| 3022 | 8039 | 13048 | | 4.56 | 9.0E-06 A1218983.1 | EST_HUMAN | Scareas_placenta_8to9weeks_2NbHP8tgcW Homo sapiens cDNA clone IMAGE:1759191 3' |
| 3529 | 8535 | | | 2.64 | 9.0E-06 M61755.1 | NT | Human alanine:pyruvate aminotransferase (AGXT) gene, exons 1 and 2 |
| 2458 | 7771 | 12543 | | 1.52 | 8.0E-06 AW362539.1 | EST_HUMAN | RC3-C_T0283-201199-01-h11 CT0283 Homo sapiens cDNA clone IMAGE:854251 3' similar to contains ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' |
| 964 | 5979 | | | 1.3 | 7.0E-06 AA669729.1 | EST_HUMAN | MER20.11 MER20 repetitive element; |
| 1412 | 6410 | 11469 | | 2.42 | 7.0E-06 7662177 | NT | Homo sapiens KIAA0555 gene product (KIAA0555), mRNA |
| 2802 | 7822 | | | 6.96 | 7.0E-06 A136B252.1 | EST_HUMAN | qw16g9.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element; |
| 2847 | 7867 | 12883 | | 1.16 | 6.0E-06 BE069189.1 | EST_HUMAN | QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA |
| 2871 | 7890 | 12912 | | 1.03 | 6.0E-06 Q01456 | SWISSPROT | OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN) |
| 3609 | 8616 | 13625 | | 0.93 | 6.0E-06 BE069189.1 | EST_HUMAN | QV3-BT0379-C-10300-105-d11 BT0379 Homo sapiens cDNA |
| 4609 | 7890 | 12912 | | 1.96 | 6.0E-06 Q01456 | SWISSPROT | OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN) |
| 4616 | 9601 | 14587 | | 2.14 | 6.0E-06 A1040099.1 | EST_HUMAN | ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER3.12 MER3 repetitive element; |
| 639 | 5667 | 10670 | | 5.76 | 4.0E-06 R16267.1 | EST_HUMAN | ya48c03.r1 Soares_infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element;contains L1 repetitive element; |
| 846 | 5855 | 10895 | | 6.98 | 4.0E-06 AW103354.1 | EST_HUMAN | xo69g12.x1 NCI_CGAP_Esc02 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element;contains element MER21 repetitive element; |
| 1314 | 6311 | 11359 | | 3.35 | 4.0E-06 A1334928.1 | EST_HUMAN | tb33ed09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1314 | 6311 | 11360 | | 3.35 | 4.0E-06 A1334928.1 | EST_HUMAN | tb33ed09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1445 | 6442 | 11500 | | 1.85 | 4.0E-06 BF365612.1 | EST_HUMAN | QV2-NT0046-20080-250-H07 NT0046 Homo sapiens cDNA |
| 2203 | 7181 | 12304 | | 1.59 | 4.0E-06 AW015401.1 | EST_HUMAN | UI-H-B10-sat-T05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA |
| 2980 | 8008 | 13021 | | 0.74 | 4.0E-06 AF198849.1 | NT | Gallus gallus Dach2 protein (Dach2)mRNA, complete cds |
| 3769 | 8802 | 13807 | | 1.07 | 4.0E-06 AW848295.1 | EST_HUMAN | IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA |
| 4663 | 9848 | 14635 | | 1.95 | 4.0E-06 A1886939.1 | EST_HUMAN | wf94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element; |

Single Exon Probes Expressed in Table 4 Page 64 of 209

| Probe SEQ ID | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal Value | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|--------------|-----------------|----------------|-------------------------|--------------------------------------|-----------------------|-------------------------|--|
| 5047 | 10018 | 14987 | 1.04 | 4.0E-06 | AW817268.1 | EST_HUMAN | QV0-ST0247-09C200-105-e05 ST0247 Homo sapiens cDNA z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to |
| 2059 | 7080 | 12194 | 1.29 | 3.0E-06 | AA700562.1 | EST_HUMAN | z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' contains L1.1L1 repetitive element; |
| 2099 | 7080 | 12195 | 1.29 | 3.0E-06 | AA700562.1 | EST_HUMAN | z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' contains L1.1L1 repetitive element; |
| 2205 | 7182 | | 1.19 | 3.0E-06 | AF202635.1 | NT | Homo sapiens Pi1200 mRNA, complete cds |
| 2851 | 7871 | 12886 | 1.09 | 3.0E-06 | AA868218.1 | EST_HUMAN | ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.3 LTR1 repetitive element; |
| 3191 | 8207 | | 2.25 | 3.0E-06 | A1857779.1 | EST_HUMAN | wl22a05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1.t2 L1 repetitive element ; |
| 3695 | 8699 | 13701 | 1.73 | 3.0E-06 | BE047094.1 | EST_HUMAN | hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 3695 | 8699 | 13702 | 1.73 | 3.0E-06 | BE047094.1 | EST_HUMAN | hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 4430 | 9420 | 14406 | 2.51 | 3.0E-06 | X54816.1 | NT | Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N terminus.) |
| 4766 | 9750 | 14738 | 0.95 | 3.0E-06 | J04038.1 | NT | Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds |
| 4766 | 9750 | 14739 | 0.95 | 3.0E-06 | J04038.1 | NT | Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds |
| 202 | 5266 | | 2.36 | 2.0E-06 | P54366 | SWISSPROT | HOMEBOX PROTEIN GOOSECOID |
| 1535 | 6533 | | 4.34 | 2.0E-06 | P21414 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 2315 | 7290 | 12411 | 3.21 | 2.0E-06 | AI672138.1 | EST_HUMAN | wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30.b1 MER30 repetitive element; |
| 2397 | 7368 | 12489 | 1.48 | 2.0E-06 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (KAHRP) |
| 2494 | 7462 | 12577 | 4.19 | 2.0E-06 | P06719 | SWISSPROT | KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP) |
| 3441 | 8449 | 13475 | 1.07 | 2.0E-06 | AV657555.1 | EST_HUMAN | AV657555 GLC Homo sapiens cDNA clone GI_CFDB05 3' |
| 3676 | 8581 | 13684 | 1.7 | 2.0E-06 | AA173518.1 | EST_HUMAN | zp02e05.r1 Stratagene ovarian cancer (#83/219) Homo sapiens cDNA clone IMAGE:595232 3' |
| 3689 | 8693 | 13595 | 1.8 | 2.0E-06 | AB030896.1 | NT | Mus musculus gene for odorant receptor A16, complete cds |
| 34 | 5114 | | 10.00 | 1.11 | 1.0E-06 | O78882 | ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER) |
| 649 | 5677 | 10584 | 1.24 | 1.0E-06 | AF084364.1 | NT | Mus musculus D6MM53 protein (D6MM53) mRNA, complete cds |
| 1425 | 6422 | 11481 | 1.53 | 1.0E-06 | P09125 | SWISSPROT | MEROZOITE SURFACE PROTEIN CMZ-8 |
| 1491 | 6489 | 11544 | 0.92 | 1.0E-06 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 1948 | 6934 | 12034 | 3.32 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 1948 | 6934 | 12035 | 3.32 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 4244 | 9238 | 14221 | 13.65 | 1.0E-06 | U07561.1 | NT | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|---|--|--------------------|
| 4933 9910 | 14887 | 1.24 | 1.0E-06 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C0855 | |
| 4933 8910 | 14888 | 1.24 | 1.0E-06 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C0855 | |
| 359 5409 | 10421 | 1.02 | 9.0E-07 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions | |
| 359 5409 | 10422 | 1.02 | 9.0E-07 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions | |
| 4625 9610 | 14598 | 5.07 | 8.0E-07 | AI288596.1 | EST_HUMAN | q8zg07_X1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:18788763' | |
| 4625 9610 | 14599 | 5.07 | 8.0E-07 | AI288596.1 | EST_HUMAN | q8zg07_X1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:18788763' | |
| 1868 6857 | 11945 | 2.73 | 6.0E-07 | AW855558.1 | EST_HUMAN | CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA hydroxylase (CYPI21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, > 2421 7392 | |
| 3895 8867 | 12513 | 2.45 | 6.0E-07 | AF019413.1 | NT | SWISSPROT HYPOTHETICAL_24.1_KD PROTEIN IN LEF4-P33 INTERGENIC REGION | |
| 324 5378 | | 1.99 | 6.0E-07 | P41479 | EST_HUMAN | wh84f10-x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:23855473' | |
| 1040 6050 | | 0.9 | 5.0E-07 | AI831893.1 | EST_HUMAN | EST83615 Supt cells Homo sapiens cDNA 5' end | |
| 4511 9501 | 14480 | 1.83 | 5.0E-07 | AA380630.1 | EST_HUMAN | Hom sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds | |
| 3893 8893 | 13892 | 1.86 | 5.0E-07 | AF14974.1 | NT | ws84h05_x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:25046973' | |
| 438 5476 | 10492 | 5.45 | 3.0E-07 | U19719.1 | EST_HUMAN | Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons | |
| 578 5610 | 10609 | 2.79 | 3.0E-07 | AJ271735.1 | NT | Human sapiens Xq pseudautosomal region; segment 1/2 | |
| 1356 6353 | 11403 | 1.32 | 3.0E-07 | MS9149.1 | NT | Human polymorphic microsatellite DNA | |
| 1586 6583 | | 1.79 | 3.0E-07 | M64857.1 | NT | Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele | |
| 2224 7201 | 12320 | 0.94 | 3.0E-07 | MS9149.1 | NT | Human polymorphic microsatellite DNA | |
| 2399 7370 | 12491 | 26.28 | 3.0E-07 | BE005077.1 | EST_HUMAN | MRO-BN0115-020300-001-111 BN0115 Homo sapiens cDNA | |
| 2399 7370 | 12492 | 26.28 | 3.0E-07 | BE005077.1 | EST_HUMAN | MRO-BN0115-020300-001-111 BN0115 Homo sapiens cDNA | |
| 2964 7982 | 12996 | 0.85 | 3.0E-07 | T84704.1 | EST_HUMAN | yd50f12_r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:111695_5' | |
| 3086 8102 | 13117 | 1.64 | 3.0E-07 | P38739 | SWISSPROT HYPOTHETICAL_63.8_KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR | | |
| 4587 9575 | 14566 | 8.15 | 3.0E-07 | AV650201.1 | EST_HUMAN | AV650201 GLC Homo sapiens cDNA clone GL0CCDD01_3' | |
| 4895 9874 | 14841 | 1.6 | 3.0E-07 | T57850.1 | EST_HUMAN | yc14h09_s1 Stratagene lung (#93/210) Homo sapiens cDNA clone IMAGE:807053' similar to similar to | |
| 4895 9874 | 14842 | 1.6 | 3.0E-07 | T57850.1 | EST_HUMAN | gb: M62982 ARACHIDONATE_12-LIPOXYGENASE (HUMAN) | |
| 29 5109 | 10094 | 2.94 | 2.0E-07 | AF262988.1 | NT | Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds | |
| 153 5219 | 10231 | 23.84 | 2.0E-07 | L77569.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end | |
| 153 5219 | 10232 | 23.84 | 2.0E-07 | L77569.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end | |
| 181 5244 | 10255 | 129.68 | 2.0E-07 | U38849.1 | NT | Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds | |

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Table 4

Single Exon Probes Expressed in HEL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--|
| 739 | 5762 | 10785 | 1.46 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 739 | 5762 | 10786 | 1.46 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 929 | 5946 | 10980 | 1.99 | 2.0E-07 | AA223260.1 | EST_HUMAN | Z08b07.s1 Stratagen NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:J31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element; |
| 930 | 5947 | 10981 | 11.68 | 2.0E-07 | T63042.1 | EST_HUMAN | yc15g04.s1 Stratagen lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element; |
| 1145 | 6149 | 11181 | 0.93 | 2.0E-07 | Q28768 | SWISSPROT | IIS AUTOANTIGEN |
| 1565 | 6562 | 11625 | 2.13 | 2.0E-07 | Q09701 | SWISSPROT | HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1 |
| 3604 | 8611 | 13619 | 20.05 | 2.0E-07 | AF125348.1 | NT | Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds |
| 1085 | 6092 | | 1.43 | 1.0E-07 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 2754 | 6488 | 11543 | 2.14 | 1.0E-07 | P09256 | SWISSPROT | GLYCOPROTEIN GPV |
| 3659 | 6092 | | 3.91 | 1.0E-07 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 4169 | 9164 | 14150 | 2.86 | 1.0E-07 | AV718662 | GLC_Homo sapiens cDNA clone GLCFNF04 5' | AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5' |
| 4169 | 9164 | 14151 | 2.86 | 1.0E-07 | AV718662 | EST_HUMAN | AV718662 GLC Homo sapiens cDNA clone IMAGE:363026 5' |
| 4973 | 9949 | 14927 | 1.22 | 1.0E-07 | AA019181.1 | EST_HUMAN | z656q02_r1 Soares retina N2b4H homo sapiens cDNA clone IMAGE:2228273 3' |
| 604 | 7725 | | 2.23 | 8.0E-08 | A911352.1 | EST_HUMAN | wd16b05_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3943976 5' |
| 1033 | 6043 | | 0.8 | 8.0E-08 | BE793469.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5' |
| 3468 | 8476 | | 1.7 | 8.0E-08 | BE793469.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5' |
| 79 | 5156 | 10167 | 3.2 | 7.0E-08 | Q02357 | SWISSPROT | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) |
| 1344 | 6341 | 11392 | 42.98 | 7.0E-08 | X04809.1 | NT | Rat mRNA for ribosomal protein L31 |
| 3495 | 8503 | 13517 | 0.7 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 3495 | 8503 | 13518 | 0.7 | 7.0E-08 | P15305 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 807 | 5828 | 10858 | 2.78 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 807 | 5828 | 10859 | 2.78 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 2302 | 7277 | 12397 | 3.8 | 6.0E-08 | BE144398.1 | EST_HUMAN | MRO-HT0166-191198-004-509 HT0166 Homo sapiens cDNA |
| 2988 | 8006 | 13019 | 2.09 | 6.0E-08 | 7662473 | NT | Homo sapiens KIAA1074 protein (KIAA1074), mRNA |
| 4126 | 9121 | 14106 | 0.92 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 83 | 5160 | 10171 | 2.15 | 5.0E-08 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2174 | 7153 | 12273 | 1.68 | 5.0E-08 | AA493851.1 | EST_HUMAN | nh03b69_s1_N_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element; |
| 1722 | 6717 | 11793 | 1.2 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR |
| 1722 | 6717 | 11794 | 1.2 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR |
| 2815 | 7835 | | 1.1 | 4.0E-08 | AL079581.1 | EST_HUMAN | DKFZp434J0426 11434 (synonym: hbae3) Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element; |

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Table 4
Single Exon Probes Expressed in HEL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 206 | 5270 | | 8.87 | 2.0E-08 | AW302986.1 | EST_HUMAN | xr8706.x1 NCI CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3' |
| 227 | 5290 | | 7.99 | 2.0E-08 | AA425598.1 | EST_HUMAN | zw4807.r1 Scores: total_fetus_Nb2-HFB_8w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element; |
| 493 | 5529 | 10537 | 2.63 | 2.0E-08 | AF198349.1 | NT | Genus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 652 | 5680 | 10686 | 9.13 | 2.0E-08 | AW886438.1 | EST_HUMAN | MFO-OT0080-24(200-001)-908 OT0080 Homo sapiens cDNA |
| 652 | 5680 | 10687 | 9.13 | 2.0E-08 | AW886438.1 | EST_HUMAN | MFO-OT0080-24(200-001)-908 OT0080 Homo sapiens cDNA |
| 975 | 5991 | | 26.56 | 2.0E-08 | BE280477.1 | EST_HUMAN | 60115532(F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:31388B93 5' |
| 1323 | 6321 | 11369 | 1.74 | 2.0E-08 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 1702 | 6697 | | 1.75 | 2.0E-08 | BE734971.1 | EST_HUMAN | 601570463(F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5' |
| 1818 | 6808 | | 3.33 | 2.0E-08 | AW270271.1 | EST_HUMAN | xp4311.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3' |
| 2352 | 7326 | 12443 | 1.22 | 2.0E-08 | AA731948.1 | EST_HUMAN | rw64h01.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.13 L1 repetitive element; |
| 2472 | 7441 | | 1.31 | 2.0E-08 | K00216.1 | NT | Sheep His-tRNA-GUG |
| 3135 | 8151 | 13173 | 6.15 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3135 | 8151 | 13174 | 6.15 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3769 | 8772 | | 1.61 | 2.0E-08 | AW813620.1 | EST_HUMAN | RC3-ST0197-161098-012-b03 ST0197 Homo sapiens cDNA |
| 4281 | 9274 | | 1.32 | 2.0E-08 | AA459040.1 | EST_HUMAN | aa26c07.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:8714380 5' similar to contains L1.12 L1 repetitive element; |
| 4800 | 9784 | | 3.44 | 2.0E-08 | AW572981.1 | EST_HUMAN | he77h08.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element; |
| 1738 | 6733 | 11810 | 1.26 | 1.0E-08 | AF125348.1 | NT | Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds |
| 1998 | 6981 | | 1.58 | 1.0E-08 | BE141959.1 | EST_HUMAN | PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA |
| 3119 | 8135 | 13155 | 1.06 | 1.0E-08 | BE246844.1 | EST_HUMAN | TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP5232 |
| 3119 | 8135 | 13156 | 1.06 | 1.0E-08 | BE246844.1 | EST_HUMAN | sapiens cDNA clone TCBAP5232 |
| 4120 | 9114 | 14100 | 3.28 | 9.0E-09 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 4120 | 9114 | 14101 | 3.28 | 9.0E-09 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 3526 | 8532 | | 1.62 | 7.0E-09 | D86842.1 | NT | Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 |
| 4310 | 9302 | 14287 | 1.19 | 6.0E-09 | AF111167.2 | NT | Homo sapiens lun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 4821 | 9805 | 14787 | 4.89 | 6.0E-09 | BE169421.1 | EST_HUMAN | PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA |
| 1390 | 6387 | 11439 | 2.89 | 5.0E-09 | BE149264.1 | EST_HUMAN | RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1816 | 6806 | 11899 | 1.29 | 5.0E-09 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 517 | 5552 | | 1.41 | 4.0E-09 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 950 | 5966 | | 2.28 | 4.0E-09 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1441 | 6438 | 11495 | 2.05 | 4.0E-09 | 9558718 | NT | Homo sapiens hypothetical protein (AF038169). mRNA |
| 2362 | 7336 | 12453 | 17.61 | 4.0E-09 | AA350878.1 | EST_HUMAN | Homo sapiens cDNA 5' end similar to heat shock protein, 90 kDa EST5885 Infant brain Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 2290 | 7265 | 12383 | 3.39 | 3.0E-09 | BE222239.1 | EST_HUMAN | hu09609_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 2482 | 7450 | 12563 | 1.04 | 3.0E-09 | BE222239.1 | EST_HUMAN | MER18 repetitive element |
| 2578 | 7541 | 12655 | 0.92 | 3.0E-09 | P23249 | SWISSPROT | hu09609_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 3254 | 8267 | 13289 | 1.29 | 3.0E-09 | BE222239.1 | EST_HUMAN | MER18 repetitive element |
| 3292 | 8303 | | 5.3 | 3.0E-09 | AA442272.1 | EST_HUMAN | NHT Homo sapiens cDNA clone IMAGE:757422.5' |
| 4302 | 9294 | 14281 | 4.42 | 3.0E-09 | AF175325.1 | NT | Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene, partial cds |
| 4381 | 9372 | 14351 | 1.63 | 3.0E-09 | Q9Y3R5 | SWISSPROT | ZV548041_1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422.5' |
| 1239 | 6237 | 11280 | 13.77 | 2.0E-09 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1618 | 6615 | | 14.91 | 2.0E-09 | AL118573.1 | EST_HUMAN | DKFZp761B1710_r1_761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 r1 |
| 2265 | 7242 | 12359 | 8.68 | 2.0E-09 | Q9Y3R5 | SWISSPROT | 258.1 kDa PROTEIN C21ORF5 (KIAA0933) |
| 3834 | 8836 | 13842 | 3.1 | 2.0E-09 | O80241 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR |
| 1092 | 6099 | 11128 | 1.68 | 1.0E-09 | 5031624 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 1092 | 6099 | 11129 | 1.68 | 1.0E-09 | 5031624 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 2428 | 7399 | | 1.35 | 1.0E-09 | A1356086.1 | EST_HUMAN | q64e11_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 |
| 2819 | 7839 | 12856 | 1.69 | 1.0E-09 | U80017.1 | NT | MER12 repetitive element |
| 2855 | 7875 | 12890 | 17.33 | 1.0E-09 | M28699.1 | NT | Homo sapiens basic transcription factor p44 (bf2p44) gene, partial cds, neuronal apoptosis inhibitor protein (nap1) and survival motor neuron protein (smn) genes, complete cds |
| 2855 | 7875 | 12891 | 17.33 | 1.0E-09 | M28699.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| 2966 | 7984 | 12898 | 0.69 | 1.0E-09 | BE535440.1 | EST_HUMAN | Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds |
| 4654 | 9639 | | 6.25 | 1.0E-09 | AA719297.1 | EST_HUMAN | 601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446177 5' |
| 1290 | 6289 | 11333 | 1.94 | 9.0E-10 | AW867740.1 | EST_HUMAN | Zh35b03_s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains |
| 2760 | 7781 | 12806 | 7.26 | 9.0E-10 | A1870071.1 | EST_HUMAN | Alu repetitive element;contains element MER22 repetitive element; |
| | | | | | | | w678h03_x1 Soares_Dlectgrafts_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RU29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element; |

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 Table 4

Single Exon Probes Expressed in HBL-100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|-------------------------|-------------------------|--|
| 146 | 5212 | 10226 | | 11.08 | 8.0E-10 U63630_2. | NT | Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds |
| 4078 | 9072 | 14059 | | 1.87 | 8.0E-10 AA376832_1 | EST_HUMAN | EST89564 Small intestine 1 Homo sapiens cDNA 5' end |
| 692 | 5716 | 10732 | | 39.41 | 7.0E-10 7706225 | NT | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| 692 | 5716 | 10733 | | 39.41 | 7.0E-10 7706225 | NT | Homo sapiens TPA inducible protein (LOC51588), mRNA |
| 1583 | 6580 | 11643 | | 1.69 | 7.0E-10 Q13342 | SWISSPROT | LysP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100) |
| 2488 | 7456 | | | 9.17 | 7.0E-10 P08547 | SWISSPROT | LysP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG |
| 3014 | 8031 | 13041 | | 2.59 | 7.0E-10 X00856_1 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 902 | 5920 | 10956 | | 2.89 | 6.0E-10 AJ400877_1 | NT | Homo sapiens DHFR gene, exon 3 |
| 2606 | 7568 | 12683 | | 1.11 | 6.0E-10 AI424405_1 | EST_HUMAN | ft02007_x1 NC_ CGAP_P128 Homo sapiens cDNA clone IMAGE:20985021 3' |
| 4598 | 9586 | | | 2.52 | 6.0E-10 AW853719_1 | EST_HUMAN | RC3-CT0254-031099-012-912 CT0254 Homo sapiens cDNA |
| 751 | 5773 | | | 4.91 | 5.0E-10 AL046804_1 | EST_HUMAN | DKFZp434N219_r1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 3395 | 8403 | 13429 | | 1.15 | 5.0E-10 Q01033 | SWISSPROT | HYPOTHETICAL GENE 48 PROTEIN |
| 4833 | 9817 | 14795 | | 1.25 | 5.0E-10 AF181897_1 | NT | Homo sapiens WRN (WRN) gene, complete cds |
| 111 | 5183 | | | 1.48 | 4.0E-10 A1221083_1 | EST_HUMAN | Q909f09_x1 Searns_placenta_8toweeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1758049 3' |
| 576 | 5608 | 10607 | | 1.35 | 4.0E-10 AA515260_1 | EST_HUMAN | similar to contains LTR8_b2_LTR8 repetitive element; |
| 1960 | 6936 | 12037 | | 1.15 | 4.0E-10 AW594709_1 | EST_HUMAN | inf64e01_s1 NC_ CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3' |
| 2499 | 7467 | 12582 | | 3.14 | 4.0E-10 AL163303_2 | NT | hg58g03_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains |
| 904 | 5921 | 10958 | | 1.72 | 3.0E-10 N36113_1 | EST_HUMAN | yy32f06_s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains |
| 1333 | 6331 | | | 4.3 | 3.0E-10 AY005150_1 | NT | L1_H1 repetitive element; |
| 36 | 5116 | 10102 | | 1.49 | 2.0E-10 P48988 | SWISSPROT | Homo sapiens extracellular glycoprotein lactitin precursor, gene, complete cds |
| 36 | 5116 | 10103 | | 1.49 | 2.0E-10 P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 1857 | 6846 | | | 2.98 | 2.0E-10 U80017_1 | NT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 2917 | 7936 | | | 1.37 | 2.0E-10 BF675047_1 | EST_HUMAN | HS21 segment HS21C103 |
| 1479 | 6476 | | | 1.01 | 1.0E-10 AW867767_1 | EST_HUMAN | EST_HUMAN |
| 1570 | 6567 | 11629 | | 2.18 | 1.0E-10 AV652123_1 | EST_HUMAN | AV652123 Gl C Homo sapiens cDNA clone GLCCXA13 |
| 2505 | 7473 | | | 2.43 | 1.0E-10 AW852001_1 | EST_HUMAN | QV0-C70226-191199-058-e08 CT0225 Homo sapiens cDNA |
| 3420 | 8428 | 13454 | | 0.69 | 1.0E-10 AW832912_1 | EST_HUMAN | QV2-T70003-181199-013-g10 TT0003 Homo sapiens cDNA |
| 3462 | 8470 | | | 0.97 | 1.0E-10 AL041685_1 | EST_HUMAN | DKFZp434N1317_r1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434N1317 5' |
| 3754 | 8470 | | | 1.16 | 1.0E-10 AL041685_1 | EST_HUMAN | DKFZp434N1317_r1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434N1317 5' |

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Single Exon Probes Expressed in HEK100 Cells

| Single Exon Probes Expressed in HEL100 Cells | | | | | | |
|--|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|
| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source |
| 3908 | 8908 | | 6.93 | 1.0E-10 | AF213884.1 | NT |
| 4007 | 9003 | 13990 | 4.83 | 1.0E-10 | U52111.2 | NT |
| 4007 | 9003 | 13991 | 4.83 | 1.0E-10 | U52111.2 | NT |
| 4013 | 9009 | 13999 | 2.16 | 1.0E-10 | AB031069.1 | NT |
| 4046 | 9042 | | 2.35 | 1.0E-10 | M30629.1 | NT |
| 2559 | 5318 | 10328 | 1.16 | 9.0E-11 | BET45600.1 | EST_HUMAN |
| 2046 | 7028 | 12139 | 4.32 | 9.0E-11 | AL134395.1 | EST_HUMAN |
| 2046 | 7028 | 12140 | 4.32 | 9.0E-11 | AL134395.1 | EST_HUMAN |
| 3289 | 8310 | 13337 | 2.54 | 9.0E-11 | AL134395.1 | EST_HUMAN |
| 3299 | 8310 | 13338 | 2.54 | 9.0E-11 | AL134395.1 | EST_HUMAN |
| 4371 | 9363 | 14343 | 0.69 | 9.0E-11 | AA775985.1 | EST_HUMAN |
| 3042 | 8059 | | 8.11 | 8.0E-11 | H19971.1 | EST_HUMAN |
| 3930 | 8930 | 13921 | 4.2 | 8.0E-11 | N23712.1 | EST_HUMAN |
| 1422 | 6419 | 11479 | 1.51 | 7.0E-11 | AA330642.1 | EST_HUMAN |
| 409 | 5446 | 10467 | 5.12 | 6.0E-11 | M55270.1 | NT |
| 409 | 5446 | 10468 | 5.12 | 6.0E-11 | M55270.1 | NT |
| 12 | 5092 | 10076 | 0.93 | 5.0E-11 | AL163283.2 | NT |
| 3284 | 5092 | 10076 | 0.92 | 5.0E-11 | AL163283.2 | NT |
| 4107 | 9101 | 14088 | 1.53 | 5.0E-11 | P48034 | SWISSPROT |
| 13777 | 6374 | | 5.75 | 4.0E-11 | AA456042.1 | EST_HUMAN |
| 2718 | 7675 | 12788 | 4.93 | 4.0E-11 | BE885900.1 | EST_HUMAN |
| 2900 | 7919 | 12940 | 1.26 | 4.0E-11 | AL163247.2 | NT |
| 4485 | 9475 | 14455 | 0.75 | 4.0E-11 | D44666.1 | EST_HUMAN |
| 1460 | 6457 | 11516 | 18.61 | 3.0E-11 | 6579077 | NT |
| 2829 | 7849 | | 0.91 | 3.0E-11 | AI816933.1 | EST_HUMAN |
| 4154 | 9149 | | 1.05 | 3.0E-11 | AA309248.1 | EST_HUMAN |
| 945 | 5962 | 10995 | 1.02 | 2.0E-11 | AI50502.1 | EST_HUMAN |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|---|
| 1166 | 8169 | 11204 | 3.84 | 2.0E-11 | R24807.1 | EST_HUMAN | J943612.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:351445' |
| 1166 | 8169 | 11205 | 3.84 | 2.0E-11 | R24807.1 | EST_HUMAN | J943612.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:351445' |
| 1576 | 6573 | 11634 | 3.97 | 2.0E-11 | L17432.1 | NT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds |
| 1576 | 6573 | 11635 | 3.97 | 2.0E-11 | L17432.1 | NT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds |
| 2691 | 7649 | 12763 | 0.93 | 2.0E-11 | AF087913.1 | NT | Human endogenous retrovirus HERV-P-T47D |
| 3123 | 8139 | 13161 | 5.68 | 2.0E-11 | P10263 | SWISSPROT | RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) |
| 3251 | 8264 | 13285 | 0.74 | 2.0E-11 | A1478617.1 | EST_HUMAN | Im54c09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:21619363' |
| 3417 | 8425 | | 0.94 | 2.0E-11 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 4321 | 9313 | | 1.04 | 2.0E-11 | BE065537.1 | EST_HUMAN | RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA |
| 4474 | 9464 | | 0.75 | 2.0E-11 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 4779 | 9763 | | 1.84 | 2.0E-11 | BE062558.1 | EST_HUMAN | QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA |
| 668 | 5693 | 10702 | 0.79 | 1.0E-11 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 775 | 5797 | 10825 | 1.24 | 1.0E-11 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1198 | 6199 | 11235 | 2.94 | 1.0E-11 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C019 |
| 1469 | 6466 | | 1.4 | 1.0E-11 | AF119914.1 | NT | Homo sapiens mRNA, complete cds |
| 1986 | 6971 | 12075 | 1.14 | 1.0E-11 | P16258 | SWISSPROT | OXYSTEROID-BINDING PROTEIN |
| 2067 | 7049 | 12157 | 2.2 | 1.0E-11 | AF000573.1 | NT | Homino sapiens homogenitalise 1,2-dioxigenase gene, complete cds |
| 3419 | 8427 | 13453 | 0.93 | 1.0E-11 | BE004315.1 | EST_HUMAN | CMM-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA |
| 4526 | 9516 | 14502 | 1.42 | 7.0E-12 | Q05904 | SWISSPROT | 34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34) |
| 3471 | 8479 | | 0.75 | 6.0E-12 | AV730554.1 | EST_HUMAN | AV730554 HTF Homo sapiens cDNA clone HTFAWF085' |
| 4222 | 9216 | 14195 | 9.87 | 6.0E-12 | AA732516.1 | EST_HUMAN | n288f1.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Ala repetitive element |
| 5074 | 10043 | 15009 | 1.48 | 6.0E-12 | M22486.1 | NT | Human chromosome 21 distal long arm DNA |
| 1026 | 6036 | 11058 | 2.25 | 5.0E-12 | T06573.1 | EST_HUMAN | EST04462 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBDV33 |
| 3306 | 8317 | 13343 | 1.16 | 5.0E-12 | BE04778.1 | EST_HUMAN | Iz42b05.y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:22912175' |
| 3644 | 8650 | 13656 | 7.07 | 5.0E-12 | AJ271736.1 | NT | Homo sapiens Xg pseudoeatosomal region, segment 2/2 |
| 242 | 5303 | 10313 | 4.12 | 4.0E-12 | AA700326.1 | EST_HUMAN | Z74g11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4606763' |
| 243 | 5303 | 10313 | 6.02 | 4.0E-12 | AA700326.1 | EST_HUMAN | Z74g11.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:22707453' similar to TR:Q13539 Q13539 |
| 4487 | 9477 | 14457 | 0.7 | 4.0E-12 | AI689984.1 | EST_HUMAN | b26h05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone MARINER TRANSPOSEASE ; |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--|--|--|
| | | | | | | | | | |
| 612 | 5639 | 10641 | 3.43 | 3.0E-12 AW341683.1 | EST_HUMAN | hd13d01_x1_Scores_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2909377 3' similar to TR:O14517 | | | |
| 612 | 5639 | 10642 | 3.43 | 3.0E-12 AW341683.1 | EST_HUMAN | hd13d01_x1_Scores_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2909377 3' similar to TR:O14517 | | | |
| 612 | 6609 | 11673 | 1.82 | 2.0E-12 AW802131.1 | EST_HUMAN | hd13d01_x1_Scores_NFL_T_GBC_S1_Homo_sapiens_cDNA IMAGE:2909377 3' similar to TR:O14517 | | | |
| 1613 | 8394 | 13418 | 0.75 | 2.0E-12 6754495 | NT | Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA | | | |
| 3386 | 8994 | 13981 | 0.85 | 2.0E-12 J01884.1 | NT | Rat U3A small nuclear RNA | | | |
| 3998 | 8994 | 13982 | 0.85 | 2.0E-12 J01884.1 | NT | Rat U3A small nuclear RNA | | | |
| 3998 | 8994 | 13982 | 2.34 | 2.0E-12 BE063509.1 | EST_HUMAN | CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA IMAGE:2909377 3' similar to TR:O14517 | | | |
| 4297 | 9289 | 14712 | 1.72 | 2.0E-12 O70306 | SWISSPROT | TBX15 PROTEIN (T-BOX PROTEIN 15) | | | |
| 4742 | 9727 | 14713 | 1.72 | 2.0E-12 O70306 | SWISSPROT | TBX15 PROTEIN (T-BOX PROTEIN 15) | | | |
| 4742 | 9727 | 14713 | 1.72 | 2.0E-12 O70306 | SWISSPROT | h9n0a9.x1 NC_02GAP GU1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to contains MER18.11 | | | |
| 123 | 5192 | 10205 | 1.65 | 1.0E-12 AW621674.1 | EST_HUMAN | MER18 repetitive element; h9n0a9.x1 NC_02GAP_U2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element; | | | |
| 1941 | 6927 | | 1.12 | 1.0E-12 AI871726.1 | EST_HUMAN | wn1f107.x1 NC_02GAP_U2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element; | | | |
| 2597 | 8015 | 13027 | 1.34 | 1.0E-12 AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds | | | |
| 2597 | 8015 | 13028 | 1.34 | 1.0E-12 AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds | | | |
| 2597 | 8015 | 13789 | 29.33 | 1.0E-12 AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' | | | |
| 3783 | 8786 | 13789 | 29.33 | 1.0E-12 AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' | | | |
| 3783 | 8786 | 13790 | 29.33 | 1.53 | 9.0E-13 AJ2/1735.1 | NT | Homo sapiens Yq pseudodautosomal region, segment 1/2 | | |
| 3543 | 8550 | | 0.85 | 9.0E-13 AB028600.1 | NT | Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5 | | | |
| 3843 | 8845 | 13854 | 0.85 | 8.0E-13 U29185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds | | | |
| 707 | 5731 | 10747 | 4.84 | 8.0E-13 U29185.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2-44) gene, partial cds, neuronal apoptosis inhibitory protein (nap1) and survival motor neuron protein (smn) genes, complete cds | | | |
| 707 | 5731 | 10748 | 4.84 | | | Homo sapiens chromosome 21 segment HS21C007 | | | |
| 1802 | 6793 | 11883 | 2.36 | 8.0E-13 U80017.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds | | | |
| 2044 | 7026 | 12137 | 3.41 | 6.0E-13 AL163207.2 | EST_HUMAN | PM2-HT0224-221099-01-11 HT0224 Homo sapiens cDNA clone IMAGE:145759 5' | | | |
| 3248 | 8261 | | 0.67 | 5.0E-13 R78383.1 | EST_HUMAN | PM2-HT0224-221099-01-11 HT0224 Homo sapiens cDNA clone IMAGE:145759 5' | | | |
| 3313 | 8324 | | | 1.36 | 5.0E-13 AA43573.1 | EST_HUMAN | PM2-HT0224-221099-01-11 HT0224 Homo sapiens cDNA clone IMAGE:145759 5' | | |
| 1830 | 6820 | | | 9.36 | 4.0E-13 AW3786-14.1 | EST_HUMAN | PM2-HT0224-221099-01-11 HT0224 Homo sapiens cDNA clone IMAGE:145759 5' | | |
| 2391 | 7362 | | | 1.32 | 4.0E-13 AF003529.1 | NT | Hom sapien's glycan 3 (GPC3) gene, partial cds and flanking repeat regions | | |
| 4604 | 9592 | | | 1.02 | 4.0E-13 AA454054.1 | EST_HUMAN | zx48d07 r1 Scores testis NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains MER22 repetitive element; | | |
| 179 | 5242 | | | 4.21 | 3.0E-13 AF003528.1 | NT | Hom sapien's X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions | | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|---|-------------------------|--|
| | | | | 3.0E-13 | Aa430310.1 | EST_HUMAN | Zm68g08_r1 Soares testis_NHt Homo sapiens cDNA clone IMAGE:781406 5' |
| 854 | 5873 | | 6.84 | 3.0E-13 | A271736.1 | NT | Homo sapiens Xq p/sedentary region; segment 21 |
| 2309 | 7284 | 12404 | 1.24 | 3.0E-13 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 2408 | 7379 | | 2.01 | 3.0E-13 | BF372962.1 | EST_HUMAN | CM3-FT0100-1407(r0-242-h08 FT0100 Homo sapiens cDNA clone IMAGE:1324035 3' |
| 2593 | 7556 | 12670 | 3.02 | 3.0E-13 | ob8d02.s1 NCL_C3AP_Kids5 Homo sapiens cDNA clone IMAGE:068d02.s1 NCL_C3AP_Kids5 Homo sapiens cDNA clone IMAGE:9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), | EST_HUMAN | ob8d02.s1 NCL_C3AP_Kids5 Homo sapiens cDNA clone IMAGE:9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), |
| 3113 | 8129 | | 2.06 | 3.0E-13 | AA745844.1 | EST_HUMAN | Homo sapiens >28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), |
| 149 | 5215 | 10229 | 2.57 | 2.0E-13 | U52111.2 | NT | Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds |
| 237 | 5299 | 10310 | 0.88 | 2.0E-13 | U23839.1 | NT | Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds |
| 1251 | 6249 | 11290 | 6.43 | 2.0E-13 | AF239710.1 | NT | Homo sapiens cDNA clone IMAGE:3' |
| 3208 | 8223 | 13245 | 1.32 | 2.0E-13 | BF431899.1 | EST_HUMAN | nsab76f05.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3' |
| 3428 | 8436 | 13462 | 1.88 | 2.0E-13 | AF105907.1 | NT | Homo sapiens DNA polymerase delta 21 segment HS21C078 |
| 3992 | 8989 | | 2.02 | 2.0E-13 | AL163278.2 | NT | Fgf-1=fibroblast growth factor 1 [human, kidney, genomic, 342 nt, segment 2 of 2] |
| 289 | 5346 | 10358 | 1.09 | 1.0E-13 | S74129.1 | NT | Homo sapiens L3MD2B gene |
| 877 | 5895 | 10936 | 4.81 | 1.0E-13 | AJ007973.1 | NT | Homo sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes |
| 1316 | 6313 | 11362 | 1.45 | 1.0E-13 | XB7344.1 | NT | nw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 genes |
| 1972 | 6957 | 12062 | 1.73 | 1.0E-13 | AA720574.1 | EST_HUMAN | THR repetitive element; |
| 4461 | 9451 | 14432 | 1.6 | 1.0E-13 | BF340987.1 | EST_HUMAN | 602038009F1 NCL CGAP_Brn64 Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 genes |
| 331 | 5383 | 10391 | 2.84 | 9.0E-14 | AA781159.1 | EST_HUMAN | aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 genes |
| 332 | 5384 | 10392 | 2.83 | 9.0E-14 | AA781159.1 | EST_HUMAN | EST repetitive element; |
| 2427 | 7398 | | 3.07 | 9.0E-14 | AW861577.1 | EST_HUMAN | repetitive element; |
| 2680 | 7638 | 12753 | 3.39 | 9.0E-14 | AB038162.1 | NT | RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA |
| 3037 | 8054 | 13062 | 5.01 | 9.0E-14 | AW513296.1 | EST_HUMAN | RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA |
| 3708 | 8712 | 13715 | 7.31 | 9.0E-14 | D14547.1 | NT | TFF gene cluster for trefoil factor, complete cds |
| 4612 | 9598 | 14584 | 1.69 | 9.0E-14 | AJ002153.1 | NT | Homo sapiens TFF gene cluster for trefoil factor, complete cds |
| 3418 | 8426 | | 1.04 | 8.0E-14 | BE468263.1 | EST_HUMAN | xo54h05.x1 NCL_CGAP_UH1 Homo sapiens cDNA |
| 3849 | | | 3.5 | 8.0E-14 | R16269.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| | | | | | | | Saguinus oedipus gene for seminal vesicle secreted protein semenogelin 1 |
| | | | | | | | hz71c09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3' |
| | | | | | | | hz71c09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:147786 3' |
| | | | | | | | y72e03.r1 Soares placentae Nb214P Homo sapiens cDNA clone IMAGE:147786 3' |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|---|--|
| | | | | | | | | | |
| 1590 | 7751 | | | 2.98 | 7.0E-14 AW151673.1 | EST_HUMAN | x67e10_x1_NCI_C3AP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10_L2 MER10 repetitive element; | | |
| 366 | 5415 | 10428 | | 13.89 | 6.0E-14 AF020503.1 | NT | I Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1) | | |
| 614 | 5641 | 10644 | | 4.27 | 5.0E-14 Q63120 | SWISSPROT | ASSOCIATED PROTEIN 2 (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) | x603b05_x1_NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.t2_L1 repetitive element; | |
| 4886 | 9865 | 14836 | | 1.45 | 5.0E-14 AW073791.1 | EST_HUMAN | S-ANTIGEN PROTEIN PRECURSOR | NT | |
| 1106 | 7739 | | | 1.59 | 4.0E-14 P04928 | SWISSPROT | Hom sapiens CGMD2B gene | Hom sapiens cDNA clone IMAGE:487858 5' | |
| 1839 | 6829 | 11918 | | 5.27 | 4.0E-14 AJ007973.1 | EST_HUMAN | 2k67a06_r1_Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:279190 3' similar to y73c12_s1_Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone | | |
| 3666 | 8671 | | | 0.88 | 4.0E-14 AA046502.1 | EST_HUMAN | contains L1.t3_L1 repetitive element; | | |
| 4168 | 9163 | 14149 | | 0.8 | 4.0E-14 NA6328.1 | EST_HUMAN | R_norvegicus mRNA for CPG2 protein | | |
| 935 | 5952 | 10984 | | 1.12 | 3.0E-14 X95466.1 | NT | Xq pseudoautosomal region; segment 2/2 | | |
| 389 | 5427 | 10442 | | 2.33 | 2.0E-14 AJ271736.1 | NT | Homo sapiens Xq pseudoautosomal region; segment 2/2 | | |
| 389 | 5427 | 10443 | | 2.33 | 2.0E-14 AJ271736.1 | NT | Homo sapiens Xq pseudoautosomal region; segment 2/2 | | |
| 389 | 5427 | 10443 | | 7.63 | 2.0E-14 AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 | | |
| 681 | 7727 | 10716 | | 1.24 | 2.0E-14 AW372868.1 | EST_HUMAN | RC5-B1037-031299-031-D12_B10377_Homo sapiens cDNA | | |
| 2324 | 7298 | | | 1.08 | 2.0E-14 765f529 | NT | Homo sapiens habdoid tumor deletion region protein 1 (RTDR1), mRNA | | |
| 2395 | 7366 | | | 1.41 | 2.0E-14 AL163209.2 | NT | Hom sapiens chromosome 21 segment HS21C009 | | |
| 2455 | 7425 | 12539 | | 1.59 | 1.0E-14 AL163246.2 | NT | Hom sapiens chromosome 21 segment HS21C046 | | |
| 1050 | 6059 | 11088 | | 4.61 | 1.0E-14 AL163268.2 | NT | Hom sapiens chromosome 21 segment HS21C058 | | |
| 1382 | 6379 | 11427 | | 4.61 | 1.0E-14 AL163268.2 | NT | Hom sapiens chromosome 21 segment HS21C059 | | |
| 1382 | 6379 | 11428 | | 4.61 | 1.0E-14 AL163268.2 | NT | Hom sapiens chromosome X region from flamin (FLN) gene to glucose-6-phosphate dehydrogenase | | |
| 1955 | 6941 | 12043 | | 21.53 | 1.0E-14 L44140.1 | NT | Hom sapiens chromosome 21 segment HS21C103 | (G6PD) gene, complete cds's | |
| 2121 | 7101 | 12213 | | 4.33 | 1.0E-14 AL163303.2 | NT | Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds | | |
| 2343 | 7317 | 12437 | | 18 | 1.0E-14 AF001689.1 | NT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-1) | | |
| 2874 | 7893 | 12916 | | 1.2 | 1.0E-14 P05227 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-1) | | |
| 3094 | 8110 | 13127 | | 5.58 | 1.0E-14 BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 C10432_Homo sapiens cDNA | | |
| 3094 | 8110 | 13128 | | 5.58 | 1.0E-14 BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 C10432_Homo sapiens cDNA | | |
| 3782 | 8795 | 13800 | | 1.7 | 1.0E-14 AA682964.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 C10432_Homo sapiens cDNA | | |
| 4348 | 9339 | 14320 | | 1.99 | 1.0E-14 AW275852.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 C10432_Homo sapiens cDNA | | |
| 1541 | 6539 | 11596 | | 1.39 | 9.0E-15 | 7427522 | NT | Hom sapiens tyrosine phosphatase, receptor type, T (PTPR), mRNA | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| | | | | | | | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and I-type calcium channel $\alpha 2$ |
| 2108 | 7088 | | | 1.04 | 9.0E-15 AF196779.1 | NT | JM10 protein, A4 differentiation-dependent protein, I-type calcium channel $\alpha 2$ |
| 2739 | 5513 | | | 1.02 | 8.0E-15 BE261482.1 | EST_HUMAN | 601148632F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5' |
| 979 | 5594 | 11027 | | 4.97 | 6.0E-15 AJ271736.1 | NT | Homo sapiens Xq1 pseudautosomal region; segment 2/2 |
| 407 | 5444 | 10464 | | 4.86 | 5.0E-15 AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| | | | | | | | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (Hh-A-H) gene, Ror2 gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 2686 | 7644 | 12759 | | 1.12 | 5.0E-15 U91328.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 424 | 5082 | 10066 | | 2.43 | 4.0E-15 AL163303.2 | NT | [Y1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 F similar to ANF(CARDIODILATIN)] |
| 4096 | 9090 | | | 7.1 | 3.0E-15 N89452.1 | EST_HUMAN | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 |
| 4770 | 9754 | | | 2.28 | 3.0E-15 P92485 | SWISSPROT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 248 | 5308 | 10319 | | 2.86 | 2.0E-15 AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 367 | 5416 | 10429 | | 2.77 | 2.0E-15 AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 367 | 5416 | 10430 | | 2.77 | 2.0E-15 AF223391.1 | NT | h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 2311 | 7286 | 12406 | | 1.11 | 2.0E-15 BE350127.1 | EST_HUMAN | MER29 repetitive element; |
| 2311 | 7286 | 12407 | | 1.11 | 2.0E-15 BE350127.1 | EST_HUMAN | h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 |
| 3430 | 8438 | | | 0.91 | 2.0E-15 AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 3430 | 8438 | 13465 | | 0.91 | 2.0E-15 AF223391.1 | NT | h109g01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:271521 3' similar to contains L1.L1 |
| 3430 | 8438 | | | 0.91 | 2.0E-15 AF223391.1 | NT | h109g01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:271521 3' similar to contains L1.L1 |
| 3954 | 8952 | 13942 | | 1.02 | 2.0E-15 AW238499.1 | EST_HUMAN | wp07f06.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q13539 Q13539 |
| 4489 | 9479 | | | 2.55 | 2.0E-15 AI080335.1 | EST_HUMAN | Q61043 NINEIN ; |
| 2702 | 7659 | | | 1.94 | 1.0E-15 AI689984.1 | EST_HUMAN | b26n05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to MARINER TRANSPONASE ; |
| 2943 | 7962 | 12982 | | 1.78 | 1.0E-15 BE043564.1 | EST_HUMAN | hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 5' |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit No. | Top Hit Acession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|---------------|----------------------|---|---|
| | | | | | | | | LIN-E-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3069 | 8085 | 13099 | 1.42 | 1.0E-15 | F08547 | | SWISSPROT | RC3-HT0649-100500-022-h05 HT0649 Homo sapiens cDNA |
| 4234 | 9228 | 14212 | 0.98 | 1.0E-15 | BE182696.1 | EST_HUMAN | EST_HUMAN | W86d04_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3' |
| 4963 | 9840 | 14917 | 0.93 | 1.0E-15 | A1984928.1 | EST_HUMAN | EST_HUMAN | EST384702 IMAGE: resequences, MAGI Homo sapiens cDNA |
| 2080 | 7061 | | | 6.0E-16 | AW972611.1 | | EST_HUMAN | |
| 1461 | 6458 | 11517 | 2.3 | 5.0E-16 | AJ251154.1 | NT | | Mus musculus olfactory receptor cluster_ OR31A, OR37B, OR37C, OR37E genes and OR37D pseudogene |
| 2609 | 7571 | 12685 | 1.58 | 5.0E-16 | AA992176.1 | EST_HUMAN | EST_HUMAN | o80c04_s1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to o80c04_s1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to o80c04_s1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' |
| 2178 | 7157 | | | 0.98 | 4.0E-16 | AB001523.1 | NT | contains element I.1 repetitive element: Homo sapiens gene for TMEV1 and PW/P2, complete and partial cds |
| 2317 | 7292 | 12412 | 1.01 | 4.0E-16 | AW797168.1 | EST_HUMAN | EST_HUMAN | QV1-JM0036-201300-115-g02 UM0036 Homo sapiens cDNA |
| 2317 | 7292 | 12413 | 1.01 | 4.0E-16 | AW797168.1 | EST_HUMAN | EST_HUMAN | QV1-JM0036-201300-115-g02 UM0036 Homo sapiens cDNA |
| 3375 | 8383 | 13403 | 4.99 | 4.0E-16 | Q16653 | SWISSPROT | MYELIN-OLIGO(G)ENDROCYTE GLYCOPROTEIN PRECURSOR | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 4019 | 9015 | 14002 | 4.76 | 4.0E-16 | BE083875.1 | EST_HUMAN | EST_HUMAN | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 4019 | 9015 | 14003 | 4.76 | 4.0E-16 | BE083875.1 | EST_HUMAN | EST_HUMAN | PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 133 | 5199 | 10215 | 0.97 | 3.0E-16 | AW022862.1 | EST_HUMAN | EST_HUMAN | df45c01_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5' |
| 133 | 5199 | 10216 | 0.97 | 3.0E-16 | AW022862.1 | EST_HUMAN | EST_HUMAN | df45c01_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5' |
| 463 | 5500 | | | 1.75 | 3.0E-16 | AL046445.1 | EST_HUMAN | DKFZp434P037_l1434 (synonym: hesc) Homo sapiens cDNA clone DKFZp434P037_l1434 |
| 472 | 5508 | | | 2.13 | 3.0E-16 | AF135446.1 | NT | Homo sapiens TSX (TSX) pseudogene, exon 5 |
| 1426 | 6423 | 11482 | 3.79 | 3.0E-16 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR | ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220] |
| 2907 | 7926 | 12944 | 4.23 | 3.0E-16 | P03200 | SWISSPROT | Homo sapiens Bento Soares Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end | EST06060 |
| 3830 | 8832 | 13839 | 0.78 | 3.0E-16 | T08159.1 | EST_HUMAN | | EST06060 |
| 3851 | 8853 | | | 0.67 | 3.0E-16 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 4785 | 9769 | 14753 | 1.06 | 3.0E-16 | AV661393.1 | EST_HUMAN | AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3' | |
| 957 | 5973 | | | 2.44 | 2.0E-16 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 2617 | 7579 | | | 0.89 | 2.0E-16 | J03061.1 | NT | Human SVA-related endogenous retroviral LTR-like element |
| 4054 | 9048 | 14036 | 0.92 | 2.0E-16 | X89211.1 | NT | H.sapiens DNA for endogenous retroviral like element | |
| 184 | 5247 | 10256 | 2.54 | 1.0E-16 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds | af39g11_s1 Shares_total_fetus_Nb2Hf8_Bw Homo sapiens cDNA clone IMAGE:1034064 3' similar to af39g11_s1 Shares_total_fetus_Nb2Hf8_Bw Homo sapiens cDNA clone IMAGE:1034064 3' |
| 381 | 5456 | | | 25.58 | 1.0E-16 | AA629592.1 | EST_HUMAN | contains OFR_12 OFR repetitive element: QV0-BN0148-070/00-293-a10 BN0148 Homo sapiens cDNA |
| 1927 | 6913 | 12009 | 1.7 | 1.0E-16 | BF327942.1 | EST_HUMAN | QV0-BN0148-070/00-293-a10 BN0148 Homo sapiens cDNA | |
| 3654 | 8660 | 13665 | 3.23 | 9.0E-17 | AW800048.1 | EST_HUMAN | CMI-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA | |
| 1002 | 6012 | | | 1.83 | 8.0E-17 | AW880701.1 | EST_HUMAN | QV0-OT0032-080300-155-a01 OT0032 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|--|---|
| 3797 | 8800 | | 2.95 | 8.0E-17 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 1431 | 6428 | | 1.93 | 7.0E-17 | 6753097 NT | Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA | |
| 203 | 5287 | 10281 | 5.89 | 6.0E-17 | AW983880.1 | EST_HUMAN | RC1-HN0003-220300-021-504 Hn0003 Homo sapiens cDNA |
| 418 | 5076 | 10060 | 2.71 | 5.0E-17 | T64110.1 | EST_HUMAN | yc05m08.r1 Strategene lung (R937210) Homo sapiens cDNA clone IMAGE:1058528 3' |
| 3550 | 8557 | 13564 | 0.94 | 4.0E-17 | AA643697.1 | EST_HUMAN | ni98e05.s1 NCI CGAP_Co10 Homo sapiens cDNA clone IMAGE:2604784 3' |
| 2041 | 7023 | 12133 | 1.06 | 3.0E-17 | AW119123.1 | EST_HUMAN | 2d89e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3' |
| 3121 | 8137 | | 1.31 | 3.0E-17 | P35410 | SWISSPROT | MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG |
| 3557 | 8564 | 13570 | 1.36 | 3.0E-17 | BE328522.1 | EST_HUMAN | hw05b04.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:31181989 3' |
| 3557 | 8564 | 13571 | 1.36 | 3.0E-17 | BE328522.1 | EST_HUMAN | hw05b04.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:31181989 3' |
| 351 | 5403 | 10413 | 2.52 | 2.0E-17 | AJ270080.1 | EST_HUMAN | qf63a06.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element |
| 352 | 5403 | 10413 | 2.83 | 2.0E-17 | AJ270080.1 | EST_HUMAN | qf63a06.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element |
| 973 | 5989 | | 2.23 | 2.0E-17 | AA722932.1 | EST_HUMAN | zg81d04.s1 Soires fetal heart NhH119W Homo sapiens cDNA clone IMAGE:399751 3' |
| 2379 | 7351 | 12471 | 1.92 | 2.0E-17 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2379 | 7351 | 12472 | 1.92 | 2.0E-17 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2859 | 7879 | 12897 | 6.43 | 2.0E-17 | P12036 | SWISSPROT | NEUROFILAMENT TRIPLET H PROTEIN (200 KDa NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) |
| 3693 | 8697 | | 4.37 | 2.0E-17 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18s), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adendoleukodystrophy protein > |
| 741 | 5764 | 10789 | 3.03 | 1.0E-17 | P08183 | SWISSPROT | MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) |
| 1670 | 6686 | | 0.97 | 1.0E-17 | AJ271736.1 | NT | Homo sapiens Xq pseudoautosomal region; segment 2/2 |
| 1730 | 6725 | 11803 | 4.26 | 1.0E-17 | AL1632017.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 2057 | 7039 | 12448 | 1.51 | 1.0E-17 | P02461 | SWISSPROT | COLLAGEN ALPHA 1(III) CHAIN PRECURSOR |
| 2274 | 7250 | 12367 | 2.06 | 1.0E-17 | U78410.1 | NT | Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B |
| 3488 | 8496 | | 1.05 | 1.0E-17 | AF224669.1 | EST_HUMAN | Homo sapiens mammotropin, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 |
| 4015 | 9011 | | 8.44 | 1.0E-17 | R09942.1 | NT | (UBE2D3) genes, complete cds |
| 3698 | 8702 | 13705 | 1.84 | 8.0E-18 | 4755977 NT | Y30807.1 Soires fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5' | |
| 347 | 5399 | 10407 | 65.43 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:120868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |
| 347 | 5399 | 10408 | 65.43 | 7.0E-18 | AW316976.1 | EST_HUMAN | xx10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:120868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3221 | 8236 | 13257 | 1.06 | 6.0E-18 | X771791.2 | NT | Rattus norvegicus partial GdnPn-1 gene for glia-derived neuropeptide nephin 1, enhancer region (TGASe C) (TGC) |
| 4603 | 9591 | | 4.28 | 6.0E-18 | P52181 | SWISSPROT | qmg5g11.x1 Soares,_placenta,_8to9weeks,_2NbHP8tGw Homo sapiens cDNA clone IMAGE:1893668_3' |
| 1130 | 6135 | 11166 | 11.59 | 5.0E-18 | A1280214.1 | EST_HUMAN | qm65g11.x1 Soares,_placenta,_8to9weeks,_2NbHP8tGw Homo sapiens cDNA clone IMAGE:3039511_3' similar to contains MER29_b3 |
| 125 | 5193 | 10206 | 1.37 | 4.0E-18 | BE044076.1 | EST_HUMAN | ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511_3' similar to contains MER29_b3 |
| 125 | 5193 | 10207 | 1.37 | 4.0E-18 | BE044076.1 | EST_HUMAN | ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:1144845_3' similar to gb:M26326 |
| 1678 | 6674 | 11749 | 21.73 | 4.0E-18 | AA621814.1 | EST_HUMAN | nr024f11.s1 NCI_CGAP_C610 Homo sapiens cDNA clone IMAGE:1144845_3' similar to gb:M26326 |
| 2138 | 7118 | 12232 | 0.98 | 4.0E-18 | Q06430 | SWISSPROT | nr024f11.s1 CYTOSKELETA18 (HUMAN); KERATIN, TYPE I CYTOSKELETA18 (HUMAN); N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (IGNT) |
| 2138 | 7118 | 12233 | 0.98 | 4.0E-18 | Q06430 | SWISSPROT | ACETYLGLUCOSAMINYLTRANSFERASE (I-BRANCHING ENZYME) (IGNT) |
| 839 | 5858 | 10899 | 34.38 | 3.0E-18 | AA814196.1 | EST_HUMAN | ACETYLGLUCOSAMINYLTRANSFERASE (I-BRANCHING ENZYME) (IGNT) |
| 917 | 5933 | 10967 | 3.2 | 3.0E-18 | BE088634.1 | EST_HUMAN | gb:Z31115.1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581_3' similar to SV_RS5_HUMAN |
| 3846 | 8848 | 13856 | 1.1 | 3.0E-18 | AL163247.2 | NT | gb:Z31115.1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581_3' similar to SV_RS5_HUMAN |
| 249 | 5309 | 10320 | 4.3 | 2.0E-18 | AW1836820.1 | EST_HUMAN | gb:Z31115.1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581_3' similar to SV_RS5_HUMAN |
| 1135 | 6140 | | 211.43 | 2.0E-18 | BE255697.1 | EST_HUMAN | gb:Z31115.1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581_3' similar to SV_RS5_HUMAN |
| 3050 | 8067 | 13076 | 0.93 | 2.0E-18 | Q39575 | SWISSPROT | ye4g05.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:712811_5' similar to contains MER19_12 |
| 4291 | 9283 | | 0.87 | 1.0E-18 | T95406.1 | EST_HUMAN | ye4g05.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:712811_5' similar to contains MER19_12 |
| 541 | 5576 | 10582 | 5.62 | 9.0E-19 | AA281961.1 | EST_HUMAN | z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811_5' similar to contains MER19_12 |
| 542 | 5576 | 10582 | 3.19 | 9.0E-19 | AA281961.1 | EST_HUMAN | z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811_5' similar to contains MER19_12 |
| 1031 | 6041 | | 1.33 | 8.0E-19 | AW974902.1 | EST_HUMAN | z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811_5' similar to contains MER19_12 |
| 2184 | 7163 | 12283 | 1.86 | 7.0E-19 | | 4758139_NT | Homo sapiens DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) mRNA |
| 3692 | 8696 | | 1.56 | 6.0E-19 | AW857930.1 | EST_HUMAN | PM0-C1024F-131089-001-001 C10248 Homo sapiens cDNA |
| 4339 | 9330 | 14314 | 1.45 | 6.0E-19 | P34986 | SWISSPROT | OLFFACTORY RECEPTOR 6 (M50) |
| 4339 | 9330 | 14315 | 1.45 | 6.0E-19 | P34986 | SWISSPROT | OLFFACTORY RECEPTOR 6 (M50) |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4655 | 9640 | | | 1.38 | 6.0E-19 AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4865 | 9845 | 14820 | | 1.45 | 6.0E-19 AL120817.1 | EST_HUMAN | DKFZp762F192 1' 762 (synonym: hmei2) Homo sapiens cDNA clone DKFZp762F192 5' |
| 550 | 5584 | 10586 | | 0.91 | 4.0E-19 AB007910.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| 2611 | 7573 | 12687 | | 1.1 | 4.0E-19 BF697362.1 | EST_HUMAN | 602130910F_NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5' |
| 3762 | 8765 | 13767 | | 0.98 | 3.0E-19 Q28997 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 3762 | 8765 | 13768 | | 0.98 | 3.0E-19 Q28997 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 4163 | 9158 | 14144 | | 1.07 | 3.0E-19 O43900 | SWISSPROT | IM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) |
| 4163 | 9158 | 14145 | | 1.07 | 3.0E-19 O43900 | SWISSPROT | IM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) |
| 4324 | 9316 | 14298 | | 1.25 | 3.0E-19 AV708136.1 | EST_HUMAN | AV708136 ADC Homo sapiens cDNA clone ADCAmA11 5' |
| 2489 | 7457 | 12572 | | 24.97 | 2.0E-19 AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4323 | 9315 | | | 1.37 | 2.0E-19 AI311783.1 | EST_HUMAN | qr91e02_x1_NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q693866 Q69386 |
| 478 | 5515 | | | 1.56 | 1.0E-19 BE408611.1 | EST_HUMAN | POLYENV GENE; |
| 2100 | 7081 | 12196 | | 1.18 | 1.0E-19 H30795.1 | EST_HUMAN | 601304125F11_NIH_MGC_21 Homo sapiens cDNA clone IMAGE:184188 5' similar to contains y079g07_r1_Soares adult brain N264H55Y Homo sapiens cDNA clone IMAGE:1915893 10 5' |
| 2645 | 7605 | | | 2.01 | 1.0E-19 D38044.1 | NT | Human gene for Ah-receptor, exon 7-9 |
| 2774 | 7795 | | | 5.45 | 1.0E-19 4758977 | NT | Human sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| | | | | | | | qr91b12_s1_Soares_ testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 |
| | | | | | | | qr91b12_s1_Soares_ testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37 repetitive element; |
| 3317 | 8327 | 13348 | | 1.46 | 1.0E-19 AA834967.1 | EST_HUMAN | MER37 repetitive element; |
| 3202 | 8217 | 13240 | | 0.74 | 7.0E-20 BF326455.1 | EST_HUMAN | PM4-AN0096-05090-03-804 AN0086 Homo sapiens cDNA |
| 3478 | 8486 | 13505 | | 3.52 | 6.0E-20 P39188 | SWISSPROT | ALU SUBFAM1_Y J SEQUENCE CONTAMINATION WARNING ENTRY |
| 4150 | 9145 | 14129 | | 2.85 | 6.0E-20 BE622434.1 | EST_HUMAN | 60144123 (F11 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5' |
| 4464 | 9454 | | | 1.02 | 5.0E-20 AV725123.1 | EST_HUMAN | AV725123 HTTC Homo sapiens cDNA clone HTCTBTA01 5' |
| 1581 | 6578 | 11642 | | 1.44 | 4.0E-20 AL163247.2 | NT | Human sapiens chromosome 21 segment HS21C047 |
| 2079 | 7060 | 12170 | | 1.22 | 3.0E-20 U03888.1 | NT | Human BXF21 gene |
| 4088 | 9082 | 14073 | | 1.46 | 3.0E-20 P23273 | SWISSPROT | OLFACTOORY RECEPTOR-LIKE PROTEIN14 |
| 4491 | 9481 | 14460 | | 1.27 | 3.0E-20 AA037616.1 | EST_HUMAN | z36b12_s1_Scates_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE |
| 820 | 5840 | | | 48.46 | 2.0E-20 AW30398.1 | EST_HUMAN | xr24e10_x1_NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:484895 3' similar to SW_RS5_MOUSE |
| 1094 | 6101 | 11130 | | 3.05 | 2.0E-20 AA516335.1 | EST_HUMAN | P97461_40S_EUBOSOMAL PROTEIN S5. ; |
| 1094 | 6101 | 11131 | | 3.05 | 2.0E-20 AA516335.1 | EST_HUMAN | ng69h09_s1_NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 |

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Table 4

Single Exon Probes Expressed in HEK100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|--|-------------------------|---|
| | | | | | x24e10_x1_NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE | | |
| 2745 | 5840 | | 36.55 | 2.0E-20 | AW303868.1 | EST_HUMAN | P97481_40S RIBOSOMAL PROTEIN S5; |
| 4789 | 9773 | 14756 | 4.58 | 2.0E-20 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 4789 | 9773 | 14757 | 4.58 | 2.0E-20 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 4969 | 9946 | | 1.73 | 2.0E-20 | 5174538_NT | | Homo sapiens metal dehydrogenase 1, NAD (soluble) (MDH1) mRNA |
| 1963 | 7703 | 12051 | 2.7 | 1.0E-20 | AA281961.1 | EST_HUMAN | z11d06_x1_NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 4316 | 8308 | 14293 | 1.12 | 1.0E-20 | BF115158.1 | EST_HUMAN | lrb4b06_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element; |
| 2842 | 7862 | | 1.16 | 9.0E-21 | AJ003514.1 | EST_HUMAN | AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1pl12-8/J21 |
| 2016 | 6999 | 12102 | 1.61 | 7.0E-21 | P15800 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3) |
| 2016 | 6999 | 12103 | 1.61 | 7.0E-21 | P15800 | SWISSPROT | LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3) |
| 4133 | 9128 | | 6.12 | 7.0E-21 | AA046502.1 | EST_HUMAN | 2k67a06_r1 Soes_Pregnant uterus_NibHPU Homo sapiens cDNA clone IMAGE:487858 5' |
| 3987 | 8985 | 13971 | 0.98 | 6.0E-21 | BE408611.1 | EST_HUMAN | 601304_125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3538310 5' |
| 913 | 5929 | 10984 | 0.79 | 5.0E-21 | 5902031_NT | | Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA |
| 4228 | 9232 | 14215 | 3.34 | 5.0E-21 | BE965839.1 | EST_HUMAN | 601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3593880 5' |
| 4548 | 5929 | 10964 | 0.83 | 5.0E-21 | 5902031_NT | | Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA |
| 4657 | 9642 | 14631 | 6.35 | 5.0E-21 | 4885474_NT | | Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA |
| 1696 | 6691 | 11767 | 1.66 | 4.0E-21 | AA970713.1 | EST_HUMAN | o06608_s1_NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 |
| 1801 | 6792 | 11882 | 1.05 | 3.0E-21 | AA218891.1 | EST_HUMAN | PMS3 mRNA; contains OFR_H1 OFF repetitive element; |
| 2212 | 7189 | 12310 | 0.99 | 3.0E-21 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3006 | 8023 | 13035 | 3.56 | 3.0E-21 | AJ007873.1 | NT | Homo sapiens GMID2B gene |
| 145 | 5211 | | 18.78 | 2.0E-21 | BE163247.1 | EST_HUMAN | QV3+HT0458_7/0200-09/012 HT0458 Homo sapiens cDNA |
| 922 | 5938 | 10969 | 0.87 | 2.0E-21 | AB007857.2 | NT | Homo sapiens mRNA for KIAA0397 protein, partial cds |
| 922 | 5938 | 10970 | 0.87 | 2.0E-21 | AB007857.2 | NT | Homo sapiens mRNA for KIAA0397 protein, partial cds |
| 1195 | 6196 | | 2.36 | 2.0E-21 | BE064410.1 | EST_HUMAN | RC4-BT0311_141109-0111-r06 BT0311 Homo sapiens cDNA |
| 2567 | 7530 | 12848 | 2.35 | 2.0E-21 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2567 | 7530 | 12849 | 2.35 | 2.0E-21 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 1236 | 6234 | 11278 | 1.4 | 1.0E-21 | AA557657.1 | EST_HUMAN | l46c04_s1_NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29_b2 |
| 1378 | 6375 | | 10.68 | 1.0E-21 | A1601284.1 | EST_HUMAN | sr88d12_x1_Barsleed clone HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3' |
| 4236 | 9278 | 14266 | 1.11 | 9.0E-22 | A1702438.1 | EST_HUMAN | l294g03_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408 |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|----------------------------|-------------------------|---|---|--|
| 934 | 5951 | | | 5.16 | 8.0E-22 BE144748.1 | EST_HUMAN | CAG-HT0179-281J99-076-h05 HT0179 Homo sapiens cDNA | |
| 857 | 5684 | 10691 | 4.6 | 7.0E-22 AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 | | |
| 4160 | 9155 | 14138 | 2.11 | 7.0E-22 Q61838 | SWISSPROT | ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M) | | |
| 4872 | 9851 | 14826 | 0.98 | 7.0E-22 AB008681.1 | NT | Homo sapiens gene for activin receptor type IIb, complete cds | | |
| 3551 | 8558 | | | 13.85 | 4.0E-22 AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 | |
| 944 | 5961 | | | 0.98 | 3.0E-22 AI469679.1 | EST_HUMAN | Hom14h10.x1 NCI CGAP_Oo14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gbl19593 HIGH | |
| 2495 | 7463 | 12578 | 2.28 | 3.0E-22 AI859038.1 | EST_HUMAN | AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN);contains L1.t1 L1 repetitive element; | | |
| 3588 | 8595 | | 1.25 | 3.0E-22 D14718.1 | NT | Wf66b04.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN | | |
| 4656 | 9641 | 14630 | 3.17 | 3.0E-22 AI090125.1 | EST_HUMAN | P46778 60S RIBOSOMAL PROTEIN L21.; | | |
| 1913 | 6899 | | 2.09 | 2.0E-22 N24942.1 | SWISSPROT | Human chromosomal protein HMG1 related gene | | |
| 2452 | 7422 | 12537 | 1.44 | 2.0E-22 P24916 | NT | qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to | | |
| 3335 | 8345 | 13363 | 3.9 | 2.0E-22 8394043 | NT | Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' | | |
| 4104 | 9098 | 14084 | 1.53 | 2.0E-22 AW817794.1 | EST_HUMAN | MEF12.12 MER12 repetitive element; | | |
| 1840 | 6830 | 11919 | 1.41 | 1.0E-22 AW865517.1 | EST_HUMAN | YX73d05.s1 Soares_melanocyte 2NbHMI Homo sapiens cDNA clone IMAGE:267369 3' | | |
| 2507 | 7475 | 12590 | 1.47 | 1.0E-22 U50871.1 | NT | IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR | | |
| 3326 | 8336 | 13356 | 1.7 | 1.0E-22 D14547.1 | NT | Homo sapiens protein kinase, gamma 3 non-catalytic subunit (PRKAG3), mRNA | | |
| 9238 | 8251 | | 2.43 | 7.0E-23 AV647246.1 | EST_HUMAN | PM1-ST0262-261189-001-d1/2 ST0262 Homo sapiens cDNA | | |
| 3349 | 8358 | | 1.59 | 6.0E-23 AF199333.1 | NT | PM4-SN0020-0 10400-009-h02 SN0020 Homo sapiens cDNA | | |
| 4146 | 9141 | 14125 | 1.04 | 6.0E-23 AL163249.2 | NT | Human familial Alzheimer's disease (STM2) gene, complete cds | | |
| 5055 | 8358 | | 1.07 | 6.0E-23 AF199333.1 | NT | Human DNA, SINE repetitive element | | |
| 658 | 5685 | 10692 | 3.39 | 2.0E-23 AJ289880.1 | NT | PM67246 GLC; Homo sapiens cDNA clone GLCAWC07 3' | | |
| 1125 | 7697 | | 3.75 | 2.0E-23 M55270.1 | NT | AV647246 GLC; Homo sapiens cDNA clone GLCAWC07 3' | | |
| 2723 | 7680 | 12793 | 1.37 | 2.0E-23 P22105 | SWISSPROT | Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds | | |
| 2723 | 7680 | 12794 | 1.37 | 2.0E-23 P22105 | SWISSPROT | TENASCIN-X PRECURSOR (TN-X)(HEXBRAUCHION-LIKE) | | |
| | | | | | EST_HUMAN | TENASCIN-X PRECURSOR (TN-X)(HEXBRAUCHION-LIKE) | | |
| 3289 | 8300 | | | 1.07 | 2.0E-23 AI201458.1 | EST_HUMAN | q573f11.x1 NC1 CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 | |
| 3634 | 8640 | | | 4.12 | 2.0E-23 BE165980.1 | EST_HUMAN | MER3-HT0487-150200-113-301 HT0487 Homo sapiens cDNA | |
| 3869 | 8870 | 13874 | 2.39 | 2.0E-23 H59981.1 | EST_HUMAN | MR3-HT0487-150200-113-301 HT0487 Homo sapiens cDNA clone IMAGE:205418 5' | | |
| 3869 | 8870 | 13875 | 2.39 | 2.0E-23 H59981.1 | EST_HUMAN | yr16ad2.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:205418 5' | | |
| 4397 | 9388 | 14371 | 1.16 | 1.0E-23 AL163252.2 | NT | yr16ad2.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:205418 5' | | |
| 4620 | 9605 | | 4.78 | 1.0E-23 AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C052 | | |
| | | | | | | Homo sapiens chromosome 21 segment HS21C052 | | |
| | | | | | | Homo sapiens chromosome 21 segment HS21C052 | | |

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Table 4
Single Exon Probes Expressed In HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|--|--|--|
| | | | | | | | ab7560B_s1 Striagene fetal retina 9372022 Homo sapiens cDNA clone IMAGE:852758 3' similar to TRE19822_E19B22 CA PROTEIN. ; |
| 548 | 5562 | | | 2.52 | 9.0E-24 AA663213.1 | EST_HUMAN SWISSPROT | OLFACTOORY RECEPTOR-LIKE PROTEIN [3] |
| 9503 | 14482 | 14482 | 1.13 | 8.0E-24 P23269 | EST_HUMAN SWISSPROT | OLFACTOORY RECEPTOR-LIKE PROTEIN [3] | |
| 4513 | 9503 | 14483 | 1.13 | 8.0E-24 P23269 | EST_HUMAN Q0V-DT0047-17020-122-606 DT0047 Homo sapiens cDNA DKFZp434A2311 5' | | |
| 3781 | 8784 | | 0.93 | 7.0E-24 AW937954.1 | EST_HUMAN DKFZp434A2311_1 434 (synonym: hies3) Homo sapiens cDNA clone IMAGE:852758 3' similar to Olfactory receptor-like protein Y (TSFY), complete cds | | |
| 4983 | 8958 | | 1.18 | 7.0E-24 AL039498.1 | EST_HUMAN Macaca fasciata mRNA for Testis-Specific Protein Y (TSFY), complete cds | | |
| 696 | 5720 | | 2.3 | 6.0E-24 AB001421.1 | NT | Homo sapiens chromosome 21 segment HS21C049 | |
| 828 | 5848 | 10885 | 33.51 | 6.0E-24 AL163249.2 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21(q22, segment 3/3 | |
| 3863 | 8865 | 13869 | 8.31 | 5.0E-24 AJ1229043.1 | NT | Homo sapiens cDNA clone c-ztc06 | |
| 4919 | 9387 | 14871 | 1.85 | 3.0E-24 F08337.1 | EST_HUMAN HSCZRC081 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:609161 5' | | |
| 2285 | 7261 | 12379 | 1.8 | 2.0E-24 AA167539.1 | EST_HUMAN ZP11109_r1 Striatogene fetal retina 9372022 Homo sapiens cDNA | | |
| 3709 | 8713 | | 0.78 | 2.0E-24 AW989189.1 | EST_HUMAN RC3-NN0068-096500-021-b03 NN0068 Homo sapiens cDNA | | |
| 1657 | 6853 | 11725 | 2.5 | 1.0E-24 | 7706340 NT | Homo sapiens CC1-127 protein (LOC515646), mRNA | |
| 2602 | 7564 | | 1.1 | 1.0E-24 AW820194.1 | EST_HUMAN QY0-ST0294-10400-185-x10 ST0294 Homo sapiens cDNA | | |
| 2954 | 7973 | 12988 | 4.21 | 1.0E-24 D86423.1 | NT | Mus musculus mRNA for HGT keratin, partial cds | |
| 4148 | 9143 | | 1.8 | 1.0E-24 AF143513.1 | NT | Homo sapiens PTEN (PTEN) gene, exon 2 | |
| 4837 | 9821 | 14798 | 3.17 | 7.0E-25 AA483944.1 | EST_HUMAN Homo sapiens cDNA clone IMAGE:121763 5' | | MER1 repetitive element; |
| 1612 | 6608 | 11672 | 1.2 | 5.0E-25 AW850271.1 | EST_HUMAN IL3-C70219-161199-031-D04 CT0218 Homo sapiens cDNA | | |
| 1421 | 6418 | 11478 | 1.64 | 4.0E-25 T98107.1 | EST_HUMAN y56n04_r1 Soay sheep fetal liver spleen 1NFLS Homo sapiens cDNA | | |
| 3318 | 8328 | | 2.89 | 4.0E-25 AW887671.1 | EST_HUMAN PM3-O70083-230200-001-g07 OT0093 Homo sapiens cDNA | | |
| 4190 | 9183 | | 3.14 | 4.0E-25 BE170957.1 | EST_HUMAN QV3-HT0543-140400-140-e11 HT0543 Homo sapiens cDNA | | |
| 3246 | 8269 | 13280 | 3.16 | 3.0E-25 | 8923321 NT | Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA | |
| 3246 | 8259 | 13281 | 3.16 | 3.0E-25 | 8923321 NT | Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA | |
| 1329 | 6327 | 11375 | 3.49 | 2.0E-25 | 5032158 NT | Homo sapiens transducin (beta)-like 1 (TBL1) mRNA | |
| 2245 | 7222 | 12341 | 6.05 | 2.0E-25 BE888016.1 | EST_HUMAN 601611530f NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5' | | |
| 2758 | 7440 | 12556 | 9.38 | 2.0E-25 P17008 | SWISSPROT 40S RIBOSOMAL PROTEIN S16 | | |
| 4066 | 9060 | 14047 | 1.69 | 2.0E-25 P17008 | SWISSPROT 40S RIBOSOMAL PROTEIN S16 | | |
| 4066 | 9060 | 14048 | 1.69 | 2.0E-25 P17008 | SWISSPROT 40S RIBOSOMAL PROTEIN S16 | | |
| 363 | 5412 | 10425 | 0.75 | 1.0E-25 AL040229.1 | EST_HUMAN DKFZp434H0313_1 434 (synonym: hies3) Homo sapiens cDNA clone IMAGE:852758 3' similar to Human endogenous retrovirus, complete genome | | |
| 1239 | 6228 | | 2.15 | 1.0E-25 | 9835487 NT | ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C) | |
| 2367 | 7341 | 12458 | 1.69 | 1.0E-25 Q06055 | SWISSPROT ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C) | | |
| 4710 | 9695 | 14679 | 2.8 | 1.0E-25 BE162737.1 | EST_HUMAN PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA | | |
| 2412 | 7383 | 12502 | 1.14 | 9.0E-26 AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 | |

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 Table 4
 Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| | | | | | | | Homo sapiens X-linked arthiodactyl dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 1542 | 6540 | 11597 | 1.66 | 7.0E-26 | AF003528.1 | NT | |
| 3873 | 8874 | 13879 | 1.32 | 7.0E-26 | X89211.1 | NT | H.sapiens DNA for endogenous retroviral like element |
| 4035 | 9031 | 14018 | 1.76 | 7.0E-26 | AW340153.1 | EST_HUMAN | hd02612x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3' |
| 2164 | 7143 | 12261 | 9.02 | 6.0E-26 | AF029308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families |
| 3271 | 8283 | 13306 | 1.78 | 6.0E-26 | AA206131.1 | EST_HUMAN | Z052R04.r1 Stratified neurepithelium (#837231) Homo sapiens cDNA clone IMAGE:2319519 3' similar to as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:WP-F49C12.11 CE03371 |
| 1168 | 6162 | 11196 | 5.17 | 5.0E-26 | A1708235.1 | EST_HUMAN | WP-F49C12.11 CE03371; as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to |
| 1158 | 6162 | 11197 | 5.17 | 5.0E-26 | A1708235.1 | EST_HUMAN | Human DNA, SIN/E repetitive element |
| 1721 | 6716 | 11792 | 1.25 | 3.0E-26 | D14547.1 | NT | Zn30d08.r1 Stratigene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' |
| 1981 | 6966 | | 2.26 | 3.0E-26 | AA115895.1 | EST_HUMAN | similar to qb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); Z030f10.r1 Stratigene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G665374 |
| 3691 | 8695 | 13697 | 1.2 | 3.0E-26 | AA152464.1 | EST_HUMAN | G665374 THYROID RECEPTOR INTERACTOR ; Z030f10.r1 Stratigene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G665374 |
| 3691 | 8695 | 13698 | 1.2 | 3.0E-26 | AA152464.1 | EST_HUMAN | G665374 THYROID RECEPTOR INTERACTOR ; |
| 673 | 5698 | 10707 | 5.99 | 2.0E-26 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 1831 | 6821 | | 2.34 | 2.0E-26 | AL038099.2 | EST_HUMAN | DKFZp56L171_s1_566 (synonym: hifid2) Homo sapiens cDNA clone DKFZp56L171_3' |
| 3160 | 8176 | 13199 | 5.27 | 2.0E-26 | X86694.1 | NT | M.musculus mRNA for astrocytic phosphoprotein, PEA-15 |
| 137 | 5203 | 10218 | 58.33 | 1.0E-26 | BE170371.1 | EST_HUMAN | QV4-H10538-C28300-123-e02 HT0538 Homo sapiens cDNA MFR2-BN0114;240500-030-907 BN0114 Homo sapiens cDNA |
| 2492 | 7460 | 12575 | 1.04 | 1.0E-26 | BE814995.1 | EST_HUMAN | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds |
| 2615 | 7577 | | 57.21 | 1.0E-26 | AF261085.1 | NT | WJ49c04.x1 NCI_CGAP_Lut19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 |
| 11 | 5091 | 10075 | 2.7 | 8.0E-27 | AI831462.1 | EST_HUMAN | THR repetitive element ; |
| 553 | 5587 | | 2.73 | 8.0E-27 | AL163227.2 | NT | au87h08.x1 segment HS21C027 |
| 1391 | 6388 | 11440 | 83.09 | 8.0E-27 | AW162737.1 | EST_HUMAN | Homo sapiens chromosome 21 segment 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558 |
| 1391 | 6388 | 11441 | 83.09 | 8.0E-27 | AW162737.1 | EST_HUMAN | TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 1391 | 6388 | 12199 | 1.71 | 8.0E-27 | AW864776.1 | EST_HUMAN | PM2-SN0018-220300-002-807 SN0018 Homo sapiens cDNA |
| 2103 | 7083 | | | | | | ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCATOR 3) (ANT 3) |
| 3111 | 8127 | 13147 | 2.66 | 8.0E-27 | P12236 | SWISSPROT | NUCLEOTIDE TRANSLOCATOR |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Acession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|----------------------|---|--|
| | | | | | | | Human endogenous retroviral element HC22 |
| 675 | 5700 | | 1.35 | 7.0E-27 | Z70664.1 | NT | h51h12_x1_Soares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2975879 3' similar to TR:O76040 |
| | | | | 2.5 | 7.0E-27 AW629172.1 | EST_HUMAN | h5040 ORF2: FUNCTION UNKNOWN; O76040 |
| 4918 | 9896 | | | 2.62 | 3.0E-27 X501658.1 | NT | Rattus RY43 mRNA for a potential ligand-binding protein |
| 1990 | 6975 | 12080 | | 1.26 | 3.0E-27 BE071924.1 | EST_HUMAN | PM0-BT0527-090100-001-d411 BT0527_Homo_sapiens_cDNA |
| 4149 | 9144 | 14128 | | 3.0E-27 AF054187.1 | NT | Homo sapiens alpha NAC mRNA, complete cds | |
| 42 | 5122 | 10110 | | 36.86 | 2.0E-27 | | nr01b10_s1_NCI_CGAP_P11_Homo_sapiens_cDNA_clone IMAGE:1000699 similar to gb:M17886 60S |
| 1855 | 6844 | | | 37.38 | 2.0E-27 AA563345.1 | EST_HUMAN | ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h51h12_x1_Soares_NFL_T_GBC_S1_Homo_sapiens_cDNA_clone IMAGE:2975879 3' similar to TR:O76040 |
| 3036 | 8053 | | | 10.93 | 2.0E-27 AW629172.1 | EST_HUMAN | C76040 ORF2: FUNCTION UNKNOWN; C76040 |
| 3153 | 8169 | 13189 | 1.99 | 2.0E-27 | AF111167.2 | NT | Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 3153 | 8169 | 13190 | 1.99 | 2.0E-27 | AF111167.2 | NT | Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 433 | 5471 | | 1.55 | 1.0E-27 | AL163246.2 | NT | HS21C046 |
| 981 | 5996 | 11028 | 1.2 | 1.0E-27 | AB026898.1 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 3966 | 8964 | | 1.02 | 1.0E-27 | BE350127.1 | EST_HUMAN | DLEC1 to ORC1L3, ORC1L4 genes, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds) |
| 141 | 5206 | | | 9.0E-28 | BE34899.1 | EST_HUMAN | SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ; hw17c11_x1_NCI_CGAP_Lu24_Homo_sapiens_cDNA_clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 |
| 309 | 5364 | 10375 | | 2.16 | 9.0E-28 | AU126260.1 | NT2RP1_Homo_sapiens_cDNA_clone NT2RP1_Homo_sapiens_cDNA_clone IMAGE:3146256 3' similar to contains MER29_b3 |
| 1162 | 6166 | 11200 | 2.37 | 9.0E-28 | AU142750.1 | EST_HUMAN | hw17c11_x1_NCI_CGAP_Lu24_Homo_sapiens_cDNA_clone IMAGE:3146256 3' similar to contains MER29_b3 |
| 316 | 5371 | | 15.2 | 7.0E-28 | AU142750.1 | EST_HUMAN | hw18c07_x1_NCI_CGAP_Pan1_Homo_sapiens_cDNA_clone IMAGE:2455652 3' similar to contains MER29_b3 |
| 3902 | 8902 | 13800 | 2.32 | 5.0E-28 | AU921003.1 | EST_HUMAN | THR repetitive element; |
| | | | 1.66 | 5.0E-28 | R79762.1 | EST_HUMAN | Y18R10.1_Soares_placenta_Nb21P_Homo_sapiens_cDNA_clone IMAGE:146443 5' |
| 2552 | 7517 | 12635 | 2.12 | 4.0E-28 | AW195066.1 | EST_HUMAN | xn33c09_x1_NCI_CGAP_Kid11_Homo_sapiens_cDNA_clone IMAGE:2695504 3' similar to SW:GG95_HUMAN |
| 2908 | 7927 | 12945 | 1.09 | 4.0E-28 | 4F05316 | NT | xn33c09_x1_NCI_CGAP_Kid11_Homo_sapiens_cDNA_clone IMAGE:3685305 5' |
| 3035 | 8052 | 13081 | 5.95 | 4.0E-28 | BE40910.1 | EST_HUMAN | Q08379_COL3N-95; Homo sapiens myosin phosphatase, target subunit 1 (MYPFT1) mRNA |
| | | | | | | | Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds |
| 1264 | 6262 | | | 1.66 | 3.0E-28 | AF155382.1 | NT |
| 87 | 5164 | 10175 | 8.92 | 2.0E-28 | BE062167.1 | EST_HUMAN | RC1-BT0254_220300-019-c05_BT0254_Homo_sapiens_cDNA |
| 1147 | 6151 | 11183 | 10.35 | 2.0E-28 | Y11107.3 | NT | Hom sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41 |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| | | | | | | | qq35006_x1_NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element; |
| 2405 | 7376 | 12496 | | 1.68 | 2.0E-28 AI348634.1 | EST_HUMAN | Human gene for Ah-receptor, exon 7-9 |
| 3281 | 8293 | 13318 | | 0.68 | 2.0E-28 AI163209.2 | NT | Human zinc finger protein ZNF131 mRNA, partial cds |
| 1448 | 6445 | 11504 | | 1.71 | 1.0E-28 D38044.1 | EST_HUMAN | QV1-B10821-1209C-360-b03 BT0821 Homo sapiens cDNA |
| 2158 | 7137 | 12256 | | 2.04 | 1.0E-28 BF33236.1 | EST_HUMAN | Human zinc finger protein ZNF131 mRNA, partial cds |
| 4436 | 9426 | | | 2.22 | 1.0E-28 U09410.1 | NT | OLFACTORY RECEPTOR 15 (OR3) |
| 5003 | 9974 | 14949 | | 1.55 | 1.0E-28 F23275 | SWISSPROT | EST378521 IMAGE resequences, MAGI Homo sapiens cDNA |
| 1567 | 6564 | 11627 | | 1.17 | 7.0E-29 AW956447.1 | EST_HUMAN | 6011149901 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356367 5' similar to TR:O15475 |
| 3476 | 8484 | | | 1.34 | 7.0E-29 BE254708.1 | EST_HUMAN | WP69601_x1_NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2465985 3' similar to TR:O15475 |
| 590 | 5621 | 10620 | | 9.68 | 6.0E-29 AI936748.1 | EST_HUMAN | O15475 UNNAMED HERV-H PROTEIN; contains LTR7.b1 LTR7 repetitive element; |
| 4839 | 9823 | | | 1.37 | 5.0E-29 AI163203.2 | NT | Homo sapiens chromosome 21 segment HS21C002 random |
| 3161 | 8177 | | | 1.75 | 4.0E-29 AI752367.1 | EST_HUMAN | cn15c02_x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone IMAGE:cn15c02 random |
| 4290 | 9282 | 14270 | | 1.29 | 3.0E-29 AB042297.1 | NT | Homo sapiens PT/S gene for 6-pyruvoyltetrahydropterin synthase, complete cds |
| 489 | 5525 | 10532 | | 1.15 | 2.0E-29 AF084869.1 | NT | Homo sapiens envelope protein RIC-6 (env) gene, complete cds |
| 489 | 5525 | 10533 | | 1.15 | 2.0E-29 AF084869.1 | NT | Homo sapiens envelope protein RIC-6 (env) gene, complete cds |
| 1501 | 6499 | 11553 | | 4.66 | 2.0E-29 AI963604.1 | EST_HUMAN | Wf65d10_x1_NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 |
| 1501 | 6499 | 11554 | | 4.66 | 2.0E-29 AI963604.1 | EST_HUMAN | HERV-E ENVEL_OPE GLYCOPROTEIN; |
| 4157 | 9152 | 14134 | | 2.09 | 2.0E-29 AL163268.2 | NT | Hom sapiens chromosome 21 segment HS21C008 |
| 1484 | 6481 | | | 1.34 | 7.0E-30 BE091133.1 | EST_HUMAN | PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA |
| 1534 | 6532 | | | 0.9 | 6.0E-30 X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 1736 | 6731 | 11808 | | 1.1 | 6.0E-30 D25303.1 | EST_HUMAN | Human mRNA for integrin alpha subunit, complete cds |
| 3117 | 8133 | 13152 | | 2.42 | 6.0E-30 BE008026.1 | EST_HUMAN | QV0-BN0147-290400-214-112 BN0147 Homo sapiens cDNA |
| 4614 | 8133 | 13152 | | 0.93 | 6.0E-30 BE008026.1 | EST_HUMAN | QV0-BN0147-290400-214-112 BN0147 Homo sapiens cDNA |
| 3906 | 8906 | 13904 | | 40.12 | 5.0E-30 A1399992.1 | EST_HUMAN | QV3-DT0043-0304200-080-006 DT0043 Homo sapiens cDNA |
| 2082 | 7063 | 12172 | | 1.93 | 4.0E-30 AW937471.1 | EST_HUMAN | QV3-DT0043-0304200-080-006 DT0043 Homo sapiens cDNA |
| 2082 | 7063 | 12173 | | 1.93 | 4.0E-30 AW937471.1 | EST_HUMAN | qq83c05_x1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains MER28_b2 MER29 repetitive element; |
| 1134 | 6139 | | | 3.35 | 3.0E-30 AI338551.1 | EST_HUMAN | contains MER28_b2 MER29 repetitive element; |
| 3672 | 8677 | 13680 | | 0.82 | 3.0E-30 AF128893.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6 |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 667 5692 | 10701 | | 1.21 | 2.0E-30 | AW857315.1 | EST_HUMAN | Cm0_CTo307_3_10110_158_H03 CTo307 Homo sapiens cDNA |
| 1068 6076 | | | 2.46 | 2.0E-30 | F08688.1 | EST_HUMAN | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105 |
| 1449 6446 | 11505 | | 8.55 | 2.0E-30 | BE175877.1 | EST_HUMAN | RG5-HT0582_11040/0-0/3-H08 HT0582 Homo sapiens cDNA |
| 2643 7603 | 12716 | | 6.5 | 2.0E-30 | BE765232.1 | EST_HUMAN | IL2-NT0101-28670(1)-116-E04 NT0101 Homo sapiens cDNA |
| 2849 7889 | 12885 | | 6.88 | 2.0E-30 | AF114156.1 | NT | Homo sapiens Y-linked zinc finger protein (ZEV) gene, complete cds |
| 3700 8704 | 13707 | | 2.23 | 2.0E-30 | AW206581.1 | EST_HUMAN | UH-BI1_afc-c-12-41-U1.5f NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722558 3' |
| 4653 9618 | 14609 | | 1.61 | 2.0E-30 | BE298945.1 | EST_HUMAN | 601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5' |
| 4653 9618 | 14610 | | 1.61 | 2.0E-30 | BE298945.1 | EST_HUMAN | 601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5' |
| 284 5342 | 10355 | | 13.84 | 1.0E-30 | C18939.1 | EST_HUMAN | C188939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5' |
| 533 5568 | 10571 | | 3.42 | 1.0E-30 | AW468897.1 | EST_HUMAN | hd30b04_xrl Sacarose_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910391 3' similar to contains MER1.3 MER1_MER1 repetitive element; |
| 706 5730 | 10746 | | 3.15 | 1.0E-30 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 2150 7129 | 12248 | | 2.78 | 1.0E-30 | AA664377.1 | EST_HUMAN | 8G77b08_51 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:868589 3' |
| 2393 7364 | 12486 | | 1.95 | 1.0E-30 | BF347728.1 | EST_HUMAN | 602022560F1 NCI CGAP_Elm67 Homo sapiens cDNA clone IMAGE:41157991 5' |
| 2980 7988 | 13011 | | 0.79 | 1.0E-30 | AA315045.1 | EST_HUMAN | EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end |
| 1060 6069 | 11100 | | 6.71 | 8.0E-31 | 8923389 | NT | Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA |
| 2347 7321 | | | 23.47 | 8.0E-31 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 4763 9747 | 14733 | | 1.01 | 8.0E-31 | F23275 | SWISSPROT | OLFACTOORY RECEPTOR 15 (OR3) |
| 4763 9747 | 14734 | | 1.01 | 8.0E-31 | F23275 | SWISSPROT | OLFACTOORY RECEPTOR 15 (OR3) |
| 701 5725 | | | 2.43 | 7.0E-31 | AA372657.1 | EST_HUMAN | EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end |
| 2597 7559 | 12675 | | 2.15 | 7.0E-31 | EE326517.1 | EST_HUMAN | hw05a11_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31820123 |
| 2597 7559 | 12676 | | 2.15 | 7.0E-31 | EE326517.1 | EST_HUMAN | hw05a11_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31820123 |
| 3594 8601 | | | 2.5 | 6.0E-31 | AE223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced |
| 192 5256 | 10268 | | 3.17 | 5.0E-31 | M60694.1 | NT | Homo sapiens type I DNA topoisomerase gene, exon 8 |
| 192 5256 | 10269 | | 3.17 | 5.0E-31 | M60694.1 | NT | Homo sapiens type I DNA topoisomerase gene, exon 8 |
| 591 5622 | | | 3.18 | 4.0E-31 | AJ271735.1 | NT | Homo sapiens Xq pseudoautosomal region; segment 1/2 |
| 1782 6774 | | | 1.4 | 4.0E-31 | AL163200.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2716 7873 | | | 1.63 | 4.0E-31 | 5730038 | NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 2519 7486 | | | 1.54 | 3.0E-31 | 6005871 | NT | Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA |
| 1873 6862 | 11951 | | 2.35 | 2.0E-31 | AW83871.1 | EST_HUMAN | QV2-LT0051-26C300-111-03 LT0051 Homo sapiens cDNA |
| 2152 7131 | 12248 | | 1.01 | 2.0E-31 | AI308388.1 | EST_HUMAN | Ig44d05_x1 SacaroseNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3' |
| 2278 7254 | 12373 | | 1.52 | 2.0E-31 | AL119245.1 | EST_HUMAN | DKF2p781G1513_I1781 (synonym: hamy2) Homo sapiens cDNA clone DKF2p781G1513 5' |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLASTE Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|-------------------------------------|-----------------------|-------------------------|--|
| | | | | | | | aab8f11_5' Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:338413 3' similar to contains THR_12 THR repetitive element; |
| 2373 | 7345 | 12465 | 4.03 | 2.0E-31 | AA458824.1 | EST_HUMAN | Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds |
| 15 | 5095 | 10079 | 10.14 | 1.0E-31 | J83163.1 | NT | OLFFACTORY RECEPTOR 2C1 |
| 1623 | 6620 | 11686 | 9.05 | 1.0E-31 | O95371 | SWISSPROT | OLFFACTORY RECEPTOR 2C1 |
| 1623 | 6620 | 11687 | 9.05 | 1.0E-31 | O95371 | SWISSPROT | OLFFACTORY RECEPTOR 2C1 |
| 1623 | 6620 | 11688 | 9.05 | 1.0E-31 | O95371 | SWISSPROT | DKFZp547B235_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5' |
| 4501 | 9491 | 14467 | 1.26 | 1.0E-31 | AL134376.1 | EST_HUMAN | DKFZp547B235_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKE7p547B235 5' |
| 4501 | 9491 | 14468 | 1.26 | 1.0E-31 | AL134376.1 | EST_HUMAN | ozt15a09_XL_Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3' |
| 2024 | 7007 | 12113 | 5.49 | 8.0E-32 | AI056770.1 | EST_HUMAN | Homo sapiens PRD1181 mRNA, complete cds |
| 1017 | 6027 | 11057 | 84.69 | 5.0E-32 | AF116827.1 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 918 | 5934 | | 1.7 | 4.0E-32 | AL163246.2 | NT | Homo sapiens FLI-1 gene, partial |
| 453 | 5490 | 10505 | 2.46 | 3.0E-32 | Y17293.1 | NT | AV731500 HTTF_Homo sapiens cDNA clone HTTFAKC07 5' |
| 1427 | 6424 | 11483 | 57.22 | 3.0E-32 | AV731500.1 | EST_HUMAN | Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds |
| 2604 | 7566 | | 1.49 | 1.0E-32 | D84430.1 | NT | Homo sapiens cDNA clone IMAGE:38344433 5' |
| 3020 | 8037 | | 1.65 | 1.0E-32 | BE743299.1 | EST_HUMAN | 601575207F1 NH_MGC_9 Homo sapiens |
| | | | | | | | to12509_XL_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 O88539 |
| 3400 | 8409 | | 5.22 | 9.0E-33 | BE327112.1 | EST_HUMAN | IWW DOMAIN EINDING PROTEIN 11. |
| 62 | 5142 | 10144 | 11.74 | 7.0E-33 | 5031736 NT | | Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA |
| 62 | 5142 | 10145 | 11.74 | 7.0E-33 | 5031736 NT | | Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA |
| 2097 | 7078 | 12192 | 1.93 | 7.0E-33 | AI590115.1 | EST_HUMAN | to12509_XL_NCI_CGAP_U24 Homo sapiens cDNA clone IMAGE:2178509 3' similar to contains OFR_11_OFR repetitive element; |
| 2576 | 7539 | | 7.4 | 7.0E-33 | AV730056.1 | EST_HUMAN | AV730056 HTTF_Homo sapiens cDNA clone HTTFANF08 5' |
| 2757 | 6655 | 11727 | 1.01 | 7.0E-33 | AV730015.1 | EST_HUMAN | AV730015 HTTF_Homo sapiens cDNA |
| 3168 | 8184 | | 14.85 | 7.0E-33 | AW971307.1 | EST_HUMAN | EST383396 MAGE resequences, MAGL_Homo sapiens cDNA |
| 3652 | 8658 | | 0.8 | 6.0E-33 | AL163285.2 | NT | Hom sapiens chromosome 21 segment HS21C085 |
| 1740 | 6735 | | 1.43 | 5.0E-33 | BF373515.1 | EST_HUMAN | QV1-FT0169 Homo sapiens cDNA |
| 1842 | 6832 | | 0.97 | 5.0E-33 | 11141884 | NT | Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA |
| 1858 | 6847 | 11934 | 4.15 | 5.0E-33 | | 4507208 | Homo sapiens spermidine synthase (SRM) mRNA |
| 1858 | 6847 | 11935 | 4.15 | 5.0E-33 | | 4507208 | Homo sapiens spermidine synthase (SRM) mRNA |
| 2210 | 7187 | | 1.61 | 5.0E-33 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 3945 | 8943 | 13933 | 1.87 | 5.0E-33 | AB014599.1 | NT | Homo sapiens mRNA for KIAA0699 protein, partial cds |
| 5055 | 10034 | 15001 | 1.07 | 5.0E-33 | M64350.1 | NT | Human TCR variable region Vα30 subfamily gene (Vα30, JA, CA segments), 5' end |
| 1111 | 6117 | | 1.87 | 4.0E-33 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |

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 Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2066 | 7048 | 12156 | 1.97 | 4.0E-33 | 4758987 | NT | Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA ab51b11.r1 Strategene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844377 5' similar to |
| 2353 | 7327 | | 1.14 | 4.0E-33 | AA626621.1 | EST_HUMAN | contains Alu repetitive element; contains MER28_b2 MER28 repetitive element; |
| 2474 | 7443 | 12558 | 2.2 | 4.0E-33 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 U1-H-B12-ghH-c-[3-O-Ui_s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3' |
| 4356 | 9347 | 14327 | 1.46 | 4.0E-33 | AW293349.1 | EST_HUMAN | h09g01_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28_b3 |
| 1073 | 6081 | | 5.08 | 3.0E-33 | BE350127.1 | EST_HUMAN | MER29 repetitive element; |
| 1074 | 6081 | | 3.92 | 3.0E-33 | BE350127.1 | EST_HUMAN | h09g01_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28_b3 |
| 2382 | 7770 | | 1.73 | 3.0E-33 | AV647851.1 | EST_HUMAN | AV647851 GLC Homo sapiens cDNA clone GLCBGF09 3' |
| 16 | 5096 | | 1.02 | 2.0E-33 | AI160189.1 | EST_HUMAN | qb67g03_x1 Socres_fetal_heart_NbH-H9W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.tif OFR repetitive element; |
| 105 | 5096 | | 2.37 | 2.0E-33 | AI160189.1 | EST_HUMAN | qb67g03_x1 Socres_fetal_heart_NbH-H9W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.tif OFR repetitive element; |
| 4295 | 9287 | | 5.1 | 2.0E-33 | BE159039.1 | EST_HUMAN | MRO-HT0405-160300-202-d08 HT0406 Homo sapiens cDNA ab51g11.r1 Strategene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to |
| 4826 | 9810 | 14791 | 30.71 | 2.0E-33 | AA626683.1 | EST_HUMAN | gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN); |
| 4922 | 9900 | 14875 | 2.2 | 2.0E-33 | 11421332 | NT | Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA |
| 4922 | 9900 | 14876 | 2.2 | 2.0E-33 | 11421332 | NT | Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA |
| 9 | 5089 | | 1.61 | 1.0E-33 | AF003528.1 | NT | Homo sapiens X-linked epidermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 4368 | 9360 | 14340 | 1.09 | 8.0E-34 | BE062570.1 | EST_HUMAN | QV2-BT0258-071289-019-007 BT0258 Homo sapiens cDNA |
| 1419 | 6416 | 11476 | 2.31 | 7.0E-34 | T70845.1 | EST_HUMAN | yd15e05_r1 Socres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5' |
| 468 | 5504 | 10517 | 1.48 | 6.0E-34 | U10991.1 | NT | Human G2 protein mRNA, partial cds |
| 468 | 5504 | 10518 | 1.48 | 6.0E-34 | U10991.1 | NT | Human G2 protein mRNA, partial cds |
| 1841 | 6831 | | 2.53 | 5.0E-34 | 7706500 | NT | Homo sapiens NpwBP-binding protein NpwBP (LOC51729), mRNA |
| 4893 | 9872 | 14839 | 5.04 | 5.0E-34 | U30883.1 | NT | Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds |
| 1952 | 6938 | 12040 | 1.36 | 4.0E-34 | AI804667.1 | EST_HUMAN | tg94c06_x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2249194 3' |
| 2647 | 7607 | 12719 | 0.92 | 4.0E-34 | 89222807 | NT | Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA |
| 3099 | 8115 | 13133 | 1.38 | 4.0E-34 | 5803166 | NT | Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) |
| 1475 | 6472 | 11530 | 14.56 | 1.0E-34 | P12236 | SWISSPROT | Homo sapiens X-linked epidermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 3589 | 8596 | 13600 | 1.32 | 1.0E-34 | AF003528.1 | NT | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--------------------|
| 3957 8955 | 13944 | 0.93 | 1.0E-34 | A7009397.1 | NT | Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds | |
| 3957 8955 | 13945 | 0.93 | 1.0E-34 | A7009397.1 | NT | Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds | |
| 4352 9343 | | 4.5 | 1.0E-34 | BE071414.1 | EST_HUMAN | RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA | |
| 3560 8567 | 13573 | 1.41 | 9.0E-35 | AW663302.1 | EST_HUMAN | hh77hb06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:29668787 5' | |
| 224 5286 | | 25.01 | 8.0E-35 | 6031190 | NT | Homo sapiens irrophitin (PHB) mRNA | |
| 1699 6694 | 11770 | 2.3 | 8.0E-35 | BF589937.1 | EST_HUMAN | neaa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:32581343' similar to TR:O75912 | |
| 1699 6694 | 11771 | 2.3 | 8.0E-35 | BF589937.1 | EST_HUMAN | neaa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:32581343' similar to TR:O75912 | |
| 4717 9702 | 14688 | 3.04 | 8.0E-35 | BF183195.1 | EST_HUMAN | O75912 DIACYL GLYCEROL KINASE IOTA. ; | |
| 1388 6385 | 11437 | 1.5 | 6.0E-35 | AA757115.1 | EST_HUMAN | 601808588bf1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5' | |
| 1925 6911 | 12006 | 1.65 | 6.0E-35 | 6005975 | NT | Homo sapiens testis_NHT Homo sapiens cDNA clone 13039397 3' | |
| 5063 10032 | | 0.75 | 6.0E-35 | 8923389 | NT | Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA | |
| 1671 6667 | 11742 | 1.53 | 5.0E-35 | X63392.1 | NT | H. sapiens immunoglobulin kappa light chain variable region L14 | |
| 2711 7668 | 12781 | 1.05 | 5.0E-35 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds | |
| 2939 7959 | 12977 | 1.22 | 5.0E-35 | 6912639 | NT | Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA | |
| | | | | | | Homo sapiens metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds | |
| 4285 9277 | 14265 | 1.3 | 5.0E-35 | AF023298.1 | NT | | |
| 1408 6406 | 11465 | 66.29 | 4.0E-35 | BE257907.1 | EST_HUMAN | 601109719f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5' | |
| 1783 6775 | 11866 | 19.99 | 4.0E-35 | H91193.1 | EST_HUMAN | Y98a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element; | |
| 1544 6542 | 11600 | 52.74 | 3.0E-35 | BE268182.1 | EST_HUMAN | 601123260f1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:33450063 5' | |
| 2269 7246 | | 1.68 | 3.0E-35 | AF224492.1 | NT | Homo sapiens phospholipid scramblase 1 gene, complete cds | |
| 108 7713 | 10192 | 1.21 | 2.0E-35 | N88965.1 | EST_HUMAN | K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT | |
| 1168 6171 | 11206 | 1.09 | 2.0E-35 | T11909.1 | EST_HUMAN | A971F Heart Homo sapiens cDNA clone A971 | |
| 2156 7135 | 12254 | 2.74 | 2.0E-35 | AB018413.1 | NT | Homo sapiens mRNA for Gab2, complete cds | |
| 2612 7574 | 12688 | 1.92 | 2.0E-35 | AW66505.1 | EST_HUMAN | hi86a12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879166 3' similar to SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12; | |
| 3480 8488 | | 0.84 | 2.0E-35 | AB020702.1 | NT | Homo sapiens mRNA for KIAA0855 protein, partial cds | |
| 3814 8817 | 13823 | 0.81 | 2.0E-35 | BE247575.1 | EST_HUMAN | TCBAP2E4323 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328 | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3814 | 8817 | 13824 | 0.81 | 2.0E-35 | BE247575.1 | EST_HUMAN | TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HGSC project=TCBA Homo sapiens cDNA clone TC3AP4328 |
| 4535 | 9525 | | 2.63 | 2.0E-35 | H49239.1 | EST_HUMAN | JY19at2.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2740795' |
| 47 | 5128 | 10119 | 6.23 | 1.0E-35 | AA631949.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12:1 |
| 47 | 5128 | 10120 | 6.23 | 1.0E-35 | AA631949.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12:1 |
| 743 | 5766 | 10790 | 140.65 | 1.0E-35 | AW389473.1 | EST_HUMAN | IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA |
| 743 | 5766 | 10791 | 140.65 | 1.0E-35 | AW389473.1 | EST_HUMAN | IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA |
| 898 | 5916 | | 1.2 | 1.0E-35 | T87947.1 | EST_HUMAN | Yd93a01.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1157525' similar to SP-A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ; |
| 2471 | 7439 | 12555 | 2.17 | 1.0E-35 | 7705994 | NT | Homo sapiens hypothetical protein (LOC51233), mRNA ht08g01.xt NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256' similar to contains MER29.b3 |
| 2694 | 7652 | 12766 | 1.37 | 1.0E-35 | BE350127.1 | EST_HUMAN | MER29 repetitive element ; ht08g01.xt NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256' similar to contains MER29.b3 |
| 2694 | 7652 | 12767 | 1.37 | 1.0E-35 | BE350127.1 | EST_HUMAN | Homo sapiens hypothetical protein (LOC51233), mRNA ht08g01.xt NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256' similar to contains MER29.b3 |
| 3070 | 8086 | 13100 | 1.24 | 1.0E-35 | 6006030 | NT | Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L), mRNA |
| 3090 | 8106 | 13121 | 2.49 | 1.0E-35 | AV650422.1 | EST_HUMAN | AV650422 GLC Homo sapiens cDNA clone GL_CCEF06 3' |
| 3090 | 8106 | 13122 | 2.49 | 1.0E-35 | AV650422.1 | EST_HUMAN | AV650422 GLC Homo sapiens cDNA clone GL_CCEF06 3' |
| 4298 | 9290 | 14276 | 4.67 | 1.0E-35 | 7656905 | NT | Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA |
| 4298 | 9290 | 14277 | 4.67 | 1.0E-35 | 7656905 | NT | Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA |
| 3879 | 8880 | 13883 | 1.75 | 9.0E-36 | AW82170.1 | EST_HUMAN | RC3-ST0315-180200-013-f12 ST0315 Homo sapiens cDNA |
| 2860 | 7880 | 12898 | 2.3 | 7.0E-36 | AW857579.1 | EST_HUMAN | CM1-CT0315-091299-003-d07 CT0315 Homo sapiens cDNA |
| 3044 | 8061 | | 4.78 | 7.0E-36 | 4557498 | NT | Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA |
| 1957 | 6943 | 12045 | 1.89 | 6.0E-36 | 7706622 | NT | Homo sapiens inquinin 2 (NINJ2), mRNA |
| 2351 | 7325 | | 5.02 | 6.0E-36 | AB035346.1 | NT | Homo sapiens TCL6 gene, exon 12 |
| 3554 | 8561 | 13567 | 1.16 | 6.0E-36 | BF515101.1 | EST_HUMAN | U1-H-BW1-anv-c12-0-U.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3' |
| 138 | 5204 | 10219 | 10.77 | 5.0E-36 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 2678 | 7636 | 12751 | 24.76 | 5.0E-36 | BS388436.1 | EST_HUMAN | 601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5' |
| 3531 | 8537 | 13542 | 1.37 | 5.0E-36 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 4643 | 9628 | 14621 | 2.22 | 5.0E-36 | 5729729 | NT | Homo sapiens API5-like 1 (API5L1), mRNA |
| 4643 | 9628 | 14622 | 2.22 | 5.0E-36 | 5729729 | NT | Homo sapiens API5-like 1 (API5L1), mRNA |
| 1205 | 6206 | 11243 | 2.05 | 4.0E-36 | BED100384.1 | EST_HUMAN | PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA |
| 1416 | 6413 | 11474 | 1.38 | 4.0E-36 | P10266 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 1606 | 6602 | 11664 | 1.78 | 4.0E-36 | BE382574.1 | EST_HUMAN | 601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5' |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|--------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--|
| 2161 | 7140 | | 4.99 | 4.0E-36 | AW247772.1 | EST_HUMAN | 2820020_5_prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020_5' |
| 3275 | 8287 | 13311 | 0.98 | 4.0E-36 | BE389298.1 | EST_HUMAN | 60128226SF1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168_5' |
| 3275 | 8287 | 13312 | 0.98 | 4.0E-36 | BE389299.1 | EST_HUMAN | 60128226SF1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168_5' |
| 687 | 5711 | 10725 | 2.91 | 3.0E-36 | AF099810.1 | NT | Homo sapiens neurexin II-alpha gene, partial cds |
| 1468 | 6465 | 11524 | 1.3 | 3.0E-36 | AF110239.1 | NT | Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds |
| 1468 | 6465 | 11525 | 1.3 | 3.0E-36 | AF110239.1 | NT | Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds |
| 2235 | 7212 | 12329 | 2.14 | 3.0E-36 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 4373 | 9365 | 14345 | 6.39 | 3.0E-36 | '0181139 | NT | Mus musculus lunotrophilin 1 (Jp1-pending), mRNA |
| 3096 | 8112 | 13130 | 6.65 | 2.0E-36 | BE259267.1 | EST_HUMAN | 60110634SF1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3342706_5' |
| 4802 | 9786 | 14768 | 17.96 | 2.0E-36 | AW880376.1 | EST_HUMAN | QV0-O70030-24030-174-h04 OT030 Homo sapiens cDNA |
| 874 | 5892 | 10933 | 1.87 | 1.0E-36 | BE409310.1 | EST_HUMAN | 60130093SF1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480_5' |
| 2084 | 7065 | 12176 | 1.85 | 1.0E-36 | BE146523.1 | EST_HUMAN | RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA |
| 2084 | 7065 | 12177 | 1.85 | 1.0E-36 | BE146523.1 | EST_HUMAN | RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA |
| 2139 | 7119 | 12234 | 1.5 | 1.0E-36 | BF673761.1 | EST_HUMAN | 60213649SF1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886_5' |
| 3269 | 8282 | 12822 | 1.42 | 1.0E-36 | AF156982.1 | NT | Homo sapiens human endogenous retrovirus W proCB-19 protease (pro) gene, partial cds |
| 3276 | 8288 | 13313 | 0.98 | 8.0E-37 | 4757979 | NT | Homo sapiens chitinin (chitinin) 2 (CHN2) mRNA |
| 1265 | 6293 | 2.96 | 7.0E-37 | AL042801.1 | EST_HUMAN | DKFZp434E0422_r1_434 (synonym: hiles3) Homo sapiens cDNA clone DKFZp434E0422_5' | |
| 1705 | 6700 | 11776 | 1.1 | 7.0E-37 | AF111167.2 | NT | Homo sapiens lun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 1705 | 6700 | 11777 | 1.1 | 7.0E-37 | AF111167.2 | NT | Homo sapiens lun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 4955 | 8932 | | 1.57 | 6.0E-37 | IR10039.1 | EST_HUMAN | Y25e02_r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:127850_5' |
| 2357 | 7331 | 12447 | 2.14 | 4.0E-37 | AA702794.1 | EST_HUMAN | Z90b04_r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015_3' |
| 5038 | 10009 | | 0.91 | 4.0E-37 | NG2051.1 | EST_HUMAN | ES152g10_WATM1 Homo sapiens cDNA clone 52g10 similar to human STS G04101 |
| 1967 | 6952 | 12056 | 1.95 | 3.0E-37 | AL048956.1 | EST_HUMAN | DKFZp434L2418_r1_434 (synonym: hiles3) Homo sapiens cDNA clone DKFZp434L2418 |
| 1967 | 6952 | 12057 | 1.95 | 3.0E-37 | AL048956.1 | EST_HUMAN | DKFZp434L2418_r1_434 (synonym: hiles3) Homo sapiens cDNA clone DKFZp434L2418 |
| 2441 | 7411 | | 1.2 | 3.0E-37 | AW961150.1 | EST_HUMAN | ES137322 MAGE sequences, MAGF Homo sapiens cDNA |
| 2895 | 7914 | | 3.82 | 3.0E-37 | AW961150.1 | EST_HUMAN | ES137322 MAGE sequences, MAGF Homo sapiens cDNA |
| 4831 | 8815 | | 0.76 | 3.0E-37 | BF035327.1 | EST_HUMAN | 60145853SF1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:35662086_5' |
| 380 | 5455 | 10472 | 1.71 | 2.0E-37 | D89780.1 | NT | Homo sapiens mRNA for AML1, complete cds |
| 380 | 5455 | 10473 | 1.71 | 2.0E-37 | D89780.1 | NT | Homo sapiens mRNA for AML1, complete cds |
| 1064 | 6072 | 11104 | 2.16 | 2.0E-37 | AU131202.1 | EST_HUMAN | AU131202_NTRP3 Homo sapiens cDNA clone NTRP3002166_5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1064 | 6072 | 11105 | 2.16 | 2.0E-37 | AU131202.1 | EST_HUMAN | AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5' |
| 1923 | 6909 | 12004 | 1.45 | 2.0E-37 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 3798 | 8801 | 13806 | 4.94 | 2.0E-37 | 45032210 | NT | Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA |
| 4123 | 9118 | 14104 | 0.78 | 2.0E-37 | 48266685 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA |
| 2034 | 7017 | 12127 | 3.59 | 1.0E-37 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 3124 | 8140 | | 0.98 | 1.0E-37 | AW862052.1 | EST_HUMAN | RC3-CT0347-210400-016-h03 C10347 Homo sapiens cDNA |
| 3855 | 8857 | 13853 | 1.18 | 1.0E-37 | AF189011.1 | NT | Homo sapiens ribonuclease III (RN3) mRNA, complete cds |
| 4783 | 9767 | 14751 | 2.02 | 1.0E-37 | BF371719.1 | EST_HUMAN | QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA |
| 1202 | 6203 | 11240 | 1.69 | 8.0E-38 | 11436955 | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571).mRNA |
| 2425 | 7396 | 12517 | 1.23 | 8.0E-38 | BF346221.1 | EST_HUMAN | 602018401 F1_NCI_CGA_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5' |
| 2119 | 7099 | 12212 | 5.28 | 7.0E-38 | AW972855.1 | EST_HUMAN | EST384920 MAGE sequences, MAGL Homo sapiens cDNA |
| 2969 | 7987 | 13001 | 2.99 | 8.0E-38 | BF030303.1 | EST_HUMAN | 601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5' |
| 717 | 5740 | 10757 | 1.86 | 5.0E-38 | AW971819.1 | EST_HUMAN | EST383908 MAGE sequences, MAGL Homo sapiens cDNA |
| 2385 | 7356 | 12478 | 4.11 | 5.0E-38 | AJ237740.1 | NT | Homo sapiens RIBIR gene (partial), exon 8 |
| 4991 | 7356 | 12478 | 1.09 | 5.0E-38 | AJ237740.1 | NT | Homo sapiens RIBIR gene (partial), exon 8 |
| 119 | 5189 | 10200 | 3.97 | 4.0E-38 | ZZ5466.1 | NT | B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS |
| 119 | 5189 | 10201 | 3.97 | 4.0E-38 | ZZ5466.1 | NT | B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS |
| 2043 | 7025 | | 2.4 | 3.0E-38 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| 3613 | 8620 | | 1.58 | 3.0E-38 | 7549807 | NT | Homo sapiens HIRA interacting protein 4 (dnal-like) [HIRIP4], mRNA |
| 3765 | 8768 | 13772 | 1.58 | 3.0E-38 | P535338 | SWISSPROT | SSU72 PROTEIN |
| 3765 | 8768 | 13773 | 1.58 | 3.0E-38 | P535338 | SWISSPROT | SSU72 PROTEIN |
| 4482 | 9472 | | 1.26 | 3.0E-38 | BE279301.1 | EST_HUMAN | 60145763F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5' |
| 51 | 5132 | 10127 | 1.71 | 2.0E-38 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 1361 | 6358 | 11408 | 8.04 | 2.0E-38 | 5902097 | NT | Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA |
| 1607 | 6603 | 11665 | 1.7 | 2.0E-38 | AA437353.1 | EST_HUMAN | zw30d01,r Seares ovary tumor NbHO-T MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; |
| 1607 | 6603 | 11666 | 1.7 | 2.0E-38 | AA437353.1 | EST_HUMAN | zw30d01,r Seares ovary tumor NbHO-T MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; |
| 3455 | 8463 | | 0.91 | 2.0E-38 | AF070670.1 | NT | Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds |
| 4448 | 9438 | 14421 | 5 | 2.0E-38 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 4953 | 9930 | 14909 | 0.75 | 2.0E-38 | BE2986224.1 | EST_HUMAN | 601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5' |
| 4953 | 9930 | 14910 | 0.75 | 2.0E-38 | BE2986224.1 | EST_HUMAN | 601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--------------------|
| 1076 6083 | | | 1.97 | 1.0E-38 AA401570.1 | EST_HUMAN | ZU62602.r1 Scarsas_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element; | |
| 1953 6939 | 12041 | | 3.28 | 1.0E-38 4885288 | NT | Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA | |
| 1970 6955 | 12059 | | 0.96 | 1.0E-38 7661969 | NT | Homo sapiens KIAA0173 gene product (KIAA0173), mRNA | |
| 2423 7394 | 12515 | | 2.9 | 1.0E-38 AF270831.1 | NT | Homo sapiens cyclin K (CCNK) gene, exon 7 | |
| 4192 9185 | 14166 | | 0.72 | 1.0E-38 4505016 | NT | Homo sapiens lcx density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products | |
| 4197 9190 | 14171 | | 1.27 | 1.0E-38 AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 | |
| 4197 9190 | 14172 | | 1.27 | 1.0E-38 AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 | |
| 4466 9456 | 14436 | | 1.06 | 1.0E-38 8922543 | NT | Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA | |
| 55 5136 | 10133 | | 6.42 | 8.0E-39 4502312 | NT | Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA | |
| 1371 6368 | 11417 | | 1.13 | 8.0E-39 4758229 | NT | Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EEBA99) mRNA | |
| 1793 6784 | | | 1.43 | 8.0E-39 AIB23404.1 | EST_HUMAN | wh55f10_X1 NC_ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 F87890 POL PROTEIN; | |
| 2038 7021 | 12130 | | 4.22 | 7.0E-39 AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 | |
| 992 6005 | 11036 | | 1.95 | 5.0E-39 AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions | |
| 2916 7935 | | 12953 | 6.76 | 5.0E-39 AI750154.1 | EST_HUMAN | er36fb4_x1 Barsteed cdn HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 | |
| 546 5580 | 10584 | | 50.63 | 4.0E-39 AB015610.1 | NT | Q15408 NEUTRAL PROTEASE LARGE SUBUNIT; contains LTR7_M LTR7 repetitive element; | |
| 392 8500 | 13514 | | 0.7 | 4.0E-39 AL163210.2 | NT | Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds | |
| 48 5129 | 10121 | | 18.3 | 3.0E-39 AA631949.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C010 | |
| 48 5129 | 10122 | | 18.3 | 3.0E-39 AA631949.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 | |
| 48 5129 | 10123 | | 18.3 | 3.0E-39 AA631949.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 | |
| 886 5904 | | | 18.94 | 2.0E-39 BE40923.1 | EST_HUMAN | fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 | |
| 901 5919 | | | 8.24 | 2.0E-39 AI525119.1 | EST_HUMAN | 601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5' | |
| 1015 6025 | | | 3.1 | 2.0E-39 AF000573.1 | NT | promma-7_D01,r blymorf Homo sapiens cDNA 5' | |
| 1498 6496 | | | 89.79 | 2.0E-39 AW372318.1 | EST_HUMAN | Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds | |
| 1929 6915 | 12012 | | 2.58 | 2.0E-39 AA720574.1 | EST_HUMAN | PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA | |
| 2556 7521 | | 12638 | 1.41 | 2.0E-39 AL163248.2 | NT | T-HR repetitive element; | |
| 4279 9272 | 14261 | | 1.83 | 2.0E-39 BF370207.1 | EST_HUMAN | Hom sapiens chromosome 21 segment HS21C048 | |
| 1482 6479 | 11535 | | 11.08 | 1.0E-39 AJ006345.1 | NT | RC4-FN037-290700-011-a10 FN0337 Homo sapiens cDNA | |
| | | | | | | Homo sapiens KVLTQ7 gene | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1482 | 6479 | 11536 | 11.08 | 1.0E-39 | AJ006345.1 | NT | Homo sapiens [VLQT1 gene |
| 1499 | 6497 | 11550 | 4.37 | 1.0E-39 | 7657020 | NT | Homo sapiens [KIFZ-p434P211 protein (DKFZP434P211), mRNA |
| 4625 | 9515 | 14500 | 15.01 | 1.0E-39 | AW951995.1 | EST_HUMAN | EST364065 MAGE sequences, MAGB Homo sapiens cDNA |
| 4525 | 9516 | 14501 | 15.01 | 1.0E-39 | AW951995.1 | EST_HUMAN | EST364065 MAGE sequences, MAGB Homo sapiens cDNA |
| 4564 | 9552 | 14538 | 7.93 | 1.0E-39 | 7657020 | NT | Homo sapiens [KIFZ-p434P211 protein (DKFZP434P211), mRNA |
| 5551 | 5585 | 10587 | 1.74 | 9.0E-40 | 5803210 | NT | Homo sapiens [DGP-glucosidase pyrophosphorylase 2 (UGP2), mRNA |
| 1215 | 6214 | 11253 | 11.93 | 9.0E-40 | 4755145 | NT | Homo sapiens AE-binding protein 1 (AEBP1) mRNA |
| 1215 | 6214 | 11254 | 11.93 | 9.0E-40 | 4755145 | NT | Homo sapiens AE-binding protein 1 (AEBP1) mRNA |
| 1423 | 6420 | 11480 | 1.06 | 9.0E-40 | 4507512 | NT | Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) |
| 3697 | 8701 | 13704 | 1.19 | 9.0E-40 | 4503764 | NT | Homo sapiens fragile X mental retardation 1 (FMR1) mRNA |
| 3866 | 10048 | 13870 | 3.4 | 9.0E-40 | AB033070.1 | NT | Homo sapiens mRNA for KIAA1244 protein, partial cds |
| 4370 | 9214 | 14193 | 0.88 | 9.0E-40 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 2968 | 7986 | 13000 | 0.96 | 8.0E-40 | AA078165.1 | EST_HUMAN | TH15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04 |
| 3823 | 8825 | | 4.61 | 8.0E-40 | BE396541.1 | EST_HUMAN | 601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5' |
| 2654 | 7614 | 12724 | 6.7 | 6.0E-40 | AA361275.1 | EST_HUMAN | EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family |
| 2654 | 7614 | 12725 | 6.7 | 6.0E-40 | AA361275.1 | EST_HUMAN | EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family |
| 2529 | 7495 | 12615 | 1.57 | 5.0E-40 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1838 | 6828 | 11917 | 1.77 | 4.0E-40 | AI686005.1 | EST_HUMAN | tg1b01.x1 NC_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873' similar to TR:O73505 O73505 POL PROTEIN . |
| 2050 | 7032 | | 2.06 | 4.0E-40 | AF003528.1 | NT | Homo sapiens X-linked arachnodactyly ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 4264 | 9257 | 14247 | 8.89 | 4.0E-40 | 7662117 | NT | Homo sapiens KIAA0433 protein (KIAA0433), mRNA |
| 4011 | 9007 | 13996 | 0.99 | 3.0E-40 | AI925949.1 | EST_HUMAN | wh1207.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3' |
| 323 | 5377 | | 3.68 | 2.0E-40 | AI223036.1 | EST_HUMAN | gg52h08.x1 NCI CGAP_Uk4 Homo sapiens cDNA clone IMAGE:1838847 3' |
| 786 | 5807 | | 47.86 | 2.0E-40 | AW303868.1 | EST_HUMAN | xr24e10.x1 NCI CGAP_UK4 RIBOSOMAL PROTEIN S5 ; |
| 1790 | 67781 | | 2.37 | 2.0E-40 | AV731601.1 | EST_HUMAN | P97461 40S AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5' |
| 1894 | 6882 | 11973 | 6.41 | 2.0E-40 | 4506188 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products |
| 1894 | 6882 | 11974 | 6.41 | 2.0E-40 | 4506188 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|--|-------------------------|--|
| 2105 | 7085 | 12200 | 1.63 | 2.0E-40 | 5453592 NT | EST_HUMAN | Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA |
| 2618 | 7580 | | 1.3 | 2.0E-40 | BE275932.1 | EST_HUMAN | 601121567F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5' |
| 3053 | 8070 | 13080 | 4.08 | 2.0E-40 | 5453592 NT | EST_HUMAN | Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA |
| 4745 | 9730 | 14717 | 1.8 | 2.0E-40 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4745 | 9730 | 14718 | 1.8 | 2.0E-40 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 5005 | 9976 | 14951 | 1 | 2.0E-40 | 46055880 NT | EST_HUMAN | Homo sapiens plasmoglobin (PLG) mRNA |
| 872 | 5890 | | 1.42 | 1.0E-40 | AA22598.1 | EST_HUMAN | nc09a09_st_NCI CGAP_Pri Homo sapiens cDNA clone IMAGE:1007608 |
| 2548 | 7513 | 12631 | 1.42 | 1.0E-40 | BF036881.1 | EST_HUMAN | 601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5' |
| | | | | | bb79a10.yt NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 | | |
| 2614 | 7576 | | 1.6 | 1.0E-40 | BE016348.1 | EST_HUMAN | SYNTAXIN 17 |
| 2663 | 7622 | 12733 | 0.89 | 1.0E-40 | BF541030.1 | EST_HUMAN | 602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5' |
| 2663 | 7622 | 12734 | 0.99 | 1.0E-40 | BF541030.1 | EST_HUMAN | 602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5' |
| 3224 | 8239 | | 1.22 | 1.0E-40 | 4507142 NT | EST_HUMAN | Homo sapiens sorting nexin 3 (SNX3) mRNA |
| 4478 | 9468 | 14448 | 5.47 | 1.0E-40 | 4508012 NT | EST_HUMAN | Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products |
| 3715 | 8719 | 13720 | 1.02 | 9.0E-41 | W01596.1 | EST_HUMAN | zg56a02.1t Sources fetal liver spleen 1NF-LS Homo sapiens cDNA clone IMAGE:294602 5' |
| 818 | 7732 | 10874 | 1.8 | 7.0E-41 | AI934364.1 | EST_HUMAN | wp04h04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3' |
| 818 | 7732 | 10875 | 1.8 | 7.0E-41 | AI934364.1 | EST_HUMAN | wp04h04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3' |
| 5041 | 10012 | 14981 | 1.23 | 7.0E-41 | 11431114 NT | EST_HUMAN | Homo sapiens hypothetical protein (FLJ10986), mRNA |
| 278 | 5336 | 10350 | 2.15 | 6.0E-41 | AB037163.1 | NT | Homo sapiens DSCR5 mRNA, complete cds |
| 2052 | 7034 | 12146 | 4.09 | 6.0E-41 | 7657042 NT | EST_HUMAN | Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA |
| 1766 | 6758 | 11844 | 1.57 | 5.0E-41 | T62628.1 | EST_HUMAN | yc03e10.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:79526 3' |
| 390 | 5428 | | 1.45 | 4.0E-41 | BE156318.1 | EST_HUMAN | QV6-HT0367-150200-114-809 HT0367 Homo sapiens cDNA |
| 1081 | 6088 | 11117 | 1.03 | 4.0E-41 | AU119344.1 | EST_HUMAN | AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5' |
| | | | | | | | ow45e06.s1 Seares_perathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1849794 3' similar to TR:O000597 C00597 CYTOCHROME C-LIKE POLYPEPTIDE..; contains LTR5.b1 LTR5 repetitive element; |
| 1385 | 6382 | 11432 | 10.1 | 4.0E-41 | A027117.1 | EST_HUMAN | ow45e06.s1 Seares_perathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1849794 3' similar to TR:O000597 C00597 CYTOCHROME C-LIKE POLYPEPTIDE..; contains LTR5.b1 LTR5 repetitive element; |
| 1385 | 6382 | 11433 | 10.1 | 4.0E-41 | A027117.1 | EST_HUMAN | Hom sapiens gene for actin receptor type IIb, complete cds |
| 1398 | 6395 | 11450 | 3.73 | 4.0E-41 | AB008681.1 | NT | tm96c04.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to OFR.b1 OFR repetitive element; |
| 1595 | 6591 | 11652 | 4.42 | 4.0E-41 | A150046.1 | EST_HUMAN | Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 2818 | 7838 | 12854 | 3.89 | 4.0E-41 | AJ228041.1 | NT | Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 2818 | 7838 | 12855 | 3.89 | 4.0E-41 | AJ228041.1 | NT | |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Most Similar BLAST E Value | Expression Signal | (Top) Hit No. | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|----------------------------|-------------------|---------------|-----------------------|---|---|
| 4021 | 9017 | 14004 | 2.21 | 4.0E-41 | X92685.1 | NT | | Homo sapiens DNase I hypersensitive site (HSS-3) enhancer element |
| 933 | 5950 | 10983 | 1.82 | 3.0E-41 | AB030176.1 | NT | | Homo sapiens PAD-H19 mRNA for peptide/Marginine deiminase type II, complete cds |
| 4208 | 9201 | 14183 | 3.05 | 3.0E-41 | AB026898.1 | NT | | [Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)] |
| 1789 | 6527 | 11586 | 49.39 | 2.0E-41 | U43701.1 | NT | | Human ribosomal protein L23a mRNA, complete cds |
| 1918 | 6904 | 11988 | 1.61 | 2.0E-41 | AA331940.1 | EST_HUMAN | EST35818 Embryo, 8 week Homo sapiens cDNA 5' end | |
| 2157 | 7136 | 12255 | 5.84 | 2.0E-41 | D85962.1 | NT | | Human mRNA for KIAA0207 gene, complete cds |
| 2206 | 7183 | 12306 | 15.51 | 2.0E-41 | X89631.1 | NT | | G.gorilla DNA for ZNF80 gene homolog |
| 2755 | 6527 | 11586 | 16.52 | 2.0E-41 | U43701.1 | NT | | Human ribosomal protein L23a mRNA, complete cds |
| 3748 | 8752 | 13751 | 0.8 | 2.0E-41 | 5032106 | NT | | [Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA] |
| 4488 | 9478 | 14458 | 1.15 | 2.0E-41 | AL163267.2 | NT | | Human sapiens chromosome 21 segment HS21C0677 |
| 4488 | 9478 | 14459 | 1.15 | 2.0E-41 | AL163267.2 | NT | | Human sapiens chromosome 21 segment HS21C0677 |
| 3133 | 8149 | 13170 | 1.16 | 1.0E-41 | BE869735.1 | EST_HUMAN | 601445647F1 NIH_MGC | |
| 3133 | 8149 | 13171 | 1.16 | 1.0E-41 | BE869735.1 | EST_HUMAN | 601445647F1 NIH_MGC | |
| 4434 | 9424 | 14409 | 15.19 | 1.0E-41 | 68678468 | NT | | Mus musculus tubulin alpha 6 (Tuba6), mRNA |
| 460 | 5497 | 10508 | 5.2 | 8.0E-42 | AF003530.1 | NT | | [Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions] |
| 4976 | 9952 | 14930 | 0.94 | 8.0E-42 | 6679031 | NT | | |
| 919 | 5935 | | 1.72 | 7.0E-42 | AL163285.2 | NT | | Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Neddt1), mRNA |
| 1819 | 6809 | 11900 | 3.13 | 6.0E-42 | AF012872.1 | NT | | Human sapiens phosphatidylinositol 4-kinase 230 (PLAK230) mRNA, complete cds |
| 1819 | 6809 | 11901 | 3.13 | 6.0E-42 | AF012872.1 | NT | | Human sapiens phosphatidylinositol 4-kinase 230 (PLAK230) mRNA, complete cds |
| | | | | | | | | xp23f05_x1_NCI_CGAP_H-N10 Homo sapiens cDNA clone IMAGE:2741798 3' similar to contains L1 t1 L1 repetitive element; |
| 2227 | 7204 | | 2.79 | 6.0E-42 | AW236865.1 | EST_HUMAN | | |
| 136 | 5202 | | 5.47 | 5.0E-42 | AJ2271735.1 | NT | | Human sapiens Xq pseudautosomal region; segment 1/2 |
| 435 | 5473 | 10489 | 1.36 | 5.0E-42 | BE217913.1 | EST_HUMAN | hV31e11-x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3' | |
| 483 | 5520 | | 8.24 | 5.0E-42 | 5730038 | NT | | Human sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 484 | 5521 | | 3.56 | 5.0E-42 | 5730038 | NT | | Human sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA |
| 744 | 5767 | 10792 | 23.3 | 4.0E-42 | AF055666.1 | NT | | Human sapiens SET domain and MHC class 1 region |
| 744 | 5767 | 10793 | 23.3 | 4.0E-42 | AF055666.1 | NT | | Human sapiens MHC class 1 region |
| 1049 | 6058 | 11087 | 4.34 | 4.0E-42 | AF188011.1 | NT | | Human sapiens ribonuclease III (RN3) mRNA, complete cds |
| 4071 | 9085 | 14055 | 1.98 | 4.0E-42 | X59417.1 | NT | | H.sapiens PROS-27 mRNA |
| 4106 | 9100 | 14087 | 0.92 | 4.0E-42 | AF246219.1 | NT | | Human sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 4127 | 9122 | 14107 | 4.17 | 4.0E-42 | 4506496 | NT | | Human sapiens regulatory factor X4 (Influences HLA class II expression) (RFX4) mRNA |
| 4451 | 9441 | 14422 | 13.19 | 4.0E-42 | 4508008 | NT | | Human sapiens zinc finger protein 177 (ZNF177) mRNA |

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Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| | | | | | | | ab14610_s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:840810_3' similar to contains THR12 THR repetitive element; |
| 104 | 5181 | | 0.9 | 3.0E-42 | AA486105.1 | EST_HUMAN | RC0-TN0079-110900-024-907 TN0079 Homo sapiens cDNA |
| 1452 | 6449 | 11510 | 2.61 | 2.0E-42 | BF376834.1 | EST_HUMAN | RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA |
| 2346 | 7320 | | 2.82 | 2.0E-42 | AW898344.1 | EST_HUMAN | 2819293_3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293_3' |
| 2358 | 7332 | 12448 | 4.89 | 2.0E-42 | AW250059.1 | EST_HUMAN | Human endogenous retrovirus pHE-1 (ERV9) |
| 724 | 5746 | 10767 | 2.19 | 1.0E-42 | X57147.1 | NT | U1-H-B11-afhe-e-04-U1_s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871_3' |
| 1025 | 6035 | 11067 | 1.09 | 1.0E-42 | AW295609.1 | EST_HUMAN | Homo sapiens partial C9 gene for complement component C9, exon 1 |
| 1084 | 6091 | 11120 | 1.08 | 1.0E-42 | AJ251818.1 | NT | Homo sapiens partial C9 gene for complement component C9, exon 1 |
| 1084 | 6091 | 11121 | 1.08 | 1.0E-42 | AJ251818.1 | NT | Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 1223 | 7742 | 11267 | 11.95 | 1.0E-42 | AF057166.1 | NT | Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds |
| 1223 | 7742 | 11268 | 11.95 | 1.0E-42 | AF067166.1 | NT | Homo sapiens partial C9 gene for complement component C9, exon 1 |
| 1661 | 6657 | 11731 | 1.13 | 1.0E-42 | 11423219 | NT | Homo sapiens partial C9 gene for complement component C9, exon 1 |
| 2473 | 7442 | 12557 | 1.26 | 1.0E-42 | 5174458 | NT | Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA, and translated products |
| 2894 | 7913 | 12984 | 5.85 | 1.0E-42 | 4505524 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 3626 | 8633 | 13638 | 2.28 | 1.0E-42 | 7692027 | NT | Homo sapiens vesicular membrane trafficking protein p18 (BET1) mRNA |
| 3705 | 8709 | 13712 | 0.92 | 1.0E-42 | 5031610 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 3825 | 8827 | 13834 | 1.08 | 1.0E-42 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4124 | 9119 | 14105 | 1.89 | 1.0E-42 | AL163280.2 | NT | Homo sapiens protein p35 (yeast homolog)-like (ORC5L) mRNA, and translated products |
| 4462 | 9452 | 14433 | 0.75 | 1.0E-42 | AW813617.1 | EST_HUMAN | RC3-ST0197-161099-012-s03 ST0197 Homo sapiens cDNA |
| 4602 | 9590 | 14577 | 2.94 | 1.0E-42 | 5803122 | NT | Homo sapiens proteasome inhibitor (P31), mRNA |
| 4602 | 9590 | 14578 | 2.94 | 1.0E-42 | 5803122 | NT | Homo sapiens proteasome inhibitor (P31), mRNA |
| 4634 | 9619 | 14611 | 5.64 | 1.0E-42 | 4506758 | NT | Homo sapiens receptor 3 (RYR3) mRNA |
| 644 | 5672 | 10676 | 12.63 | 8.0E-43 | AV736824.1 | EST_HUMAN | AV736824 CB Homo sapiens cDNA clone CBLAK1H08_5' |
| 644 | 5672 | 10677 | 12.63 | 8.0E-43 | AV736824.1 | EST_HUMAN | AV736824 CB Homo sapiens cDNA clone CBLAK1H08_5' |
| 691 | 5715 | 10729 | 5.28 | 8.0E-43 | 8923276 | NT | Homo sapiens hypothetical protein FLJ20297, mRNA |
| 691 | 5715 | 10730 | 5.28 | 8.0E-43 | 8923276 | NT | Homo sapiens hypothetical protein FLJ20297, mRNA |
| 691 | 5715 | 10731 | 5.28 | 8.0E-43 | 8923276 | NT | Homo sapiens hypothetical protein FLJ20297, mRNA |
| 3556 | 8563 | 13569 | 8.21 | 7.0E-43 | AW216442.1 | EST_HUMAN | 2822251_5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251_5' |
| 1324 | 6322 | | 24.66 | 6.0E-43 | AA491890.1 | EST_HUMAN | net2d06_s1 NC1_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:8009803 similar to gb:U05095 60S RIBOSOMAL PROTEIN L30 (HUMAN); |
| 2516 | 7484 | | 2.96 | 6.0E-43 | AV708201.1 | EST_HUMAN | AV708201 ADC Homo sapiens cDNA clone ADCACC10_5' |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 142 | 5208 | | 1.96 | 5.0E-43 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 499 | 5535 | 10541 | 3.04 | 5.0E-43 | AA382780.1 | EST_HUMAN | EST96033 Testis Homo sapiens cDNA clone HS ANIC06 5' |
| 2773 | 7794 | 12814 | 1.62 | 5.0E-43 | AV732578.1 | EST_HUMAN | AV732578 HIT Homo sapiens cDNA clone HIT ANIC06 5' |
| 958 | 7696 | 11007 | 5.71 | 4.0E-43 | AF003528.1 | NT | Homo sapiens X-linked arthrodystrophic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 1194 | 6195 | | 3.19 | 3.0E-43 | AF223391.1 | NT | Homo sapiens calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 1656 | 6652 | 11724 | 4.45 | 3.0E-43 | X97869.1 | NT | H.sapiens gene encoding La autoantigen |
| 3491 | 8499 | 13513 | 1.29 | 3.0E-43 | S69002.1 | NT | AML1-EVI-1=AML1-EVI-1 fusion protein [rearranged translocation] [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt] |
| 4167 | 9162 | 14148 | 0.69 | 3.0E-43 | AA548154.1 | EST_HUMAN | nk55006_s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419 |
| 183 | 5246 | | 21.1 | 2.0E-43 | AI190764.1 | EST_HUMAN | qd61c09_x1 Soares,_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.3 |
| 1610 | 6606 | 11669 | 2.07 | 1.0E-43 | AF154836.1 | NT | PTR7 PTR7 repetitive element; |
| 1610 | 6606 | 11670 | 2.07 | 1.0E-43 | AF154836.1 | NT | Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2 |
| 1666 | 6662 | 11737 | 1.71 | 1.0E-43 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 2652 | 7612 | 127722 | 4.87 | 1.0E-43 | BF348283.1 | EST_HUMAN | 602022313 F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157666 5' |
| 879 | 5897 | 10938 | 4.62 | 8.0E-44 | AI222985.1 | EST_HUMAN | qf23g01_x1 Soeres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3' |
| 879 | 5897 | 10939 | 4.62 | 8.0E-44 | AI222985.1 | EST_HUMAN | qf23g01_x1 Soeres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3' |
| 4721 | 9706 | 14692 | 1.2 | 8.0E-44 | AW373185.1 | EST_HUMAN | RC5-BT0503_031299-011-912 BT0503 Homo sapiens cDNA |
| 4721 | 9706 | 14683 | 1.2 | 8.0E-44 | AW373185.1 | EST_HUMAN | RC5-BT0503_031299-011-912 BT0503 Homo sapiens cDNA |
| 651 | 5679 | | 1.08 | 7.0E-44 | R06035.1 | EST_HUMAN | ye89e01_r1 Soeres fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:124920 5 |
| 2172 | 7151 | 12270 | 1.31 | 7.0E-44 | 5031886 | NT | Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA |
| 2896 | 7915 | 12935 | 2.47 | 7.0E-44 | AF048729.1 | NT | Homo sapiens minisatellite ms32 repeat region |
| 2896 | 7915 | 12936 | 2.47 | 7.0E-44 | AF048729.1 | NT | Homo sapiens minisatellite ms32 repeat region |
| 3772 | 8775 | 13779 | 2.74 | 7.0E-44 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4119 | 9113 | 14098 | 1.21 | 7.0E-44 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 4119 | 9113 | 14099 | 1.21 | 7.0E-44 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 301 | 5358 | | 3.07 | 5.0E-44 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTF1 gene |
| 330 | 5382 | | 1.86 | 5.0E-44 | AJ289880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTF1 gene |
| 3330 | 8340 | 13358 | 3.09 | 4.0E-44 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 4854 | 9835 | | 1.24 | 4.0E-44 | AI435225.1 | EST_HUMAN | fr11d02_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3' |
| 1748 | 8742 | | 1.97 | 3.0E-44 | 6912477 | NT | Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA |
| 2460 | 7429 | 12546 | 1.98 | 3.0E-44 | BE880626.1 | EST_HUMAN | 601491529F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5' |

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Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1521 | 6518 | | 1.01 | 6.0E-45 | AL675425.1 | EST_HUMAN | wb99c06_x1_NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.1 L1 repetitive element; |
| 3871 | 8872 | | 9.19 | 6.0E-45 | AW157570.1 | EST_HUMAN | eu83n07_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ; |
| 881 | 5899 | | 1.17 | 5.0E-45 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C033 |
| 1956 | 6942 | 12044 | 2.41 | 5.0E-45 | BF533627.1 | EST_HUMAN | CMA-CN0044-B02020-515-f01 CN0044 Homo sapiens cDNA |
| 3137 | 8153 | 13176 | 2.09 | 5.0E-45 | AL523766.1 | EST_HUMAN | tg9af07_x1_NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1. ; |
| 1126 | 6131 | 11161 | 13.11 | 4.0E-45 | X95826.1 | NT | H_sapiens ART4 gene |
| 2229 | 7206 | 12321 | 3.69 | 4.0E-45 | BE265622.1 | EST_HUMAN | 6011944401 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5' |
| 3946 | 8944 | 13934 | 1.07 | 4.0E-45 | 4503422 | NT | Homo sapiens dUTP pyrophosphatase (DUT) mRNA |
| 3256 | 8269 | | 1.58 | 3.0E-45 | T71480.1 | EST_HUMAN | yd35f07_r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:110245 5 |
| 3971 | 8269 | | 1.78 | 3.0E-45 | T71480.1 | EST_HUMAN | yd35f07_r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:110245 5 |
| 2429 | 7400 | | 1.54 | 2.0E-45 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 2962 | 7980 | 12994 | 1.28 | 2.0E-45 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 124 | 5443 | | 3.37 | 1.0E-45 | BE389855.1 | EST_HUMAN | 6012843601_F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5' |
| 406 | 5443 | | 3.74 | 1.0E-45 | BE389855.1 | EST_HUMAN | 6012843601_F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5' |
| 469 | 5505 | 10519 | 1.3 | 1.0E-45 | 4506412 | NT | Homo sapiens RAPIA, member of RAS oncogene family (RAPIA), mRNA |
| 1155 | 8159 | 11183 | 1.76 | 1.0E-45 | 7657290 | NT | Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA |
| 3030 | 8047 | 13057 | 7.83 | 1.0E-45 | U32169.1 | NT | Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds |
| 3412 | 8421 | 13450 | 0.79 | 1.0E-45 | 8659858 | NT | Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA |
| 4350 | 9341 | 14322 | 4.49 | 1.0E-45 | BE396633.1 | EST_HUMAN | 601289116_F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5' |
| 2374 | 7346 | 12466 | 26.07 | 8.0E-46 | AI432261.1 | EST_HUMAN | f32f08_x1_NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN); |
| 2374 | 7346 | 12467 | 26.07 | 8.0E-46 | AI432261.1 | EST_HUMAN | f32f08_x1_NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN); |
| 2177 | 7156 | 12276 | 1.08 | 7.0E-46 | U46007.1 | NT | Rattus norvegicus espin mRNA, complete cds |
| 4447 | 9437 | | 9.38 | 7.0E-46 | BE388165.1 | EST_HUMAN | 601277292_F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5' |
| 4662 | 9847 | | 1.73 | 7.0E-46 | BE064386.1 | EST_HUMAN | RC+BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 2681 | 7639 | 12754 | 3.59 | 6.0E-46 | AI884381.1 | EST_HUMAN | wm31f08_x1_NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element; |
| 2681 | 7639 | 12755 | 3.59 | 6.0E-46 | AI884381.1 | EST_HUMAN | wm31f08_x1_NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element; |
| 204 | 5268 | | 4.44 | 5.0E-46 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |

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Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3450 | 8458 | 13484 | 1.07 | 5.0E-46 | BE677194.1 | EST_HUMAN | 7d81901_x1_lipinski_dorsal_root_ganglion_Homo_sapiens_cDNA_clone IMAGE:3279408_3' |
| 3450 | 8458 | 13485 | 1.07 | 5.0E-46 | BE677194.1 | EST_HUMAN | 7d81901_x1_lipinski_dorsal_root_ganglion_Homo_sapiens_cDNA_clone IMAGE:3279408_3' |
| 635 | 5663 | | 2.5 | 4.0E-46 | AA601143.1 | EST_HUMAN | nc84e09_s1_NCL_CGAP_SS1 Homo_sapiens_cDNA_clone IMAGE:1104520_3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); |
| 1665 | 6661 | 11735 | 8.01 | 4.0E-46 | AW770544.1 | EST_HUMAN | h186cd3_x1_NCL_CGAP_Lu24 Homo_sapiens_cDNA_clone IMAGE:3008836_3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ; |
| 1665 | 6661 | 11736 | 8.01 | 4.0E-46 | AW770544.1 | EST_HUMAN | h186cd3_x1_NCL_CGAP_Lu24 Homo_sapiens_cDNA_clone IMAGE:3008836_3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ; |
| 2666 | 7625 | 12737 | 2.58 | 4.0E-46 | M18048.1 | NT | Human endogenous retrovirus RTVL-H2 |
| 4293 | 9285 | 14272 | 0.97 | 4.0E-46 | AB014522.1 | NT | Homo sapiens mRNA for KIAA0622 protein, partial cds |
| 4293 | 9285 | 14273 | 0.97 | 4.0E-46 | AB014522.1 | NT | Homo sapiens mRNA for KIAA0622 protein, partial cds |
| 2222 | 7199 | 12319 | 1.23 | 3.0E-46 | 7657203 | NT | Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA |
| 2361 | 7335 | 12452 | 2.18 | 3.0E-46 | AF160212.1 | NT | Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds |
| 4269 | 9262 | 14252 | 0.72 | 3.0E-46 | 4506376 | NT | Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA |
| 4630 | 9615 | 14605 | 1.22 | 3.0E-46 | Z73660.1 | NT | H.sapiens Ig_lambda light chain variable region gene (7c.11.2) germline; Ig_Light-Lambda; VLambda |
| 4630 | 9615 | 14606 | 1.22 | 3.0E-46 | Z73660.1 | NT | H.sapiens Ig_lambda light chain variable region gene (7c.11.2) germline; Ig_Light-Lambda; VLambda |
| 827 | 5847 | 10884 | 8.39 | 2.0E-46 | AA468646.1 | EST_HUMAN | ne06a09_s1_NCL_CGAP_Co3 Homo_sapiens cDNA_clone IMAGE:880408_3' similar to contains THR.B2 THR repetitive element; |
| 1601 | 6597 | 11658 | 2.53 | 2.0E-46 | U78027.1 | NT | 2t58e02_r1_Scares_testis_NHT Homo_sapiens cDNA_clone IMAGE:726650_5' similar to SW.RSP1_MOUSE Q01730 RSP-1 PROTEIN ; |
| 4815 | 9799 | 14780 | 1.31 | 2.0E-46 | AA399286.1 | EST_HUMAN | Homo sapiens cell division cycle 10 (homologous to CDC10 of <i>S. cerevisiae</i>) (CDC10) mRNA |
| 1213 | 6212 | 11252 | 5.7 | 1.0E-46 | 4502694 | NT | Homo sapiens, KIAA0555 gene product (KIAA0555), mRNA |
| 1538 | 6536 | 11594 | 1.27 | 1.0E-46 | 7662177 | NT | Homo sapiens, KIAA0555 gene product (KIAA0555), mRNA |
| 1538 | 6536 | 11895 | 1.27 | 1.0E-46 | 7662177 | NT | Homo sapiens, KIAA0555 gene product (KIAA0555), mRNA |
| 2218 | 7195 | 12317 | 3.91 | 1.0E-46 | AW978516.1 | EST_HUMAN | EST390625 MAGE resequences, MAGP Homo_sapiens cDNA EST48b095 WATM1 Homo_sapiens cDNA clone 48b095 |
| 2336 | 7310 | 12431 | 2.62 | 1.0E-46 | H97330.1 | EST_HUMAN | EST78b02_s1_NCL_CGAP_Pt2 Homo_sapiens cDNA_clone IMAGE:1132395 similar to gb:X76717 H.sapiens |
| 3176 | 8192 | 13213 | 8.47 | 1.0E-46 | AA631912.1 | EST_HUMAN | MT-11 mRNA (HUMAN); |
| 4723 | 9708 | | 3 | 1.0E-46 | AB023197.1 | NT | Homo sapiens mRNA for KIAA0980 protein, partial cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 757 | 5778 | | 3.81 | 9.0E-47 | AJ271735.1 | NT | Homo sapiens Xq pseudoautosomal region; segment 1/2 |
| 4776 | 9760 | 14747 | 2.41 | 9.0E-47 | AW770928.1 | EST_HUMAN | h193e04_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703 |
| 1772 | 6764 | 11852 | 90.6 | 8.0E-47 | Y18536.1 | NT | Homo sapiens HLA-C gene, exon 5, individual 19323 |
| 1772 | 6764 | 11853 | 90.6 | 8.0E-47 | Y18536.1 | NT | Homo sapiens HLA-C gene, exon 5, individual 19323 |
| 2644 | 7604 | 12717 | 1.38 | 8.0E-47 | 5453955 | NT | Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA |
| 2957 | 7976 | 12991 | 1.73 | 8.0E-47 | AJ228043.1 | NT | Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 2477 | 7446 | 12559 | 1.23 | 6.0E-47 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1376 | 6373 | 11423 | 5.93 | 4.0E-47 | 4557556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 5440 | 5575 | 10580 | 3.84 | 3.0E-47 | BE907634.1 | EST_HUMAN | 601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5' |
| 5440 | 5575 | 10581 | 3.84 | 3.0E-47 | BE907634.1 | EST_HUMAN | 601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5' |
| 8018 | 58239 | 10860 | 4.98 | 3.0E-47 | N57483.1 | EST_HUMAN | YY4604_s1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:3899721 5' |
| 931 | 5948 | 10982 | 7.81 | 3.0E-47 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3230 | 8245 | 13267 | 0.94 | 3.0E-47 | 4504416 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 3859 | 8861 | | 6.7 | 3.0E-47 | U93181.1 | NT | Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds |
| 4237 | 9231 | 14214 | 1.25 | 3.0E-47 | M12959.1 | NT | Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds |
| 147 | 5213 | 10227 | 1.29 | 2.0E-47 | 4505318 | NT | Homo sapiens myosin phosphatase, target subunit 2 (MYPT2) mRNA |
| 9553 | 5969 | 11001 | 2.67 | 2.0E-47 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 9553 | 5969 | 11002 | 2.67 | 2.0E-47 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1558 | 6555 | 11616 | 2 | 2.0E-47 | 7662109 | NT | Homo sapiens KIAA0426 gene product (KIAA0426) mRNA |
| 1638 | 6635 | 11705 | 3.76 | 2.0E-47 | AA524514.1 | EST_HUMAN | ng49h12_s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3' |
| 4221 | 9215 | 14194 | 1.6 | 2.0E-47 | 4504866 | NT | Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8) mRNA |
| 4259 | 9253 | 14240 | 1.82 | 2.0E-47 | AA568592.1 | EST_HUMAN | nt23907_s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:914652 |
| 4259 | 9253 | 14241 | 1.82 | 2.0E-47 | AA568592.1 | EST_HUMAN | nt23907_s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:914652 |
| 4376 | 9367 | 14347 | 2.23 | 2.0E-47 | 574648 | NT | Homo sapiens Fev/Rex activation domain binding protein-related (RAB-R) mRNA |
| 4667 | 9852 | 14640 | 1.32 | 2.0E-47 | AW965166.1 | EST_HUMAN | EST377239 IMAGE resequences, MAGI Homo sapiens cDNA clone IMAGE:1821189 3 |
| 1381 | 6378 | 11426 | 4.13 | 1.0E-47 | AI333429.1 | EST_HUMAN | sp89h03_x1 Soares fetal lung Nb-H19W Homo sapiens cDNA clone IMAGE:3138893 5' |
| 3731 | 8735 | 13732 | 2.17 | 1.0E-47 | BE280477.1 | EST_HUMAN | 601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5' |
| 3731 | 8735 | 13733 | 2.17 | 1.0E-47 | BE280477.1 | EST_HUMAN | RC3-ST0197-13040-017-h02 ST0197 Homo sapiens cDNA clone IMAGE:3138893 5' |
| 4904 | 9883 | 14854 | 3.23 | 1.0E-47 | AW813906.1 | EST_HUMAN | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 1575 | 6572 | 11633 | 3.85 | 9.0E-48 | AF223391.1 | NT | Homo sapiens amine oxidase 1 (ACY1), mRNA |
| 1231 | 6230 | | 1.49 | 8.0E-48 | 4501900 | NT | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|---------------------|-------------------|--------------------------------------|-----------------------|--|--|
| 1232 6230 | | 1.54 | 8.0E-48 | 4501900 NT | | Homo sapiens an inoecyclase 1 (ACY1), mRNA |
| 3062 8079 | 13092 | 3.91 | 8.0E-48 AW768477.1 | EST_HUMAN | hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:30011133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); | |
| 3062 8079 | 13093 | 3.91 | 8.0E-48 AW768477.1 | EST_HUMAN | hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:30011133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN); | |
| 487 5524 | | 1.31 | 7.0E-48 AB033035.1 | NT | Homo sapiens mRNA for KIAA1209 protein, partial cds | |
| 488 5524 | | 19.03 | 7.0E-48 AB033035.1 | NT | Homo sapiens mRNA for KIAA1209 protein, partial cds | |
| 1467 8464 | 11523 | 1.05 | 7.0E-48 | 6912719 NT | Homo sapiens tousled-like kinase 1 (TLK1) mRNA | |
| 1597 6593 | 11654 | 5.73 | 7.0E-48 | 5730038 NT | Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA | |
| 3518 8526 | 13537 | 7.99 | 6.0E-48 A1761111.1 | EST_HUMAN | wf68103.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3' | |
| 3237 10046 | 13272 | 1.51 | 5.0E-48 | 4826891 NT | Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA | |
| 1931 69117 | 12015 | 28.02 | 3.0E-48 | 4885170 NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA | |
| 1931 69117 | 12016 | 28.02 | 3.0E-48 | 4885170 NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA | |
| 4125 9120 | | 0.99 | 3.0E-48 AA009541.1 | EST_HUMAN | z104g3.11 Saccharomyces cerevisiae fetal liver, spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:810052 5' | |
| 5 5086 | 10071 | 1.14 | 2.0E-48 AA465007.1 | EST_HUMAN | z280c03.11 Saccharomyces cerevisiae ovary_tumor NbHOT Homo sapiens cDNA clone CR17-26 | |
| 46 5127 | 10118 | 2.18 | 2.0E-48 AA631940.1 | EST_HUMAN | fmc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone TCBAP1D3842: Pediatric pre-B cell acute lymphocytic leukemia Baylor-HGSC project=TCBA_Homo | |
| 4401 9592 | 14376 | 0.95 | 2.0E-48 BE246065.1 | EST_HUMAN | TCBAP1D3842: Pediatric pre-B cell acute lymphocytic leukemia Baylor-HGSC project=TCBA_Homo | |
| 4803 9787 | 14769 | 1.1 | 2.0E-48 T03176.1 | EST_HUMAN | seipins cDNA clone TCBAp3842 | |
| 4803 9787 | 14770 | 1.1 | 2.0E-48 T03176.1 | EST_HUMAN | FB2E2 Fetel brain, Strategene Homo sapiens cDNA clone FB2E2 3' end | |
| 5064 10033 | 15000 | 1.11 | 2.0E-48 AW470877.1 | EST_HUMAN | FB2E2 Fetel brain, Strategene Homo sapiens cDNA clone FB2E2 3' end | |
| 57 5137 | 10135 | 8.01 | 1.0E-48 | 7706534 NT | Human endogenous retroviral DNA (4-1), complete retroviral segment | |
| 862 5881 | 10922 | 4.37 | 1.0E-48 | 4502166 NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA | |
| 1059 6068 | 11098 | 3.12 | 1.0E-48 | 7657430 NT | Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA | |
| 1059 6068 | 11099 | 3.2 | 1.0E-48 | 7657430 NT | Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA | |
| 1277 6276 | 11317 | 4.07 | 1.0E-48 | 5032032 NT | Homo sapiens RNA binding motif protein 6 (RBM6) mRNA | |
| 1874 6863 | 11952 | 15.16 | 1.0E-48 AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 | |
| 3408 8417 | 13445 | 1.25 | 1.0E-48 AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 | |
| 4959 9936 | 14914 | 0.91 | 1.0E-48 M10976.1 | NT | Mus musculus MyoSPDZ mRNA for myosin containing PDZ domain, complete cds | |
| 1959 6945 | 12047 | 0.92 | 8.0E-49 AB026497.1 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit ATPase, 4 (PSMC4) mRNA | |
| 139 5430 | 10445 | 4.24 | 7.0E-49 | 5729990 NT | Homo sapiens proteasome (prosome, macropain) 26S subunit ATPase, 4 (PSMC4) mRNA | |
| 139 5430 | 10445 | 4.24 | 7.0E-49 | 5729990 NT | Homo sapiens proteasome (prosome, macropain) 26S subunit ATPase, 4 (PSMC4) mRNA | |
| 392 5430 | 10445 | 3.24 | 7.0E-49 | 5729990 NT | Homo sapiens proteasome (prosome, macropain) 26S subunit ATPase, 4 (PSMC4) mRNA | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 392 | 5430 | 10446 | 3.24 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 393 | 5430 | 10445 | 2.99 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 393 | 5430 | 10446 | 2.99 | 7.0E-49 | 5729990 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA |
| 1201 | 6202 | 11239 | 3.59 | 7.0E-49 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| | | | | | | | ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb: X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); ob: M20632 Mouse L1Rcp3 protein mRNA from a repetitive element, |
| 197 | 5261 | 10274 | 180.31 | 6.0E-49 | AW751740.1 | EST_HUMAN | complete (MOUSE); |
| 1340 | 6338 | 11387 | 0.99 | 6.0E-49 | BF038269.1 | EST_HUMAN | 601457738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3861272 5' |
| 1340 | 6338 | 11388 | 0.99 | 6.0E-49 | BF038269.1 | EST_HUMAN | 601457738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3861272 5' |
| 3999 | 8995 | 13983 | 0.98 | 6.0E-49 | AL162091.1 | EST_HUMAN | DKFZp761A136_s1_76 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A136 3' |
| 702 | 5726 | 10741 | 7.25 | 5.0E-49 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 702 | 5726 | 10742 | 7.25 | 5.0E-49 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| | | | | | | | zp28c07.11 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to complete (MOUSE); |
| 1758 | 6751 | 11835 | 3.85 | 5.0E-49 | AA172121.1 | EST_HUMAN | TR:G233226 G233228 RTVL-H PROTEIN; contains LTR7.13 LTR7 LTR7 repetitive element; |
| 2677 | 7635 | 12750 | 7.57 | 5.0E-49 | U17714.1 | NT | Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds |
| 3199 | 8215 | 13236 | 9.74 | 5.0E-49 | 11436355 | NT | Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC33362), mRNA |
| 521 | 5556 | 10558 | 22.86 | 4.0E-49 | AW189533.1 | EST_HUMAN | x08801.x1 NC1_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP: B0350.2B CE08703 ; |
| 556 | 5590 | 10591 | 0.9 | 3.0E-49 | X68968.1 | NT | H.sapiens mRNA for acetyl-CoA carboxylase |
| | | | | | | | z231c05.11 Scores retina N2b4H1R Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.B3.L1 repetitive element; |
| 2575 | 7538 | | 1.21 | 3.0E-49 | AA016131.1 | EST_HUMAN | Human type IV collagen (COL4A6) gene, exon 40 |
| 4824 | 9808 | 14790 | 2.5 | 3.0E-49 | U46999.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 4999 | 8970 | | 0.94 | 3.0E-49 | L78810.1 | NT | MR3-HT0487:150200-113_g01 HT0487 Homo sapiens cDNA |
| 653 | 5681 | | 3.06 | 2.0E-49 | BE165980.1 | EST_HUMAN | y23d06.r1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2622571 5' |
| 3151 | 8167 | 13187 | 1.44 | 2.0E-49 | N26446.1 | EST_HUMAN | 601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 888 | 5906 | | 5.66 | 1.0E-49 | BF035327.1 | EST_HUMAN | Homo sapiens keratin 18 (KRT18) mRNA |
| 1522 | 6519 | 11575 | 27.09 | 1.0E-49 | 4557887 | NT | 601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5' |
| 1765 | 6757 | 11843 | 5.52 | 1.0E-49 | BE255216.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C002 |
| 169 | 5234 | 10244 | 2.76 | 8.0E-50 | AL163202.2 | NT | Homo sapiens mRNA for VIP receptor 2 |
| 709 | 5733 | 10749 | 1.82 | 8.0E-50 | X95097.2 | NT | Homo sapiens mRNA for VIP receptor 2 |
| 709 | 5733 | 10750 | 1.82 | 8.0E-50 | X95097.2 | NT | Homo sapiens actinin, alpha 1 (ACTN1) mRNA |
| 1726 | 6721 | 11789 | 13.5 | 8.0E-50 | 4501890 | NT | Homo sapiens actinin, alpha 1 (ACTN1) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2411 | 7382 | 12500 | 1.29 | 8.0E-50 | 7706394 | NT | Homo sapiens p47 (LOC51674), mRNA |
| 2411 | 7382 | 12501 | 1.29 | 8.0E-50 | 7706394 | NT | Homo sapiens p47 (LOC51674), mRNA |
| 2827 | 7587 | 12699 | 3.51 | 8.0E-50 | 4826658 | NT | Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA |
| 4217 | 9210 | | 0.88 | 6.0E-50 | BE794381.1 | EST_HUMAN | 601589565F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5' |
| 1757 | 6750 | 118933 | 1.19 | 5.0E-50 | BF532938.1 | EST_HUMAN | CMD-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA |
| 1757 | 6750 | 11894 | 1.19 | 5.0E-50 | BF532938.1 | EST_HUMAN | CMD-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA |
| 906 | 5923 | | 1.83 | 4.0E-50 | AA601143.1 | EST_HUMAN | no54e09_s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_m1 |
| 3365 | 8373 | 13393 | 0.98 | 4.0E-50 | AL163248.2 | NT | FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS2TC048 |
| 1898 | 6886 | | 2.31 | 3.0E-50 | M18048.1 | NT | Human endogenous retrovirus RTVL-H2 |
| 2447 | 7417 | 12532 | 1.05 | 3.0E-50 | BE259196.1 | EST_HUMAN | 601109717F1 NIH MGC_16 Homo sapiens cDNA clone IMAGE:33650309 5' |
| 3225 | 8240 | 13262 | 0.89 | 3.0E-50 | AA746142.1 | EST_HUMAN | ob03f06_s1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3' |
| 5032 | 10003 | 14974 | 1.04 | 3.0E-50 | AW593866.1 | EST_HUMAN | hg26e01_x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948744 3' similar to SW:C1TC_HUMAN |
| 769 | 5790 | | 14.02 | 2.0E-50 | AF055066.1 | NT | P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;contains Alu repetitive element; |
| 1063 | 6071 | 11103 | 5.6 | 2.0E-50 | 4557752 | NT | Homo sapiens MHC class 1 region |
| 1417 | 6414 | 11475 | 1.29 | 2.0E-50 | AF138303.1 | NT | Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA |
| 3214 | 8229 | 13250 | 0.78 | 2.0E-50 | AF411168.2 | NT | Homo sapiens complete cds, alternatively spliced |
| 4138 | 9133 | 14116 | 1.11 | 2.0E-50 | D86424.1 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 459 | 5496 | 10507 | 1.74 | 1.0E-50 | AL163209.2 | NT | Mus musculus mRNA for high-sulfur keratin protein, partial cds |
| 2304 | 7278 | | 7.62 | 1.0E-50 | AJ271735.1 | NT | Homo sapiens chromosome 21 segment HS2TC009 |
| 4435 | 9425 | 14410 | 12.15 | 8.0E-51 | AA610842.1 | EST_HUMAN | Heterogeneous NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); |
| 2950 | 7989 | 12986 | 1.33 | 7.0E-51 | AW274720.1 | EST_HUMAN | xn34e03_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 |
| 3209 | 8224 | 13246 | 1.83 | 7.0E-51 | AW889219.1 | EST_HUMAN | Q9Z340_A_TYPICAL_PKC_SPECIFIC BINDING PROTEIN ; |
| 3282 | 8294 | 13319 | 0.82 | 7.0E-51 | AW274720.1 | EST_HUMAN | QV4-N70028-200400-180-d05 NT0028 Homo sapiens cDNA |
| 4043 | 9039 | 14029 | 1.25 | 7.0E-51 | AL079628.1 | EST_HUMAN | xn34e03_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 |
| 4043 | 9039 | 14030 | 1.25 | 7.0E-51 | AL079628.1 | EST_HUMAN | Q9Z340_A_TYPICAL_PKC_SPECIFIC BINDING PROTEIN ; |
| 4225 | 9219 | 14198 | 2.54 | 7.0E-51 | AW295603.1 | EST_HUMAN | DKFZp43B229_r1434 (synonym: hies3) Homo sapiens cDNA clone IMAGE:2695564 3' |
| 1496 | 6494 | 11549 | 1.16 | 6.0E-51 | 6678763 | NT | UI-H-BW0-air_b-05-o-U1 s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728817 3' |
| | | | | | | | Homo sapiens putative DNA binding protein (M96), mRNA |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|--------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--------------------|
| 1934 | 6920 | 12019 | 3.34 | 6.0E-51 | 7657266 NT | Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA | |
| 3393 | 8401 | 13427 | 15.79 | 6.0E-51 | 7657266 NT | Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA | |
| 783 | 5804 | 10834 | 5.86 | 5.0E-51 | AL163203.2 NT | Homo sapiens chromosome 21 segment HS21C003 | |
| 794 | 5815 | 10846 | 1.74 | 5.0E-51 | 4507500 NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA | |
| 976 | 7736 | 11024 | 1.07 | 5.0E-51 | AL133204.1 NT | Novel human gene mapping to chromosome X | |
| 1571 | 6568 | 11630 | 1.42 | 5.0E-51 | 5031980 NT | Homo sapiens proteasome-associated pd1 homolog (POH1) mRNA | |
| 2517 | 7485 | 12601 | 8.01 | 5.0E-51 | AJ007558.1 NT | Homo sapiens mRNA for nucleoporin 155 | |
| 3841 | 8843 | 13850 | 3.67 | 5.0E-51 | M30938.1 NT | Human Ku (p70/p80) subunit mRNA, complete cds | |
| 3841 | 8843 | 13851 | 3.67 | 5.0E-51 | M30938.1 NT | Human Ku (p70/p80) subunit mRNA, complete cds | |
| 4900 | 9879 | 14848 | 1.54 | 5.0E-51 | AB037832.1 NT | Homo sapiens mRNA for KIAA1411 protein, partial cds | |
| 135 | 5201 | 10217 | 20.61 | 3.0E-51 | AL587348.1 EST_HUMAN | tr81c09_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); tr81c09_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); | |
| 1157 | 6161 | 11195 | 35.84 | 3.0E-51 | AL587348.1 EST_HUMAN | zq87901_s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:6490083' | |
| 1882 | 6871 | 11980 | 1.08 | 3.0E-51 | AA211296.1 EST_HUMAN | Novel human gene mapping to chromosome 22 | |
| 4200 | 9193 | 14175 | 2.01 | 3.0E-51 | AL159142.1 NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA | |
| 365 | 5414 | 10427 | 2.45 | 2.0E-51 | 4507798 NT | 601285694_F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5' | |
| 679 | 5704 | 10712 | 1.65 | 2.0E-51 | BE391063.1 EST_HUMAN | 601285694_F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5' | |
| 679 | 5704 | 10713 | 1.65 | 2.0E-51 | BE391063.1 EST_HUMAN | z30a05_r1 Stratagene NT2 neuronal precursor g37230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:c233226 G233226 RTVL-H PROTEIN ;contains LTR7 13 LTR7 repetitive element ; | |
| 1649 | 8645 | 11718 | 6.36 | 2.0E-51 | AA233352.1 EST_HUMAN | t27g03_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3' | |
| 3648 | 8654 | 13860 | 2.94 | 2.0E-51 | AI492415.1 EST_HUMAN | Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA | |
| 114 | 5186 | 10195 | 45.03 | 1.0E-51 | 4503328 NT | AV742248 CB Homo sapiens cDNA clone CBFBCC12 5' | |
| 1462 | 6459 | 5124 | 1.24 | 1.0E-51 | AV742248.1 EST_HUMAN | nw21g02_s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element; | |
| 1466 | 6463 | 11522 | 1.35 | 8.0E-52 | X84900.1 NT | H.sapiens mRNA for laminin-5, alpha3b chain | |
| 1614 | 6610 | 11674 | 2.31 | 8.0E-52 | 11968028 NT | Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA | |
| 1614 | 6610 | 11675 | 2.31 | 8.0E-52 | 11968028 NT | Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3888 | 6610 | 11674 | 6.2 | 8.0E-52 | 11968028 | NT | Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA |
| 3888 | 6610 | 11675 | 6.2 | 8.0E-52 | 11968028 | NT | Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA |
| 1655 | 6651 | 11723 | 3.39 | 6.0E-52 | AF109807.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 4318 | 9310 | 14296 | 2.8 | 5.0E-52 | Z78898.1 | NT | H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18h17 |
| 1622 | 6619 | 11685 | 1.32 | 4.0E-52 | AF257318.1 | NT | Homo sapiens Sh3-containing protein SH3GLB1 mRNA, complete cds |
| 1750 | 6744 | 11823 | 2.08 | 4.0E-52 | 4758843 | NT | Homo sapiens nucleophorin 155KD (NUP155) mRNA |
| 3826 | 8328 | 13835 | 0.81 | 4.0E-52 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 4514 | 9504 | 14484 | 1.28 | 4.0E-52 | 5174590 | NT | Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA |
| 3975 | 8973 | | 10.25 | 3.0E-52 | 11437042 | NT | Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA |
| 558 | 5592 | 10592 | 1.85 | 2.0E-52 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 558 | 5592 | 10593 | 1.85 | 2.0E-52 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 1718 | 6713 | 11790 | 1.15 | 2.0E-52 | AB007899.1 | NT | Homo sapiens mRNA for KIAA1249 protein, partial cds |
| 1964 | 6949 | 12052 | 1 | 2.0E-52 | AB033075.1 | NT | Homo sapiens mRNA for KIAA1249 protein, partial cds |
| 2426 | 7397 | 12518 | 3.12 | 2.0E-52 | BE207515.1 | EST HUMAN | bb68b07.y 1_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X76483 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE); |
| 2662 | 7621 | | 19.48 | 2.0E-52 | BF677892.1 | EST HUMAN | 602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5' |
| 4818 | 9802 | 14782 | 3.17 | 2.0E-52 | AL131788.3 | NT | Novel human gene mapping to chromosome 20, similar to membrane transporters |
| 4853 | 9834 | 14808 | 1.1 | 2.0E-52 | AI41802.1 | EST HUMAN | qas56e05.s1 1 Scares_NhMPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3' |
| 4853 | 9834 | 14809 | 1.1 | 2.0E-52 | AI41802.1 | EST HUMAN | qas56e05.s1 1 Scares_NhMPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3' |
| 529 | 5564 | 10568 | 1.37 | 1.0E-52 | AA634445.1 | EST HUMAN | zU75h12.s1 1 Scares_NH testis cDNA clone IMAGE:743878 3' |
| 1354 | 6351 | 11401 | 9.59 | 1.0E-52 | 4504026 | NT | Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA |
| 2465 | 7434 | | 1.67 | 1.0E-52 | 4502238 | NT | Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA |
| 2985 | 8003 | 13015 | 1.99 | 1.0E-52 | S61070.1 | NT | pol=reverse transcriptase homolog [retroviral element] [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt] |
| 3702 | 8706 | 13708 | 1.3 | 9.0E-53 | 4505064 | NT | Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA |
| 4267 | 9260 | 14250 | 1.22 | 9.0E-53 | AF001446.1 | NT | Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3 |
| 5033 | 10004 | 14975 | 1.19 | 9.0E-53 | AB040937.1 | NT | Homo sapiens mRNA for KIAA1504 protein, partial cds |
| 3982 | 8980 | 13965 | 15.99 | 5.0E-53 | 47559543 | NT | Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA |
| 50 | 5131 | 10125 | 1.53 | 4.0E-53 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 50 | 5131 | 10126 | 1.53 | 4.0E-53 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--------------------|
| 4675 | 9860 | 14643 | 0.96 | 4.0E-53 | 7705414 NT | Homo sapiens hook1 protein (HOOK1), mRNA | |
| 2589 | 7552 | 12667 | 1.47 | 3.0E-53 | AB026898.1 NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) | |
| 3647 | 8653 | 13659 | 1.94 | 3.0E-53 | AW050836.1 EST_HUMAN | w22cg7_x1_Scares_Dieckgraefe_colon_NHCD_Homo sapiens cDNA clone IMAGE:2558798 3' | |
| 4457 | 9447 | 14427 | 0.73 | 3.0E-53 | AW803563.1 EST_HUMAN | IL2-UM0081-2-0300-055-D03 UM0081_Homo sapiens cDNA EST/T7525 Pancreas tumor III_Homo sapiens cDNA 5' end | |
| 455 | 5492 | | 3.58 | 2.0E-53 | AA366556.1 EST_HUMAN | | |
| 2266 | 7243 | 12360 | 20.13 | 2.0E-53 | U78027.1 NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTF3 (FTP3) genes, complete cds | |
| 2466 | 7435 | | 7.48 | 2.0E-53 | 4502316 NT | Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA | |
| 3147 | 8163 | 13183 | 0.92 | 2.0E-53 | 7705687 NT | Homo sapiens eudine aminopeptidase (LOC51056), mRNA | |
| 3172 | 8188 | 13210 | 2.53 | 2.0E-53 | AF083822.1 NT | Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6 | |
| 3947 | 8945 | 13935 | 2.5 | 2.0E-53 | M61873.1 NT | Human Krueppel-related DNA-binding protein (TF34) gene, partial cds | |
| 4365 | 9356 | 14336 | 0.92 | 2.0E-53 | 4506962 NT | Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA | |
| 1420 | 6417 | 11477 | 1.56 | 1.0E-53 | AJ271736.1 NT | Homo sapiens Xg pseudautosomal region; segment 2/2 | |
| 3325 | 8335 | 13355 | 1.23 | 1.0E-53 | AB026898.1 NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) | |
| 4807 | 9791 | 14773 | 1.54 | 1.0E-53 | BE296386.1 EST_HUMAN | 601176725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5' | |
| 5039 | 1010 | 14979 | 0.97 | 1.0E-53 | AW957429.1 EST_HUMAN | EST369619 MAGE resequences, MAGE Homo sapiens cDNA | |
| 207 | 5271 | 10283 | 4.09 | 8.0E-54 | BE386785.1 EST_HUMAN | 601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5' | |
| 1799 | 6790 | 11880 | 2.71 | 8.0E-54 | 4504610 NT | Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA | |
| 4596 | 9584 | 14573 | 0.71 | 8.0E-54 | 4507848 NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA | |
| 4596 | 9584 | 14574 | 0.71 | 8.0E-54 | 4507848 NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA | |
| 383 | 5458 | 10475 | 1.58 | 7.0E-54 | AA812537.1 EST_HUMAN | ai79c12_s1_Scares_NHT_Homo sapiens cDNA clone 1377046 3' similar to contains MER30_k3 MER30 repetitive element; | |
| 1794 | 6785 | 11875 | 1.37 | 7.0E-54 | Y16845.1 NT | Homo sapiens mRNA for monocyte chemoattractant protein-2 | |
| 2142 | 7121 | 12237 | 4.24 | 7.0E-54 | N27177.1 EST_HUMAN | yw68d12_s1_Scares_placenta_8to9weeks_2NbHP8t9W_Homo sapiens cDNA clone IMAGE:257399 3' | |
| 5043 | 10014 | 14983 | 1.08 | 7.0E-54 | A1276750.1 EST_HUMAN | similar to contains LTR7_b3 LTR7 repetitive element; | |
| 23 | 5103 | 10088 | 5.96 | 6.0E-54 | AB003618.1 NT | qf64e10_x1_Scares_NhHMpu_S1_Homo sapiens cDNA clone IMAGE:1877130 3' | |
| 384 | 5459 | 10476 | 1.73 | 6.0E-54 | 8922148 NT | Homo sapiens DNA for M1CB, exon 4, 5 and partial cds | |
| 384 | 5459 | 10477 | 1.73 | 6.0E-54 | 8922148 NT | Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA | |
| 3210 | 8225 | 13247 | 2.1 | 6.0E-54 | 8922148 NT | Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA | |
| 3898 | 8898 | 13896 | 1.11 | 6.0E-54 | 4502872 NT | Homo sapiens chloride channel 6 (CLCN6) mRNA | |

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4656 | 9681 | 14664 | 1.19 | 6.0E-54 | 4505806 | NT | Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PI4KA) mRNA |
| 4724 | 9709 | | 2.36 | 6.0E-54 | Y09846.1 | NT | H sapiens shc pseudogene, p66 isoform |
| 4841 | 9709 | | 2.18 | 6.0E-54 | Y09846.1 | NT | H sapiens shc pseudogene, p66 isoform |
| 2090 | 7071 | 12185 | 3.25 | 5.0E-54 | P51523 | SWISSPROT | ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) |
| 1812 | 5245 | | 263.62 | 4.0E-54 | AF110103.1 | NT | Tupala belangeri beta-actin mRNA, partial cds |
| 941 | 5958 | 10991 | 140.55 | 4.0E-54 | AA306764.1 | EST_HUMAN | EST177698_Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase |
| 1769 | 6761 | 11848 | 2.55 | 4.0E-54 | D38521.1 | NT | Human mRNA for KIAA0077 gene, partial cds |
| 1769 | 6761 | 11849 | 2.55 | 4.0E-54 | D38521.1 | NT | Human mRNA for KIAA0077 gene, partial cds |
| 3131 | 8147 | | 1.39 | 4.0E-54 | AI835086.1 | EST_HUMAN | wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711 |
| 92 | 5169 | 10179 | 30.76 | 3.0E-54 | AA313487.1 | EST_HUMAN | O02711 PRO-POL-DUTTASE POLYPROTEIN : |
| 2551 | 7516 | | 1.04 | 3.0E-54 | AI908757.1 | EST_HUMAN | EST185371_Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 636 | 5664 | 10668 | 6.13 | 2.0E-54 | 5031900 | NT | IL-BT189-180389-007 BT189 Homo sapiens cDNA |
| 1347 | 6344 | 11395 | 2.11 | 2.0E-54 | 4507164 | NT | Homo sapiens killer cell lectin-like receptor subfamily G member 1 (KLRG1), mRNA |
| 1515 | 6513 | 11569 | 1.19 | 2.0E-54 | AA655008.1 | EST_HUMAN | nf78a09.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element; |
| 2469 | 7437 | 12554 | 1.47 | 2.0E-54 | AW163175.1 | EST_HUMAN | au92603.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to |
| 2524 | 7490 | 12610 | 1.65 | 2.0E-54 | AL163210.2 | NT | SW_CUL1_HUMAN Q13616 CUL1N HOMOLOG 1 ; Homo sapiens chromosome 21 segment HS21C010 |
| 2824 | 7845 | 12865 | 1.51 | 2.0E-54 | AW057524.1 | EST_HUMAN | wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084_Q62084 PHOSPHOLIPASE C NEIGHBORING : |
| 3472 | 8480 | | 7.32 | 2.0E-54 | AA532925.1 | EST_HUMAN | n45g08.s1 NCI_CGAP_P19 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); |
| 4082 | 9076 | | 3.11 | 2.0E-54 | 4502642 | NT | Homo sapiens chaperonin containing T-complex subunit 6 (CC16) mRNA |
| 4319 | 9311 | | 1.14 | 2.0E-54 | AF208161.1 | NT | Homo sapiens synctin precursor, mRNA, complete cds |
| 5052 | 10023 | 14992 | 0.92 | 2.0E-54 | 45069962 | NT | Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA |
| 4341 | 9332 | | 1.35 | 1.0E-54 | BF315418.1 | EST_HUMAN | 601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5' |
| 1298 | 6296 | | 1.8 | 8.0E-55 | Y07829.2 | NT | Homo sapiens RFB30 gene for RING finger protein |
| 1065 | 6073 | 11106 | 1.85 | 7.0E-55 | R09346.1 | EST_HUMAN | y26e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1278988 5' similar to |
| 1733 | 6728 | 11804 | 2.5 | 5.0E-55 | AA704971.1 | EST_HUMAN | SP:CS61_BOVIN P10897 CYTOCHROME ; |
| 1733 | 6728 | 11805 | 2.5 | 5.0E-55 | AA704971.1 | EST_HUMAN | 295b09.s1 Soares_fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3' |
| 4626 | 9611 | 14600 | 1.31 | 5.0E-55 | AW206021.1 | EST_HUMAN | 295b09.s1 Soares_fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3' U1-H-B1-efy9-09-0-Ui s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2728536 3' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLASTE Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|-------------------------------------|-----------------------|-------------------------|--|
| 56 | 7712 | 10134 | 6.49 | 4.0E-55 | AW957994.1 | EST_HUMAN | EST370064 MAGE resequences, MAGE Homo sapiens cDNA [IMAGE:1644160 3' |
| 664 | 5690 | 10699 | 29.4 | 4.0E-55 | 4826973 | NT | Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM/YA1) mRNA |
| 1414 | 6412 | 11471 | 1.58 | 4.0E-55 | 7661713 | NT | Homo sapiens predicted osteoblast protein (GS3786), mRNA |
| 1414 | 6412 | 11472 | 1.58 | 4.0E-55 | 7661713 | NT | Homo sapiens predicted osteoblast protein (GS3786), mRNA |
| 1483 | 6480 | | 1.43 | 4.0E-55 | BF061411.1 | EST_HUMAN | 7f52b10.x1 Scores_NSF_F8_9W_O^PA_P_S1 Homo sapiens cDNA clone [IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element, |
| 1974 | 6959 | 12064 | 1.95 | 4.0E-55 | 4506180 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA |
| 1974 | 6959 | 12065 | 1.95 | 4.0E-55 | 4506180 | NT | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA |
| 2032 | 7015 | 12123 | 3.3 | 4.0E-55 | 4503314 | NT | Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA |
| 2032 | 7015 | 12124 | 3.3 | 4.0E-55 | 4503314 | NT | Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA |
| 2247 | 7224 | 12344 | 4.51 | 4.0E-55 | 4507794 | NT | Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA |
| 3206 | 8221 | 13243 | 1.2 | 4.0E-55 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 4985 | 9959 | 14936 | 2.08 | 4.0E-55 | BE698671.1 | EST_HUMAN | RC2-UU0023-290700-011-f03 UT0023 Homo sapiens cDNA |
| 376 | 5423 | 10438 | 2 | 2.0E-55 | X57147.1 | NT | Human endogenous retrovirus pHE-1 (ERV9) |
| 547 | 5581 | | 1.08 | 2.0E-55 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 641 | 5669 | 10673 | 4.78 | 2.0E-55 | 4507296 | NT | Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products |
| 2889 | 7908 | 12929 | 1.7 | 2.0E-55 | 4507798 | NT | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA |
| 4620 | 9614 | 14604 | 2.97 | 2.0E-55 | BE719986.1 | EST_HUMAN | CM1-HT0876-150800-357-903 HT0876 Homo sapiens cDNA |
| 95 | 5172 | 10182 | 2.86 | 1.0E-55 | 4505060 | NT | Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA |
| 189 | 5253 | 10264 | 113.02 | 1.0E-55 | U09823.1 | NT | Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (RefSeq) mRNA, complete cds |
| 569 | 5602 | 10600 | 14.24 | 1.0E-55 | A1026718.1 | EST_HUMAN | ov85g09.x1 Scores_ntests_NHT Homo sapiens cDNA clone [IMAGE:1644160 3' |
| 1132 | 6137 | 11168 | 6.88 | 1.0E-55 | AB020710.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds |
| 1911 | 6897 | 11991 | 5 | 1.0E-55 | BE277861.1 | EST_HUMAN | 601120116F1 NIH MGCG_20 Homo sapiens cDNA clone [IMAGE:2867027 5' |
| 1911 | 6897 | 11992 | 5 | 1.0E-55 | BE277861.1 | EST_HUMAN | 601120116F1 NIH MGCG_20 Homo sapiens cDNA clone [IMAGE:2867027 5' |
| 2263 | 7240 | | 6.39 | 1.0E-55 | 5803174 | NT | Homo sapiens SMA3 (SMA3) mRNA |
| 2446 | 7416 | 12531 | 63.73 | 1.0E-55 | X13111.1 | NT | Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex) |
| 2483 | 7451 | 12564 | 3.06 | 1.0E-55 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 2483 | 7451 | 12565 | 3.08 | 1.0E-55 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 2538 | 7503 | 12622 | 14.65 | 1.0E-55 | L54057.1 | NT | Homo sapiens CLP mRNA, partial cds |
| 2717 | 7674 | 12787 | 0.98 | 1.0E-55 | AB033045.1 | NT | Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate synthetase (MTHFD) mRNA |
| 3399 | 8397 | 13422 | 1.83 | 1.0E-55 | 5174590 | NT | cyclohydrate, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3389 | 8397 | 13423 | 1.83 | 1.0E-55 | 5174590 | NT | Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methyltetrahydrofolate synthetase (MTHFD) mRNA cyclhydratase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA |
| 3883 | 8884 | 13882 | 3.86 | 1.0E-55 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 4170 | 9165 | 14152 | 1.64 | 1.0E-55 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 4592 | 9580 | | 1.01 | 1.0E-55 | N77261.1 | EST_HUMAN | y44g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5' |
| 4938 | 8935 | 14913 | 1.08 | 1.0E-55 | 8923125 | NT | Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA |
| 5015 | 9986 | 14962 | 2.2 | 1.0E-55 | BE077198.1 | EST_HUMAN | RC5-BT065-150200-031-B11 BT0605 Homo sapiens cDNA |
| 2659 | 7619 | 12730 | 3.83 | 7.0E-56 | H19934.1 | EST_HUMAN | yf62g03.r1 Soares adult brain N265fIB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element : |
| 1653 | 6649 | 11721 | 1.83 | 5.0E-58 | AW997712.1 | EST_HUMAN | RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA |
| 28 | 5108 | 10092 | 44.14 | 4.0E-58 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 28 | 5108 | 10093 | 44.14 | 4.0E-58 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds |
| 2636 | 7596 | 12709 | 7.3 | 4.0E-58 | 4507728 | NT | Homo sapiens tubulin, beta polypeptide (TUBB) mRNA |
| 2636 | 7596 | 12710 | 7.3 | 4.0E-58 | 4507728 | NT | Homo sapiens tubulin, beta polypeptide (TUBB) mRNA |
| 2740 | 5557 | 10560 | 3.56 | 4.0E-56 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 1322 | 6320 | 11368 | 3.78 | 3.0E-56 | 8924029 | NT | Homo sapiens hypothetical protein PRC01304 (PRC01304), mRNA |
| 1727 | 6722 | 11800 | 3.22 | 3.0E-56 | 6912743 | NT | Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA |
| 2089 | 7070 | 12184 | 1.19 | 3.0E-56 | 6912687 | NT | Homo sapiens oncogene TC21 (TC21), mRNA |
| 3052 | 8069 | 13078 | 1.47 | 3.0E-56 | AA325826.1 | EST_HUMAN | EST12888Q Cerebellum II Homo sapiens cDNA 5' end |
| 3052 | 8069 | 13079 | 1.47 | 3.0E-56 | AA325826.1 | EST_HUMAN | EST12888Q Cerebellum II Homo sapiens cDNA 5' end |
| 3745 | 8749 | | 2.03 | 3.0E-58 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 3818 | 8820 | 13827 | 1.28 | 3.0E-56 | BE393512.1 | EST_HUMAN | 60131020357 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5' |
| 4263 | 9256 | 14246 | 1.01 | 3.0E-56 | 7657042 | NT | Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA |
| 4300 | 9292 | 14279 | 4.75 | 3.0E-56 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 4440 | 9430 | 14414 | 2.24 | 3.0E-56 | 5902085 | NT | Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA |
| 4941 | 9918 | 14898 | 0.72 | 3.0E-56 | 6912593 | NT | Homo sapiens phosphotidylinositol transfer protein, beta (PTPNB), mRNA |
| 4984 | 9918 | 14898 | 0.83 | 3.0E-56 | 6912593 | NT | Homo sapiens phosphotidylinositol transfer protein, beta (PTPNB), mRNA |
| 520 | 5555 | | 1.87 | 2.0E-56 | AA199818.1 | EST_HUMAN | zq52ap08.s1 Stratagene neuroepithelium (#3723) Homo sapiens cDNA clone IMAGE:645206 3' |
| 723 | 7729 | 10765 | 1.67 | 2.0E-56 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 723 | 7729 | 10766 | 1.67 | 2.0E-56 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 2321 | 7296 | 12416 | 0.94 | 2.0E-56 | M26061.1 | NT | Human cGMP phosphodiesterase alpha subunit (GPR-A) mRNA, complete cds |
| 2321 | 7296 | 12417 | 0.94 | 2.0E-56 | M26061.1 | NT | Human cGMP phosphodiesterase alpha subunit (GPR-A) mRNA, complete cds |
| 2919 | 7838 | 12955 | 1.04 | 2.0E-56 | AB037835.1 | NT | Homo sapiens mRNA for KIAA1414 protein, partial cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 3242 | 8255 | | 1.89 | 2.0E-56 | AB008681.1 | NT | Homo sapiens gene for activin receptor type IIb, complete cds |
| 3456 | 8464 | 13491 | 1.29 | 2.0E-56 | AV703184.1 | EST_HUMAN | AV703184 AD13 Homo sapiens cDNA clone ADBCFG10 5' |
| 965 | 5980 | | 4.42 | 1.0E-56 | AF190930.1 | NT | Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds |
| 1489 | 6486 | 11541 | 2.19 | 1.0E-56 | AA293036.1 | EST_HUMAN | Z546b09.11 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:726137 5' similar to gb:MP4654 INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN); |
| 3590 | 8597 | 13601 | 2.26 | 1.0E-56 | AW589833.1 | EST_HUMAN | hg23c11_x1 NCI CGAP Gc8 Homo sapiens cDNA clone IMAGE:2946452 3' |
| 3590 | 8597 | 13602 | 2.26 | 1.0E-56 | AW589833.1 | EST_HUMAN | hg23c11_x1 NCI CGAP Gc8 Homo sapiens cDNA clone IMAGE:2946452 3' |
| 620 | 5647 | | 1.82 | 9.0E-57 | AW880885.1 | EST_HUMAN | QV6-OT0033-J70300-152-h03 OT0033 Homo sapiens cDNA |
| 4081 | 9075 | 14063 | 0.97 | 9.0E-57 | | 4758279 NT | Homo sapiens EphA4 (EPHA4) mRNA |
| 4081 | 9075 | 14064 | 0.97 | 9.0E-57 | | 4758279 NT | Homo sapiens EphA4 (EPHA4) mRNA |
| 295 | 5352 | 10365 | 2.81 | 8.0E-57 | AW816405.1 | EST_HUMAN | QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 873 | 5891 | 10932 | 7.02 | 8.0E-57 | AW264599.1 | EST_HUMAN | x05d10_x1 NCI CGAP Bm53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875 |
| 1780 | 6772 | 11864 | 1.69 | 8.0E-57 | AA496109.1 | EST_HUMAN | INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN); Zv51b12.r1 Soares_ testis_NHT Homo sapiens cDNA clone IMAGE:757161 5' |
| 3297 | 8308 | 13333 | 1.37 | 8.0E-57 | | 4758279 NT | Homo sapiens EphA4 (EPHA4) mRNA |
| 3297 | 8308 | 13334 | 1.37 | 8.0E-57 | | 4758279 NT | Homo sapiens EphA4 (EPHA4) mRNA |
| 4889 | 9848 | 14825 | 0.81 | 8.0E-57 | BE289916.1 | EST_HUMAN | 60084440f7 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960864 5' |
| 2561 | 7525 | 12642 | 0.97 | 7.0E-57 | 7657592 NT | Hom sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA | |
| 2561 | 7525 | 12643 | 0.97 | 7.0E-57 | 7657592 NT | Hom sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA | |
| 3177 | 8193 | 13214 | 1.16 | 7.0E-57 | 7242158 NT | Hom sapiens NMET7 (NMET7) mRNA | |
| 3177 | 8193 | 13215 | 1.16 | 7.0E-57 | 7242158 NT | Hom sapiens NMET7 (NMET7) mRNA | |
| 3197 | 8213 | 13226 | 0.74 | 7.0E-57 | 6005979 NT | Hom sapiens Kruppel-like factor 8 (KLF8), mRNA | |
| 3786 | 8789 | 13793 | 2.1 | 7.0E-57 | AF012872.1 | NT | Hom sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds |
| 3786 | 8789 | 13794 | 2.1 | 7.0E-57 | AF012872.1 | NT | Hom sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds |
| 4308 | 9300 | | 1.78 | 7.0E-57 | AF020503.1 | NT | Hom sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 3668 | 8673 | 13677 | 2.42 | 4.0E-57 | AB026898.1 | NT | Hom sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 795 | 5816 | 10847 | 1.52 | 3.0E-57 | 4507788 NT | | Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (U3E3A) mRNA |
| 1311 | 6308 | | 153.33 | 3.0E-57 | AA230279.1 | EST_HUMAN | nc13f07.s1 NCI CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10 ; |
| 2327 | 7301 | 12421 | 1.31 | 3.0E-57 | AA348335.1 | EST_HUMAN | EST54770 Hippocampus II Homo sapiens cDNA 5' end |

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|--|--|---|--|
| 2631 7591 | 12703 | 1.45 | 3.0E-57 | BE8768622.1 | EST_HUMAN | 7833b10>1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298443 3' similar to WP:Y47H8C.2 CE20263 ; | | |
| 2631 | 7591 | 12704 | 1.45 | 3.0E-57 | BE8768622.1 | EST_HUMAN | 7833b10>1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3298443 3' similar to WP:Y47H8C.2 CE20263 ; | |
| 3482 8490 | 13506 | 1.73 | 3.0E-57 | AF232708.1 | NT | Homo sapiens cell lines tsA201a chloride ion current inducer protein (Cln) gene, complete cds | | |
| 3614 8621 | 31.12 | 3.0E-57 | AW853984.1 | EST_HUMAN | RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA | | | |
| 1471 6468 | 11526 | 1.55 | 2.0E-57 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds | | |
| 1471 6468 | 11527 | 1.55 | 2.0E-57 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds | | |
| 2337 7311 | 12432 | 1.04 | 2.0E-57 | BE172526.1 | EST_HUMAN | MR0-HT0551-010400-009-h10 HT0559 Homo sapiens cDNA | | |
| 3354 8362 | 3.52 | 2.0E-57 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 | | | |
| 3474 8482 | 13501 | 0.68 | 2.0E-57 | R07702.1 | EST_HUMAN | ye88h01>1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5' | | |
| 3474 8482 | 13502 | 0.68 | 2.0E-57 | R07702.1 | EST_HUMAN | ye88h01>1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5' | | |
| 3828 8830 | 13837 | 0.83 | 2.0E-57 | BE073264.1 | EST_HUMAN | MR0-BT0551-060300-103-b03 B10551 Homo sapiens cDNA | | |
| 4063 9057 | 14044 | 1.05 | 2.0E-57 | AA018299.1 | EST_HUMAN | ze40c05>1 Soares retina N2p4TR Homo sapiens cDNA clone IMAGE:361450 5' | | |
| 4063 9057 | 14045 | 1.05 | 2.0E-57 | AA018299.1 | EST_HUMAN | ze40c05>1 Soares retina N2p4TR Homo sapiens cDNA clone IMAGE:361450 5' | | |
| 4379 9370 | 14349 | 8.09 | 2.0E-57 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 | | |
| 2170 7149 | 12266 | 1.48 | 1.0E-57 | AW503208.1 | EST_HUMAN | UI-HF-BN0-ekt-g-07-0-U1>1 NIH MGIC_50 Homo sapiens cDNA clone IMAGE:3078348 5' | | |
| 584 5615 | 1.9 | 8.0E-58 | BE868715.1 | EST_HUMAN | 601445948F1 NIH MGIC_65 Homo sapiens cDNA clone IMAGE:3850211 5' | | | |
| 646 5674 | 10679 | 4.07 | 8.0E-58 | AI798376.1 | EST_HUMAN | UNNAMED HERV-H PROTEIN : | | |
| 646 5674 | 10680 | 4.07 | 8.0E-58 | AI798376.1 | EST_HUMAN | UNNAMED HERV-H PROTEIN : | | |
| 1820 6810 | 11902 | 1.74 | 8.0E-58 | 11434921 | NT | Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA | | |
| 1820 6810 | 11903 | 1.74 | 8.0E-58 | 11434921 | NT | Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA | | |
| 2906 7925 | | 2.79 | 8.0E-58 | 7706132 | NT | Homo sapiens DHHC1 protein (LOC51304), mRNA | | |
| 2192 7171 | 12292 | 0.98 | 8.0E-58 | BE395661.1 | EST_HUMAN | 601309465F1 NIH MGIC_44 Homo sapiens cDNA clone IMAGE:3631000 5' | | |
| 2314 7289 | 12410 | 10.37 | 6.0E-58 | AU130889.1 | EST_HUMAN | AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5' | | |
| 2831 7851 | 12870 | 0.94 | 6.0E-58 | BE242150.1 | EST_HUMAN | TCAAPE1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Hom sapiens cDNA clone TCAAPE1219 | | |
| 2831 7851 | 12871 | 0.94 | 6.0E-58 | BE242150.1 | EST_HUMAN | TCAAPE1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Hom sapiens cDNA clone TCAAPE1219 | | |
| 298 5355 | 10367 | 3.24 | 5.0E-58 | 4507334 | NT | Homo sapiens synaptotagmin 1 (SYN1), mRNA | | |
| 700 5724 | 10740 | 6.5 | 5.0E-58 | BE763984.1 | EST_HUMAN | RC4-NT0057-160600-016-505 NT0057 Homo sapiens cDNA | | |
| 1175 6178 | 11213 | 3.64 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA | | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1175 | 6178 | 11214 | 3.64 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043_240300-127-e07 UM0043 Homo sapiens cDNA |
| 1176 | 6178 | 11213 | 2.81 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043_240300-127-e07 UM0043 Homo sapiens cDNA |
| 1176 | 6178 | 11214 | 2.81 | 5.0E-58 | AW797948.1 | EST_HUMAN | CM3-UM0043_240300-127-e07 UM0043 Homo sapiens cDNA |
| 3249 | 8262 | 13283 | 9.15 | 5.0E-58 | AA988183.1 | EST_HUMAN | or98e07_x1_NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3' |
| 4136 | 9131 | 14114 | 0.98 | 5.0E-58 | AI636745.1 | EST_HUMAN | ls89e07_x1_NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA_P19984 PROFILIN II; |
| 372 | 5421 | 10435 | 8.26 | 4.0E-58 | 4502302 NT | | Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA |
| 788 | 5809 | 10839 | 1.73 | 4.0E-58 | 4504634 NT | | Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA |
| | | | | | | | Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) |
| 1440 | 6437 | 11494 | 1.06 | 4.0E-58 | 4503648 NT | | (F9) mRNA |
| 2559 | 7524 | 12640 | 2.19 | 4.0E-58 | U36251.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 3 |
| 3655 | 8661 | 13666 | 1.09 | 4.0E-58 | 5031660 NT | | Homo sapiens EGFR-like repeats and discoidin I-like domains 3 (EDIL3), mRNA |
| 333 | 5385 | | 1.23 | 3.0E-58 | R17879.1 | EST_HUMAN | yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' |
| 1366 | 6363 | 11412 | 1.98 | 3.0E-58 | 4758981 NT | | Homo sapiens peptide YY (PYY) mRNA |
| 3105 | 8121 | 13138 | 3.33 | 3.0E-58 | BF699848.1 | EST_HUMAN | 602185789F1 NIH_MCGC_45 Homo sapiens cDNA clone IMAGE:4309943 5' |
| 3105 | 8121 | 13139 | 3.33 | 3.0E-58 | BF699848.1 | EST_HUMAN | 602185789F1 NIH_MCGC_45 Homo sapiens cDNA clone IMAGE:4309943 5' |
| 926 | 5943 | 10977 | 7.87 | 2.0E-58 | AF068624.1 | NT | Homo sapiens 5-aminoeuvinate synthase 2 (ALAS2) gene, complete cds |
| | | | | | | | ba08b07_x1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X89391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE); |
| 1271 | 6269 | | 27.01 | 2.0E-58 | BE208532.1 | EST_HUMAN | |
| 7112 | 5736 | 10752 | 0.84 | 1.0E-58 | M65134.1 | NT | Human complement component C5 mRNA, 3' end |
| 1051 | 6060 | 11089 | 9.81 | 1.0E-58 | 6274549 NT | | Homo sapiens: NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA |
| 1307 | 6305 | 11352 | 1.03 | 1.0E-58 | AW957782.1 | EST_HUMAN | EST369252 MAGE resequences, MAGD Homo sapiens cDNA |
| 1307 | 6305 | 11353 | 1.04 | 1.0E-58 | AW957182.1 | EST_HUMAN | EST369252 MAGE resequences, MAGD Homo sapiens cDNA |
| 1373 | 6370 | 11419 | 3.35 | 1.0E-58 | AJ238094.1 | NT | Homo sapiens: partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| 1624 | 6621 | 11689 | 1.46 | 1.0E-58 | BE466132.1 | EST_HUMAN | hy10f08_x1_NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3196935 3' |
| 2582 | 7545 | 12659 | 0.96 | 1.0E-58 | AF217514.1 | NT | Homo sapiens: uncharacterized bone marrow protein BM038 mRNA, complete cds |
| 2730 | 7687 | 12801 | 1.98 | 1.0E-58 | 4759169 NT | | Homo sapiens: steroid regulatory element binding transcription factor 2 (SRREF2) mRNA |
| 4811 | 9195 | 14778 | 5.66 | 1.0E-58 | AI141063.1 | EST_HUMAN | az43h01_x1 Soares NIHIMPU_S1 Homo sapiens cDNA clone IMAGE:1678129 3' |
| 2168 | 7147 | 12264 | 69.17 | 8.0E-59 | 4507378 NT | | Homo sapiens: TATA box binding protein (TBP) mRNA |
| 177 | 7714 | | 2.96 | 6.0E-59 | BF035327.1 | EST_HUMAN | 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1715 | 6710 | 11786 | 9.16 | 5.0E-59 | AW157281.1 | EST_HUMAN | au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 C175786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.; |
| 1715 | 6710 | 11787 | 9.16 | 5.0E-59 | AW157281.1 | EST_HUMAN | au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 C175786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.; |
| 3054 | 8071 | 13081 | 6.86 | 5.0E-59 | AI807484.1 | EST_HUMAN | wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3' |
| 4533 | 9513 | 14498 | 9.33 | 5.0E-59 | X83497.1 | NT | H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat |
| 785 | 5806 | 10837 | 2.84 | 4.0E-59 | D80006.1 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 1218 | 6217 | 11258 | 0.67 | 4.0E-59 | 4505818 | NT | Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products |
| 1218 | 6217 | 11259 | 0.67 | 4.0E-59 | 4505818 | NT | Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products |
| 5017 | 9888 | 14964 | 0.96 | 4.0E-59 | AI990847.1 | EST_HUMAN | ws32e12-x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498826 3' |
| 10 | 5090 | | 4.74 | 3.0E-59 | AW965524.1 | EST_HUMAN | EST377582 MAGE sequences, MAGI Homo sapiens cDNA |
| 225 | 5287 | 10295 | 4.43 | 3.0E-59 | 7662247 | NT | Homo sapiens KIAA0680 gene product (KIAA0680), mRNA |
| 1672 | 6668 | 11743 | 8.3 | 3.0E-59 | 4505860 | NT | Homo sapiens plasminogen activator, tissue (PLAT) mRNA |
| 1672 | 6668 | 11744 | 8.3 | 3.0E-59 | 4505860 | NT | Homo sapiens plasminogen activator, tissue (PLAT) mRNA |
| 2071 | 7053 | 12162 | 5.59 | 3.0E-59 | AB029035.1 | NT | Homo sapiens mRNA for KIAA1112 protein, partial cds |
| 2071 | 7053 | 12163 | 5.59 | 3.0E-59 | AB029035.1 | NT | Homo sapiens mRNA for KIAA1112 protein, partial cds |
| 2697 | 7779 | 12769 | 0.98 | 3.0E-59 | AF232299.1 | NT | Homo sapiens NF-1-2 pseudogene, exon 17 |
| 3056 | 8073 | 13085 | 3.67 | 3.0E-59 | 4502014 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA |
| 3056 | 8073 | 13086 | 3.67 | 3.0E-59 | 4502014 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA |
| 3735 | 8739 | 13738 | 1.33 | 3.0E-59 | 4508044 | NT | Homo sapiens zona pelucida glycoprotein 2 (sperm receptor) (ZP2) mRNA |
| 4547 | 9536 | 14523 | 1.09 | 3.0E-59 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4693 | 9678 | 14662 | 1.64 | 3.0E-59 | 7427522 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 4884 | 9863 | | 0.92 | 3.0E-59 | M95961.1 | NT | Human prohormone converting enzyme (NEC2) gene, exon 2 |
| 162 | 5228 | | 37.68 | 1.0E-59 | BE296411.1 | EST_HUMAN | 601176757F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5' |
| 2544 | 7509 | | 2.32 | 1.0E-59 | AA748468.1 | EST_HUMAN | ca56f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537 |
| 754 | 5776 | 10803 | 2.17 | 8.0E-60 | AW977845.1 | EST_HUMAN | EST389849 MAGE sequences, MAGO Homo sapiens cDNA |
| 1443 | 6440 | 11497 | 8.32 | 8.0E-60 | 4759159 | NT | Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA |
| 2107 | 7087 | 12201 | 1.59 | 8.0E-60 | 5174656 | NT | Homo sapiens differentiation-related gene 1 (nicotin-specific induction protein) (RTP) mRNA |
| 2107 | 7087 | 12202 | 1.59 | 8.0E-60 | 5174656 | NT | Homo sapiens differentiation-related gene 1 (nicotin-specific induction protein) (RTP) mRNA |
| 745 | 5768 | 10794 | 33.65 | 7.0E-60 | AF055666.1 | NT | Homo sapiens MHC class 1 region |
| 746 | 5768 | 10794 | 108.11 | 7.0E-60 | AF055666.1 | NT | Homo sapiens MHC class 1 region |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 805 | 5826 | 10856 | 1.3 | 7.0E-60 | 4504634 | NT | Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA |
| 2070 | 7052 | 12161 | 1.23 | 7.0E-60 | AF077188.1 | NT | Homo sapiens cullin 4A (CUL4A) mRNA, complete cds |
| 2712 | 7669 | 12782 | 0.98 | 7.0E-60 | AB011153.1 | NT | Homo sapiens mRNA for KIAA0581 protein, partial cds |
| 4055 | 9049 | 14037 | 4.26 | 7.0E-60 | 4505488 | NT | Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA |
| 2114 | 7094 | 12208 | 1.15 | 6.0E-60 | BE564974.2 | EST_HUMAN | 60165875TR1 NIH MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3' |
| 82 | 5159 | 10169 | 0.96 | 5.0E-60 | AI807917.1 | EST_HUMAN | wf52607_X1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2559212 3' |
| 82 | 5159 | 10170 | 0.96 | 5.0E-60 | AI807917.1 | EST_HUMAN | wf52607_X1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2559212 3' |
| 2173 | 7152 | 12271 | 1.15 | 4.0E-60 | AW503208.1 | EST_HUMAN | U1-HF-BN0-akt-g-9-0-U1..1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5' |
| 2173 | 7152 | 12272 | 1.15 | 4.0E-60 | AW503208.1 | EST_HUMAN | U1-HF-BN0-akt-g-9-0-U1..1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5' |
| 2903 | 7922 | | 1.51 | 4.0E-60 | AA298037.1 | EST_HUMAN | EST11408 Uterus Homo sapiens cDNA 5' end similar to similiar to retrovirus-related pol |
| 1822 | 6812 | 11905 | 3.27 | 3.0E-60 | BE562611.1 | EST_HUMAN | 60133644GF1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5' |
| 1822 | 6812 | 11906 | 3.27 | 3.0E-60 | BE562611.1 | EST_HUMAN | 60133644GF1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5' |
| 1832 | 6822 | | 9.77 | 3.0E-60 | 6031190 | NT | Homo sapiens prohibitin (PHB) mRNA |
| 4335 | 9326 | 14311 | 1.67 | 3.0E-60 | AJ27735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 31 | 5111 | 10097 | 1.22 | 2.0E-60 | AY008285.1 | NT | Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product |
| 1399 | 6396 | 11451 | 6.79 | 2.0E-60 | Z11694.1 | NT | H.sapiens 47kDa protein kinase related to rat ERK2 |
| 1683 | 6679 | 11752 | 1.46 | 2.0E-60 | M24603.1 | NT | Human bcr protein mRNA, 5' end |
| 1692 | 6688 | 11763 | 1.24 | 2.0E-60 | AY008285.1 | NT | Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product |
| 2532 | 7497 | 12617 | 1.04 | 2.0E-60 | 7657229 | NT | Homo sapiens interleukin 17 receptor (IL17R) mRNA |
| 3498 | 8506 | 13521 | 0.82 | 2.0E-60 | 4757867 | NT | Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA |
| 3817 | 8819 | 13826 | 0.8 | 2.0E-60 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 518 | 5553 | 10556 | 1 | 1.0E-60 | BE178586.1 | EST_HUMAN | PM3-HT0805-27020-001-e06 HT0605 Homo sapiens cDNA |
| 3806 | 8809 | 13815 | 1.97 | 1.0E-60 | AU143389.1 | EST_HUMAN | AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5' |
| 4799 | 9783 | 14766 | 1.67 | 1.0E-60 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C086 |
| 1082 | 6089 | 11118 | 2.32 | 9.0E-61 | AU118344.1 | EST_HUMAN | AU118344 HEBA1 Homo sapiens cDNA clone HEMBA1005583 5' |
| 2599 | 7561 | 12678 | 1.72 | 8.0E-61 | AW006478.1 | EST_HUMAN | wf05b10-x1 NCI CGAP C03 Homo sapiens cDNA clone IMAGE:2506555 3' |
| 2599 | 7561 | 12679 | 1.72 | 8.0E-61 | AW008478.1 | EST_HUMAN | wf05b10-x1 NCI CGAP C03 Homo sapiens cDNA clone IMAGE:2506555 3' |
| 2880 | 7899 | | 2.34 | 8.0E-61 | X57147.1 | NT | Human endogenous retrovirus pHE-1 (ERV9) |
| 128 | 5195 | 10209 | 1.8 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 128 | 5195 | 10210 | 1.8 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 4923 | 5195 | 10209 | 2.92 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |
| 4923 | 5195 | 10210 | 2.92 | 7.0E-61 | 7706670 | NT | Homo sapiens PXR2b protein (PXR2b), mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Top Hit Accession No. | Most Similar (Top) Hit BLAST E Value | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|-----------------------|--------------------------------------|-------------------------|---|
| 263 | 5322 | 10331 | 4.42 | 6.0E-61 | BE409310.1 | EST_HUMAN | 601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5' |
| 802 | 5823 | 10853 | 2.26 | 6.0E-61 | BE409310.1 | EST_HUMAN | 601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5' |
| 1301 | 6299 | 11345 | 12.89 | 6.0E-61 | AF119866.1 | NT | Homo sapiens PRO2014 mRNA, complete cds |
| 1609 | 6605 | 11668 | 2.82 | 6.0E-61 | AA596033.1 | EST_HUMAN | mn66t09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3' |
| 2068 | 7050 | 12158 | 0.95 | 6.0E-61 | AY008285.1 | NT | Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product |
| 3234 | 8249 | 13270 | 13.67 | 6.0E-61 | AU130689.1 | EST_HUMAN | AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5' |
| 358 | 5408 | 10420 | 0.86 | 5.0E-61 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 1639 | 6636 | 11706 | 3.51 | 5.0E-61 | 4506008 | NT | Homo sapiens protein phosphatase 1, regulatory subunit 10 (PP1R10) mRNA |
| 2965 | 7983 | 12997 | 2.15 | 5.0E-61 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 3125 | 8141 | 13162 | 1.7 | 5.0E-61 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 3874 | 8875 | | 1.66 | 5.0E-61 | AJ228041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4843 | 5408 | 10420 | 1.16 | 5.0E-61 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 495 | 5531 | 10538 | 1.33 | 2.0E-61 | 8922829 | NT | Homo sapiens hypothetical protein FLJ11026 (FLJ11026) mRNA |
| 1193 | 6194 | 11231 | 3.21 | 2.0E-61 | BE168410.1 | EST_HUMAN | QV3+HT0513-j6D40-147-d01 HT0513 Homo sapiens cDNA |
| 1193 | 6194 | 11232 | 3.21 | 2.0E-61 | BE168410.1 | EST_HUMAN | QV3+HT0513-j6D40-147-d01 HT0513 Homo sapiens cDNA |
| 1626 | 6623 | 11692 | 1.75 | 2.0E-61 | N53039.1 | EST_HUMAN | yw53d11.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:125444 60S RIBOSOMAL PROTEIN L35A (HUMAN); |
| 2570 | 7533 | | 1.36 | 2.0E-61 | N39397.1 | EST_HUMAN | y03f11.r1 Socres melanocyte 2NbHm Homo sapiens cDNA clone IMAGE:270189 5' |
| 432 | 5470 | | 0.75 | 1.0E-61 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C03 |
| 764 | 5785 | 10814 | 1.16 | 1.0E-61 | 5453829 | NT | Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA |
| 1732 | 6727 | | 0.96 | 1.0E-61 | U32657.1 | NT | Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region |
| 1821 | 6811 | 11904 | 4.18 | 1.0E-61 | 60056983 | NT | Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A) mRNA |
| 2134 | 7114 | 12227 | 1.82 | 1.0E-61 | AW827281.1 | EST_HUMAN | xn11b09.y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSRI repetitive element; |
| 2761 | 7782 | 12807 | 2.42 | 1.0E-61 | BE386363.1 | EST_HUMAN | 601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5' |
| 3291 | 8302 | 13328 | 0.73 | 1.0E-61 | 7662319 | NT | Homo sapiens KIAA0806 gene product (KIAA0806), mRNA |
| 4317 | 9309 | 14294 | 0.75 | 1.0E-61 | 4759249 | NT | Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA |
| 4317 | 9309 | 14295 | 0.75 | 1.0E-61 | 4759249 | NT | Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA |
| 4708 | 9693 | 14676 | 9.13 | 1.0E-61 | AW298181.1 | EST_HUMAN | Ui-H-BW0-aj->-08-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3' |
| 4708 | 9693 | 14677 | 9.13 | 1.0E-61 | AW298181.1 | EST_HUMAN | Ui-H-BW0-aj->-08-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3' |
| 4420 | 9410 | 14398 | 0.92 | 8.0E-62 | AA830420.1 | EST_HUMAN | oc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SWPOL_MLVRK P31795 POLFOLYPROTEIN ; |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1090 | 6097 | 11126 | 1.09 | 7.0E-62 | AV714334.1 | EST_HUMAN | AV714334 DC3 Homo sapiens cDNA clone DCBAMA08 5' NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1)(UBF-1) |
| 3427 | 8435 | 13461 | 0.93 | 7.0E-62 | P17480 | SWISSPROT | (AUTOANTIGEN NOR-90) |
| 2930 | 7949 | | 1.56 | 6.0E-62 | U09410.1 | NT | Human zinc finger protein ZNF131 mRNA, partial cds |
| 3300 | 8311 | | 4.7 | 6.0E-62 | 11418255 | NT | Homo sapiens CGI-56 protein (CGI-56), mRNA |
| 413 | 5450 | 10470 | 3.65 | 5.0E-62 | AI950528.1 | EST_HUMAN | wx51e07_x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLCIN-95; contains element MER22 repetitive element; |
| 2341 | 7315 | 12435 | 3.43 | 5.0E-62 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 2341 | 7315 | 12436 | 3.43 | 5.0E-62 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 2515 | 7483 | 12599 | 0.98 | 5.0E-62 | U39487.1 | NT | Human xanthine dehydrogenase/oxidase mRNA, complete cds |
| 2515 | 7483 | 12600 | 0.98 | 5.0E-62 | U39487.1 | NT | Human xanthine dehydrogenase/oxidase mRNA, complete cds |
| 3334 | 8344 | 13362 | 2.46 | 5.0E-62 | 4506758 | NT | Homo sapiensryanodine receptor 3 (RYR3) mRNA zw78ed9_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT |
| 4201 | 9194 | 14176 | 1.82 | 5.0E-62 | AA431033.1 | EST_HUMAN | P47245 NARDILYSIN ; RCS-NN1089-100500-021-H103 NN1089 Homo sapiens cDNA |
| 4427 | 9417 | | 1.12 | 5.0E-62 | AW905887.1 | EST_HUMAN | bu71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 |
| 830 | 5850 | 10887 | 5.18 | 4.0E-62 | AW161479.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); eu71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 |
| 830 | 5850 | 10888 | 5.18 | 4.0E-62 | AW161479.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 |
| 831 | 5850 | 10887 | 3.63 | 4.0E-62 | AW161479.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); eu71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 |
| 831 | 5850 | 10888 | 3.63 | 4.0E-62 | AW161479.1 | EST_HUMAN | ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_m1 HISTONE H2B.2 (HUMAN); |
| 2389 | 7360 | 12482 | 4.43 | 4.0E-62 | AI827900.1 | EST_HUMAN | wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_m1 HISTONE H2B.2 (HUMAN); |
| 2389 | 7360 | 12483 | 4.43 | 4.0E-62 | AI827900.1 | EST_HUMAN | gb:X57138_m1 HISTONE H2B.2 (HUMAN); |
| 3315 | 8326 | | 7.88 | 4.0E-62 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 5023 | 9994 | 14967 | 0.97 | 4.0E-62 | 4758323 | NT | Homo sapiens enhancer of zeste (Drosophila) homolog 2 (EZH2) mRNA |
| 73 | 5151 | 10160 | 1.46 | 3.0E-62 | 4557794 | NT | Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA |
| 2972 | 7990 | 13003 | 0.71 | 3.0E-62 | AB040909.1 | NT | Homo sapiens mRNA for KIAA1476 protein, partial cds |
| 2972 | 7890 | 13004 | 0.71 | 3.0E-62 | AB040909.1 | NT | Human cyclolin-related processed pseudogene |
| 3615 | 8622 | 13630 | 8.12 | 3.0E-62 | X52858.1 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1211 | 6211 | 11251 | 2.89 | 2.0E-62 | AL163284.2 | NT | |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1027 | 6037 | 11069 | 1.58 | 1.0E-62 | AF248540.1 | NT | Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds |
| 1512 | 6510 | 11567 | 15.3 | 1.0E-62 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 1763 | 6755 | 11840 | | 1.92 | 1.0E-62 | AA625207.1 | EST_HUMAN |
| 2844 | 7864 | 12882 | | 1.18 | 1.0E-62 | AL039044.1 | EST_HUMAN |
| 3339 | 8348 | | | 2.49 | 1.0E-62 | AB040911.1 | NT |
| 4395 | 9386 | 14369 | | 1.63 | 1.0E-62 | | Homo sapiens mRNA for KIAA1478 protein, partial cds |
| 4956 | 9933 | 14911 | | 0.98 | 1.0E-62 | AA1488522.1 | EST_HUMAN |
| 336 | 5388 | 10395 | | 1.82 | 9.0E-63 | AW816405.1 | EST_HUMAN |
| 2284 | 7260 | | | 1.09 | 9.0E-63 | C18159.1 | EST_HUMAN |
| 3928 | 8928 | 13918 | | 9.26 | 9.0E-63 | AB002348.2 | NT |
| 3928 | 8928 | 13919 | | 9.26 | 9.0E-63 | AB002348.2 | NT |
| 5056 | 10026 | 14995 | | 4.71 | 9.0E-63 | AA015938.1 | EST_HUMAN |
| 2282 | 7258 | 12376 | | 2.39 | 8.0E-63 | | |
| 2313 | 7288 | 12409 | | 5.14 | 8.0E-63 | 5031810 | NT |
| 3379 | 8387 | 13408 | | 4.89 | 8.0E-63 | AF198349.1 | NT |
| 3379 | 8387 | 13409 | | 4.89 | 8.0E-63 | AF198349.1 | NT |
| 4143 | 9138 | 14122 | | 3.27 | 8.0E-63 | AL163263.2 | NT |
| 916 | 5932 | | | 1.84 | 7.0E-63 | AI872137.1 | EST_HUMAN |
| 3247 | 8260 | 13282 | | 0.7 | 4.0E-63 | AL163278.2 | NT |
| 3719 | 8723 | 13722 | | 2.01 | 4.0E-63 | AB014607.1 | NT |
| 3719 | 8723 | 13723 | | 2.01 | 4.0E-63 | AB014607.1 | NT |
| 1895 | 6883 | 11975 | | 2.67 | 3.0E-63 | AB018260.1 | NT |
| 2706 | 7663 | 12774 | | 1.34 | 3.0E-63 | J00310.1 | NT |
| 2748 | 6219 | 11262 | | 10.16 | 3.0E-63 | 6005963 | NT |
| 191 | 5255 | 10267 | | 2.47 | 2.0E-63 | U07804.1 | NT |
| 198 | 5262 | 10275 | | 1.85 | 2.0E-63 | 4885226 | NT |
| 494 | 5530 | | | 1.36 | 2.0E-63 | 4557624 | NT |
| 816 | 5837 | 10872 | | 4.72 | 2.0E-63 | 7857042 | NT |
| 1533 | 6531 | 11591 | | 1.52 | 2.0E-63 | AB030388.1 | NT |

Single Exon Probes Expressed in HBL100 Cells

| Probe Seq ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|----------------------------|-------------------------|-----------------------|---|---|---|
| 1533 | 6531 | 11592 | 1.52 | 2.0E-63 | AB030388.1 | NT | Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds | 60_301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36336103 5' | |
| 1729 | 6724 | 11802 | 3 | 2.0E-63 | BE410739.1 | EST_HUMAN | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)(APP), mRNA | 60_301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36336103 5' | |
| 3083 | 8099 | 13114 | 1.58 | 2.0E-63 | 4502166 | NT | Homo sapiens chromosome 3 subtelomeric region | Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds | |
| 3212 | 8227 | 13249 | 2.2 | 2.0E-63 | AF109718.1 | NT | Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene | Homo sapiens cDNA clone c-Zvd11 | |
| 3809 | 8812 | 13818 | 1.4 | 2.0E-63 | L39891.1 | NT | Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene | HSCZVD11 normalized infant brain cDNA Homo sapiens cDNA clone c-Zvd11 | |
| 4716 | 9701 | 14687 | 1.23 | 2.0E-63 | AF111167.2 | NT | Homo sapiens Bm23 normalized infant brain cDNA Homo sapiens cDNA clone c-Zvd11 | HSCZVD11 normalized infant brain cDNA Homo sapiens cDNA clone c-Zvd11 | |
| 4216 | 9209 | 14188 | 3.33 | 1.0E-63 | F08485.1 | EST_HUMAN | Homo sapiens Bm23 normalized infant brain cDNA Homo sapiens cDNA clone c-Zvd11 | 60_1155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5' | |
| 4216 | 9209 | 14189 | 3.33 | 1.0E-63 | F08485.1 | EST_HUMAN | Homo sapiens Bm23 normalized infant brain cDNA Homo sapiens cDNA clone c-Zvd11 | 60_1155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5' | |
| 1029 | 6039 | | | 9.14 | 8.0E-64 | BE280796.1 | EST_HUMAN | 60_1155232F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5' | |
| 3451 | 8459 | | | 0.9 | 7.0E-64 | BE394321.1 | EST_HUMAN | 60_111455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5' | |
| 4593 | 9581 | 14570 | 3.25 | 7.0E-64 | 4507490 | NT | Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA | Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA | |
| 4593 | 9581 | 14571 | 3.25 | 7.0E-64 | 4507490 | NT | Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | |
| 1684 | 6680 | 11753 | 5.45 | 6.0E-64 | AI651992.1 | EST_HUMAN | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | |
| 1684 | 6680 | | | 5.45 | 6.0E-64 | AI651992.1 | EST_HUMAN | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): |
| 3049 | 8066 | 13074 | 5.09 | 6.0E-64 | AW026445.1 | EST_HUMAN | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | |
| 3049 | 8066 | 13075 | 5.09 | 6.0E-64 | AW026445.1 | EST_HUMAN | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | wb51607_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BEta-GLUCURONIDASE PRECURSOR (HUMAN): | |
| 810 | 5831 | 10863 | 3.24 | 5.0E-64 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA | Homo sapiens chromosome 21 unknown mRNA | |
| 810 | 5831 | 10864 | 3.24 | 5.0E-64 | AF231919.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds | Homo sapiens mRNA for KIAA0903 protein, partial cds | |
| 1318 | 6316 | 11364 | 2.38 | 5.0E-64 | AB020710.1 | NT | Homo sapiens phosphoglucomutase-related protein (PGMMP) gene, complete cds | Homo sapiens phosphoglucomutase-related protein (PGMMP) gene, complete cds | |
| 1397 | 6394 | 11448 | 1.35 | 5.0E-64 | L40933.1 | NT | Homo sapiens phosphoglucomutase-related protein (PGMMP) gene, complete cds | Homo sapiens phosphoglucomutase-related protein (PGMMP) gene, complete cds | |
| 1397 | 6394 | 11449 | 1.35 | 5.0E-64 | L40933.1 | NT | Homo sapiens putative transcription factor CR33 (CR33) mRNA, partial cds | Homo sapiens putative transcription factor CR33 (CR33) mRNA, partial cds | |
| 1673 | 6669 | 11745 | 1.5 | 5.0E-64 | UB89458.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds | Homo sapiens mRNA for KIAA0903 protein, partial cds | |
| 2753 | 6447 | 11506 | 4.17 | 5.0E-64 | 7662205 | NT | C18895 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-569E02 5' | C18895 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-569E02 5' | |
| 2753 | 6447 | 11507 | 4.17 | 5.0E-64 | 7662205 | NT | C18895 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-569E02 5' | C18895 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-569E02 5' | |
| 3852 | 8854 | 13859 | 8.23 | 5.0E-64 | AF017433.1 | NT | AV711714 DCAAMC01 5' | AV711714 DCAAMC01 5' | |
| 3988 | 8986 | 13972 | 1.02 | 5.0E-64 | AB020710.1 | NT | AV711714 DCAAMC01 5' | AV711714 DCAAMC01 5' | |
| 2135 | 7115 | 12228 | 3.23 | 3.0E-64 | C18895.1 | EST_HUMAN | AV711714 DCAAMC01 5' | AV711714 DCAAMC01 5' | |
| 3359 | 8367 | 13385 | 1.37 | 3.0E-64 | AV711714.1 | EST_HUMAN | AV711714 DCAAMC01 5' | AV711714 DCAAMC01 5' | |
| 3359 | 8367 | 13386 | 1.37 | 3.0E-64 | AV711714.1 | EST_HUMAN | AV711714 DCAAMC01 5' | AV711714 DCAAMC01 5' | |
| 1072 | 6080 | 11111 | 1.32 | 2.0E-64 | AA6039940.1 | EST_HUMAN | ef09d0B_s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1031151 3' | ef09d0B_s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1031151 3' | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1374 | 6371 | 11420 | 5.42 | 2.0E-64 | 4757701 | NT | Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA |
| 2454 | 7424 | | 1.92 | 2.0E-64 | AI927030.1 | EST_HUMAN | w087601.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element; |
| 2459 | 7428 | 12544 | 2.92 | 2.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 2459 | 7428 | 12545 | 2.92 | 2.0E-64 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 3067 | 8083 | 13097 | 0.91 | 2.0E-64 | 4504068 | NT | Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA |
| 256 | 5316 | 10325 | 1.58 | 1.0E-64 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 1741 | 6736 | 11812 | 51.93 | 1.0E-64 | AI929419.1 | EST_HUMAN | eu60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:1;21696 cds1 PROTHYMOGIN ALPHA (HUMAN);contains element MSFR1 repetitive element; |
| 2942 | 7961 | 12981 | 0.81 | 1.0E-64 | 4507334 | NT | Homo sapiens synaptophysin 1 (SYN1), mRNA |
| 3432 | 8440 | 13467 | 5 | 1.0E-64 | AF196779.1 | NT | Homo sapiens transcription factor TGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α> |
| 3503 | 8511 | 13525 | 1.46 | 1.0E-64 | AF228527.1 | NT | Homo sapiens TRIAD3 mRNA, partial cds |
| 3503 | 8511 | 13526 | 1.46 | 1.0E-64 | AF228527.1 | NT | Homo sapiens TRIAD3 mRNA, partial cds |
| 3805 | 8808 | 13814 | 0.87 | 1.0E-64 | 8922829 | NT | Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA |
| 2214 | 7191 | 12312 | 1.09 | 9.0E-65 | X89211.1 | NT | H.sapiens DNA_Y for endogenous retroviral like element |
| 2214 | 7191 | 12313 | 1.09 | 9.0E-65 | X89211.1 | NT | H.sapiens DNA_Y for endogenous retroviral like element |
| 1039 | 6049 | 11079 | 3.17 | 6.0E-65 | AV721898 | EST_HUMAN | AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5' |
| 1880 | 6869 | | 48.55 | 6.0E-65 | AA550929.1 | EST_HUMAN | nj86d10.s1 NCI CGAP P11 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN); |
| 625 | 5652 | 10656 | 0.96 | 5.0E-65 | AF064604.1 | NT | Homo sapiens K03 protein mRNA, partial cds |
| 1335 | 6333 | 11381 | 1.94 | 5.0E-65 | 7661951 | NT | Homo sapiens KIAA0156 gene product (KIAA0156), mRNA |
| 1335 | 6333 | 11382 | 1.94 | 5.0E-65 | 7661951 | NT | Homo sapiens KIAA0156 gene product (KIAA0156), mRNA |
| 3181 | 8197 | 13220 | 1.88 | 5.0E-65 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 3181 | 8197 | 13221 | 1.88 | 5.0E-65 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 193 | 5257 | 10270 | 3.82 | 4.0E-65 | AL120419.1 | EST_HUMAN | DKF7p761G118_11761 (synonym: hany2) Homo sapiens cDNA clone DKF7p761G108 5' |
| 736 | 5759 | 10781 | 1.07 | 4.0E-65 | AI266468.1 | EST_HUMAN | qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3' |
| 736 | 5759 | 10782 | 1.07 | 4.0E-65 | AI266468.1 | EST_HUMAN | qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3' |
| 1062 | 6070 | 11102 | 6.88 | 4.0E-65 | 4826735 | NT | Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA |
| 1455 | 6452 | 11511 | 18.94 | 4.0E-65 | 4506636 | NT | Homo sapiens ribosomal protein L34 (RPL34) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2275 | 7251 | 12368 | 3.52 | 4.0E-65 | BE221469.1 | EST_HUMAN | hu25804_x1_NCI_CGAP_Mai15 Homo sapiens cDNA clone IMAGE:3171102 3' |
| 2275 | 7251 | 12369 | 3.52 | 4.0E-65 | BE221469.1 | EST_HUMAN | hu25804_x1_NCI_CGAP_Mai15 Homo sapiens cDNA clone IMAGE:3171102 3' |
| 3845 | 8847 | 13855 | 1.07 | 4.0E-65 | AW983185.1 | EST_HUMAN | RC2-BN0033-160200-013-a03_Bn0033 Homo sapiens cDNA |
| 96 | 5174 | 10185 | 1.82 | 3.0E-65 | 5031976 | NT | Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA |
| 97 | 5174 | 10185 | 1.75 | 3.0E-65 | 5031976 | NT | Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA |
| 1212 | 7699 | | 12.12 | 3.0E-65 | X78932.1 | NT | H. sapiens IIZ_F9 mRNA for zinc finger protein |
| 1527 | 6524 | 11581 | 1.55 | 3.0E-65 | 4504626 | NT | Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products |
| 1787 | 6779 | 11871 | 1.62 | 3.0E-65 | A0000692.1 | EST_HUMAN | ov23f03_s1_Spares_tests_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element |
| 2921 | 7940 | 12956 | 0.89 | 3.0E-65 | D87078.2 | NT | MSR1 repetitive element; |
| 3203 | 8218 | 13241 | 0.83 | 3.0E-65 | 4504950 | NT | Homo sapiens mRNA for KIAA0235 protein, partial cds |
| 3638 | 8644 | 13650 | 1.17 | 3.0E-65 | A0000692.1 | EST_HUMAN | ov23f03_s1_Spares_tests_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element |
| 4515 | 9505 | 14485 | 1.45 | 3.0E-65 | 6912385 | NT | MSR1 repetitive element; |
| 3320 | 8330 | 13351 | 6.2 | 2.0E-65 | BF680294.1 | EST_HUMAN | (Homo sapiens tab6 GTPase activating protein (GAP) and centrosome-associated) (GAPCENA), mRNA |
| 89 | 5166 | | 1.12 | 1.0E-65 | BF125544.1 | EST_HUMAN | 6021550621F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5' |
| 534 | 5569 | 10572 | 1.79 | 1.0E-65 | 7657495 | NT | 6017634881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5' |
| 1989 | 6974 | 12079 | 1.12 | 1.0E-65 | AB040946.1 | NT | Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA |
| 3290 | 8301 | 13327 | 0.79 | 1.0E-65 | BE466681.1 | EST_HUMAN | h224a09_x1_NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208888 3' |
| 3892 | 8892 | 13890 | 1.89 | 1.0E-65 | 4504082 | NT | Homo sapiens glypican 4 (GPC4) mRNA |
| 3892 | 8892 | 13891 | 1.89 | 1.0E-65 | 4504082 | NT | Homo sapiens glypican 4 (GPC4) mRNA |
| 4084 | 9078 | 14066 | 3.43 | 1.0E-65 | AW028340.1 | EST_HUMAN | wx09c09_x1_NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3' |
| 4084 | 9078 | 14067 | 3.43 | 1.0E-65 | AW028340.1 | EST_HUMAN | wx09c09_x1_NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3' |
| 70 | 5149 | 10156 | 1.28 | 9.0E-66 | AL160311.1 | NT | Novel human gene mapping to chromosome 22 |
| 70 | 5149 | 10157 | 1.28 | 9.0E-66 | AL160311.1 | NT | Novel human gene mapping to chromosome 22 |
| 1336 | 6334 | 11383 | 2.47 | 9.0E-66 | 5031980 | NT | Novo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 1336 | 6334 | 11384 | 2.47 | 9.0E-66 | 5031980 | NT | Novo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA |
| 1453 | 6450 | | 3.8 | 9.0E-66 | M87299.1 | NT | Human transposon-like element, partial |
| 4553 | 9541 | 14526 | 0.96 | 9.0E-66 | AL137163.1 | NT | Novo sapiens gene mapping to chromosome X |
| 4240 | 9234 | 14216 | 1.02 | 6.0E-66 | AI924653.1 | EST_HUMAN | wn57h07_x1_NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A |
| 4240 | 9234 | 14217 | 1.02 | 6.0E-66 | AI924653.1 | EST_HUMAN | CE18595 ; |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4240 | 92234 | 14218 | 1.02 | 6.0E-66 | A1924653.1 | EST_HUMAN | wn57h07.x1_NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE15595 ; |
| 1349 | 83446 | 11397 | 1.86 | 5.0E-66 | BE064410.1 | EST_HUMAN | RC4-BT0311-141158-011-h06_BT0311 Homo sapiens cDNA |
| 4939 | 99116 | 14895 | 0.81 | 5.0E-66 | BE898644.1 | EST_HUMAN | 601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5' |
| 4939 | 99116 | 14896 | 0.81 | 5.0E-66 | BE898644.1 | EST_HUMAN | 601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5' |
| 782 | 5803 | 10833 | 2.44 | 4.0E-66 | 6679816 NT | | Mus musculus; fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA |
| 1698 | 6693 | 11769 | 1.24 | 4.0E-66 | AW897798.1 | EST_HUMAN | RC1-NN0063-100500-022-ed02 NN0063 Homo sapiens cDNA |
| 2217 | 7194 | 12316 | 2.12 | 4.0E-66 | X89211.1 | NT | H. sapiens cDNA for endogenous retroviral like element |
| 2403 | 7374 | | 2.81 | 4.0E-66 | AJ223364.1 | NT | Homo sapiens germ-line DNA upstream of J kappa locus |
| 4638 | 9623 | | 4.36 | 4.0E-66 | 9635487 NT | | Human endogenous retrovirus, complete genome |
| 1402 | 6399 | 11455 | 34.87 | 3.0E-66 | 4502098 NT | | Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA |
| 1402 | 6399 | 11456 | 34.87 | 3.0E-66 | 4502098 NT | | Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA |
| 1936 | 6922 | 12020 | 1.02 | 3.0E-66 | N55323.1 | EST_HUMAN | y27g12.1r1 Scares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:2843265' similar to SW:H2B1_TIGCA P35058 HISTONE_H2B.1/H2B.2. [2] PIR:B56612 ; |
| 1936 | 6922 | 12021 | 1.02 | 3.0E-66 | N55323.1 | EST_HUMAN | y27g12.1r1 Scares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:2843265' similar to SW:H2B1_TIGCA P35058 HISTONE_H2B.1/H2B.2. [2] PIR:B56612 ; |
| 1936 | 6922 | 12022 | 1.02 | 3.0E-66 | N55323.1 | EST_HUMAN | y27g12.1r1 Scares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:2843265' similar to SW:H2B1_TIGCA P35058 HISTONE_H2B.1/H2B.2. [2] PIR:B56612 ; |
| 2635 | 7595 | 12708 | 2.42 | 3.0E-66 | 11141880 NT | | Homo sapiens TGF(beta)-induced transcription factor 2 (TGF2), mRNA |
| 3043 | 8060 | 13069 | 7.45 | 3.0E-66 | 7662223 NT | | Homo sapiens KIAA0549 gene product (KIAA0549), mRNA |
| 52 | 5133 | 10128 | 1.38 | 2.0E-66 | 7657334 NT | | Homo sapiens Misspacer/NIK-related kinase (Mlnk), mRNA |
| 52 | 5133 | 10129 | 1.38 | 2.0E-66 | 7657334 NT | | Homo sapiens Misspacer/NIK-related kinase (Mlnk), mRNA |
| 419 | 5077 | 10061 | 1.14 | 2.0E-66 | 4505524 NT | | Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products |
| 419 | 5077 | 10062 | 1.14 | 2.0E-66 | 4505524 NT | | Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products |
| 1791 | 6782 | 11874 | 2.52 | 2.0E-66 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 2905 | 7924 | 12943 | 0.98 | 2.0E-66 | X65859.1 | NT | H. sapiens pseudogene for the low affinity IL-8 receptor |
| 3679 | 8684 | 13686 | 0.82 | 2.0E-66 | AL117233.1 | NT | Novel human gene mapping to chromosome 1 |
| 4137 | 9132 | 14115 | 0.91 | 2.0E-66 | 8923768 NT | | Homo sapiens histone deacetylase 8 (HDAC8 gene) (HSA277724), mRNA |
| 4521 | 9511 | 14495 | 39.41 | 2.0E-66 | AJ133267.2 | NT | Homo sapiens HLA-B gene for human leucocyte antigen B |
| 4521 | 9511 | 14496 | 39.41 | 2.0E-66 | AJ133267.2 | NT | Homo sapiens HLA-B gene for human leucocyte antigen B |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1644 | 6640 | | | 1.17 | 1.0E-66 BE887173.1 | EST_HUMAN | 601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909831 5' |
| 2823 | 7844 | 12863 | | 1.49 | 1.0E-66 AV717817.1 | EST_HUMAN | AV717817 DCB3 Homo sapiens cDNA clone DCBADC07 5' |
| 2823 | 7844 | 12864 | | 1.49 | 1.0E-66 AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |
| 4260 | 7844 | 12863 | | 3.88 | 1.0E-66 AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |
| 4260 | 7844 | 12864 | | 3.88 | 1.0E-66 AV717817.1 | EST_HUMAN | AV717817 DCB Homo sapiens cDNA clone DCBADC07 5' |
| 379 | 5454 | 10471 | | 4.95 | 7.0E-67 AW162232.1 | EST_HUMAN | au75d02_x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); EST96812 Testis Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid ZK353 |
| 1363 | 6360 | 11410 | | 2.15 | 7.0E-67 AA383416.1 | EST_HUMAN | Zh56d05_r1 Scares fetal liver spleen_1NF1S S1 Homo sapiens cDNA clone IMAGE:416049 5' |
| 1523 | 6520 | 11576 | | 1.98 | 7.0E-67 W85947.1 | EST_HUMAN | Zh56d05_r1 Scares fetal liver spleen_1NF1S S1 Homo sapiens cDNA clone IMAGE:416049 5' |
| 1523 | 6520 | 11577 | | 1.98 | 7.0E-67 W85947.1 | EST_HUMAN | Homo sapiens Inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA |
| 1982 | 6967 | 12072 | | 1.31 | 7.0E-67 | 7657243 NT | Homo sapiens Inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA |
| 1982 | 6967 | 12073 | | 1.31 | 7.0E-67 | 7657243 NT | au75d02_x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); |
| 2738 | 5454 | 10471 | | 4.77 | 7.0E-67 AW162232.1 | EST_HUMAN | H.sapiens mRNA for acetyl-CoA carboxylase |
| 555 | 5589 | 10590 | | 1.53 | 6.0E-67 X58968.1 | NT | Homo sapiens mRNA for transmembrane receptor protein |
| 787 | 5808 | 10838 | | 2.36 | 6.0E-67 Z17227.1 | NT | Homo sapiens PMP69 gene, exons 3,4,5,6 & 7 |
| 1254 | 6252 | 11293 | | 1.35 | 6.0E-67 Y14320.1 | NT | Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA |
| 3095 | 8111 | 13129 | | 1.52 | 6.0E-67 4506434 NT | NT | Homo sapiens Synapsin III (SYN3) mRNA, and translated products |
| 3353 | 8361 | 13377 | | 1.44 | 6.0E-67 4507332 NT | NT | Homo sapiens Synapsin III (SYN3) mRNA, and translated products |
| 3353 | 8361 | 13378 | | 1.44 | 6.0E-67 4507332 NT | NT | Homo sapiens DkFZp434P211 protein (DkFZp434P211), mRNA |
| 4567 | 9555 | 14542 | | 3.45 | 6.0E-67 7657020 NT | NT | Homo sapiens DkFZp434P211 protein (DkFZp434P211), mRNA |
| 4567 | 9555 | 14543 | | 3.45 | 6.0E-67 7657020 NT | NT | Homo sapiens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA |
| 4805 | 9789 | | | 0.86 | 6.0E-67 4507848 NT | NT | Homo sapiens B-ATF gene, complete cds |
| 5012 | 9983 | 14958 | | 1.01 | 6.0E-67 AF016898.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3a2 to TCRBV12S2 region |
| 5012 | 9983 | 14959 | | 1.01 | 6.0E-67 AF016898.1 | NT | yn02d11.1 Scares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5' |
| 3150 | 8166 | 13186 | | 2.02 | 5.0E-67 AF005660.1 | EST_HUMAN | EST37903 Embryo, 9 week Homo sapiens cDNA 5' end |
| 1308 | 6306 | 11354 | | 1.2 | 4.0E-67 R90819.1 | EST_HUMAN | RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA |
| 2741 | 5654 | 10659 | | 1.65 | 3.0E-67 AA333768.1 | EST_HUMAN | MR3-SN0065-040500-008-f01 SN0068 Homo sapiens cDNA |
| 3371 | 8379 | 13399 | | 1.01 | 3.0E-67 BE064410.1 | EST_HUMAN | hw16g09.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183736 3' similar to WP:F23H11.9 CE09817; |
| 4555 | 9543 | 14528 | | 3.04 | 3.0E-67 AW889159.1 | EST_HUMAN | QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 188 | 5252 | 10263 | | 1.1 | 2.0E-67 BE348354.1 | EST_HUMAN | |
| 835 | 5854 | 10894 | | 5.38 | 2.0E-67 AW816405.1 | EST_HUMAN | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1088 | 6095 | | 2.11 | 2.0E-67 | AF167460.1 | NT | Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4 ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 O94892 |
| 1845 | 6834 | 11924 | 1.28 | 2.0E-67 | BE303037.1 | EST_HUMAN | KIAA0798 PROTEIN ; |
| 1845 | 6834 | 11925 | 1.28 | 2.0E-67 | BE303037.1 | EST_HUMAN | KIAA0798 PROTEIN ; |
| 2179 | 7158 | 12277 | 1.81 | 2.0E-67 | 11422946 NT | | Homo sapiens hypothetical protein dJ462O23.2 (D.J462O23.2), mRNA |
| 2179 | 7158 | 12278 | 1.81 | 2.0E-67 | 11422946 NT | | Homo sapiens hypothetical protein dJ462O23.2 (D.J462O23.2), mRNA |
| 2323 | 7297 | 12419 | 1.29 | 2.0E-67 | AF309561.1 | NT | Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds |
| 2364 | 7338 | 12455 | 2.28 | 2.0E-67 | 4758795 NT | | Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA |
| 3387 | 8395 | 13419 | 3.66 | 2.0E-67 | AA625755.1 | EST_HUMAN | zu91901.s1 Soares, testis_NH _T Homo sapiens cDNA clone IMAGE:7453923' |
| 3896 | 8896 | 13894 | 2.87 | 2.0E-67 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS2TC100 |
| 251 | 5311 | 10322 | 2.94 | 1.0E-67 | 4502166 NT | | |
| 698 | 5722 | 10738 | 2.16 | 1.0E-67 | AA702794.1 | EST_HUMAN | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA z90504.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3' |
| 2111 | 7091 | 12205 | 2.23 | 8.0E-68 | BE870732.1 | EST_HUMAN | zq144855EF1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5' |
| 3778 | 8781 | 13784 | 4.83 | 8.0E-68 | AA209456.1 | EST_HUMAN | zq82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SA9_SULAC Q07590 SAV PROTEIN ; |
| 3778 | 8781 | 13785 | 4.83 | 8.0E-68 | AA209456.1 | EST_HUMAN | zq82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SA9_SULAC Q07590 SAV PROTEIN ; |
| 1851 | 6840 | | 1.93 | 6.0E-68 | AW503842.1 | EST_HUMAN | UI-HF-BND-alb-c-07-0-1U.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5' |
| 809 | 5830 | 10861 | 3.82 | 5.0E-68 | AF23191.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 809 | 5830 | 10862 | 3.82 | 5.0E-68 | AF23191.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 2707 | 7664 | 12775 | 1.09 | 5.0E-68 | AF23191.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 3074 | 8090 | 13104 | 3.02 | 5.0E-68 | AB037852.1 | NT | Homo sapiens mRNA for KIAA1431 protein, partial cds |
| 4057 | 8051 | | 0.68 | 5.0E-68 | 4826967 NT | | Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA |
| 4363 | 9354 | 14333 | 0.66 | 5.0E-68 | AL157645.1 | EST_HUMAN | DKFZp547D207_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D207 5' |
| 2456 | 7426 | 12540 | 1.15 | 4.0E-68 | 11421388 NT | | Homo sapiens transcription factor NRF (NRF), mRNA |
| 2456 | 7426 | 12541 | 1.15 | 4.0E-68 | 11421388 NT | | Homo sapiens transcription factor NRF (NRF), mRNA |
| 4816 | 9800 | | 16.14 | 4.0E-68 | P04406 SWISSPROT | | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER |
| 3577 | 8584 | 13589 | 7.2 | 3.0E-68 | AF236082.1 | NT | Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds |
| 2791 | 10054 | | 39.36 | 2.0E-68 | D00522.1 | NT | Cricetulus lori/caudatus mRNA for EIF-1 alpha, complete cds |
| 3915 | 8915 | 13909 | 0.68 | 2.0E-68 | BE67576.1 | EST_HUMAN | 715f02.x1 NCI CGAP_CLI_1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:080828 O80828 |
| 4543 | 9532 | 14520 | 1.64 | 2.0E-68 | AB009681.1 | NT | Homo sapiens gene for actinin receptor type IIb, complete cds |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|--|
| | | | | | | | | |
| 78 | 5155 | 10166 | 0.94 | 1.0E-68 | 45052222 | NT | Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA | |
| 294 | 5351 | 10364 | 11.12 | 1.0E-68 | AW816405.1 | EST_HUMAN | QV4-ST0234-181189-03-f05 ST0234 Homo sapiens cDNA | |
| 2190 | 7169 | 12289 | 1.74 | 1.0E-68 | AB011149.1 | NT | Homo sapiens mRNA for KIAA0577 protein, complete cds | |
| 2190 | 7169 | 12290 | 1.74 | 1.0E-68 | AB011149.1 | NT | Homo sapiens mRNA for KIAA0577 protein, complete cds | |
| 3903 | 8903 | 13901 | 0.97 | 1.0E-68 | BE296032.1 | EST_HUMAN | 601177002f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5' | |
| 4901 | 9880 | 14849 | 1.18 | 1.0E-68 | BE296032.1 | EST_HUMAN | 601177002f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5' | |
| 20 | 5100 | 10083 | 7.87 | 9.0E-69 | 5031976 | NT | Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA | |
| 20 | 5100 | 10084 | 7.87 | 9.0E-69 | 5031976 | NT | Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA | |
| 1011 | 6021 | 11050 | 2.59 | 9.0E-69 | 5031980 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA | |
| 1011 | 6021 | 11051 | 2.59 | 9.0E-69 | 5031980 | NT | Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA | |
| 5035 | 10006 | 14977 | 0.94 | 9.0E-69 | 4507164 | NT | Homo sapiens nuclear antigen Sp100 (SP100) mRNA | |
| 3302 | 8313 | | 1.28 | 8.0E-69 | AJ237744.1 | NT | Homo sapiens RIBLIR gene (partial), exon 12 | |
| 516 | 5551 | | 0.99 | 4.0E-69 | AI873630.1 | EST_HUMAN | wm26h11_x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3' | |
| 385 | 5460 | 10478 | 5.07 | 3.0E-69 | BE258012.1 | EST_HUMAN | 60110371f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5' | |
| 608 | 5635 | 10636 | 2.03 | 3.0E-69 | AF221712.1 | NT | Homo sapiens Smad- and Olfr-interacting zinc finger protein mRNA, partial cds | |
| 1524 | 6521 | | | | | | yd08a02_r1 Scores infant brain 1NB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP_A48836 | |
| 4804 | 9788 | 14771 | 1.63 | 3.0E-69 | T80514.1 | EST_HUMAN | A48836 SPEGF III=EGF REPEAT-CONTAINING FIBROPELLIN-LIKE PROTEIN - SEA URCHIN ; | |
| 4804 | 9788 | 14771 | 0.97 | 3.0E-69 | AB037732.1 | NT | Homo sapiens mRNA for KIAA1311 protein, partial cds | |
| 4971 | 8965 | 13954 | 1.66 | 3.0E-69 | AI765888.1 | EST_HUMAN | wh66gp8_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3' | |
| 129 | 5438 | 10457 | 2.01 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1hb protein gene, partial cds | |
| 129 | 5438 | 10458 | 2.01 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1hb protein gene, partial cds | |
| 402 | 5438 | 10457 | 5.22 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1hb protein gene, partial cds | |
| 402 | 5438 | 10458 | 5.22 | 2.0E-69 | AF160252.1 | NT | Homo sapiens KIAA0553 protein gene, complete cds; and alpha1hb protein gene, partial cds | |
| 1846 | 6835 | 11926 | 2.59 | 2.0E-69 | BE257887.1 | EST_HUMAN | 60110944f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5' | |
| 2770 | 7791 | | 3.44 | 2.0E-69 | AA431157.1 | EST_HUMAN | zw716g02_r1 Soares testis NIH Homo sapiens cDNA clone IMAGE:781682 5' | |
| 4970 | 9947 | 14924 | 1.2 | 2.0E-69 | 4504148 | NT | Homo sapiens glutamate receptor, metabotropic 8 (GRM8) mRNA | |
| 4970 | 9947 | 14925 | 1.2 | 2.0E-69 | 4504148 | NT | Homo sapiens glutamate receptor, metabotropic 8 (GRM8) mRNA | |
| 1664 | 6660 | 11734 | 1.7 | 1.0E-69 | AF053768.1 | NT | Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds | |
| 2270 | 7766 | 12363 | 1.55 | 8.0E-70 | AA230303.1 | EST_HUMAN | nc13d12_r1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023 | |
| 4248 | 9242 | 14226 | 2 | 8.0E-70 | L77566.1 | NT | Homo sapiens DGS-I mRNA, 3' end | |
| 1777 | 6769 | 11860 | 4.59 | 7.0E-70 | AI497807.1 | EST_HUMAN | tm8901_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3' | |
| 1777 | 6769 | 11861 | 4.59 | 7.0E-70 | AI497807.1 | EST_HUMAN | tm8901_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3' | |
| 1890 | 6879 | 11969 | 2.37 | 7.0E-70 | AA282955.1 | EST_HUMAN | z15h04_r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5' | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 2011 | 6994 | | 6.81 | 7.0E-70 | 5031668 NT | | Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA |
| 4103 | 9097 | 14083 | 3.55 | 7.0E-70 | 4757723 NT | | Homo sapiens adenylylate cyclase 3 (ADCY3) mRNA |
| 860 | 5879 | 10920 | 4.09 | 6.0E-70 | 4502166 NT | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 2078 | 7059 | 12169 | 4.32 | 6.0E-70 | M30938.1 NT | | Human Ku (p70/p80) subunit mRNA, complete cds |
| 2437 | 7408 | 12525 | 1.12 | 6.0E-70 | 8923899 NT | | Homo sapiens CMF-N-acetylneuraminic acid synthase (LOC55907), mRNA |
| 2481 | 7772 | 12561 | 1.53 | 5.0E-70 | 7662307 NT | | Homo sapiens KIAA0792 gene product (KIAA0792), mRNA |
| 2481 | 7772 | 12562 | 1.53 | 5.0E-70 | 7662307 NT | | Homo sapiens KIAA0792 gene product (KIAA0792), mRNA |
| 1554 | 6551 | 11610 | 3.24 | 3.0E-70 | BE071796.1 EST_HUMAN | RC0-BT0522-0712989-011-a12 BT0522 Homo sapiens cDNA | |
| 1554 | 6551 | 11611 | 3.24 | 3.0E-70 | BE071796.1 EST_HUMAN | RC0-BT0522-0712989-011-a12 BT0522 Homo sapiens cDNA | |
| 39 | 5119 | 10107 | 1.16 | 2.0E-70 | AF012872.1 NT | | Homo sapiens phosphatidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds |
| 680 | 5705 | 10714 | 11.75 | 2.0E-70 | N42161.1 EST_HUMAN | yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3H1_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR; | |
| 680 | 5705 | 10715 | 11.75 | 2.0E-70 | N42161.1 EST_HUMAN | yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3H1_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR; | |
| 69 | 5719 | 10737 | 1.73 | 2.0E-70 | A1246599.1 EST_HUMAN | q51h01_x1_NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3' | |
| 1005 | 6015 | 11045 | 2.33 | 2.0E-70 | B923669 NT | Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA | |
| 1165 | 6198 | 11202 | 1.5 | 2.0E-70 | 7661983 NT | Homo sapiens KIAA0193 gene product (KIAA0193), mRNA | |
| 1165 | 6198 | 11203 | 1.5 | 2.0E-70 | 7661983 NT | Homo sapiens KIAA0193 gene product (KIAA0193), mRNA | |
| 1615 | 6612 | 11678 | 1.22 | 2.0E-70 | AA180093.1 EST_HUMAN | zz45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR-G1041293 G1041293 D2085.5; | |
| 1615 | 6612 | 11679 | 1.22 | 2.0E-70 | AA180093.1 EST_HUMAN | zz45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR-G1041293 G1041293 D2085.5; | |
| 1703 | 6698 | 11774 | 1.85 | 2.0E-70 | AL1763202.2 NT | Homo sapiens chromosome 21 segment HS21C002 | |
| 2256 | 7233 | | 7.98 | 2.0E-70 | AA054010.1 EST_HUMAN | Z48g04.r1 Soares retina N284HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A P03345 GAC POLYPROTEIN; | |
| 2415 | 7386 | 12506 | 1.57 | 2.0E-70 | AB011173.1 NT | Homo sapiens mRNA for KIAA0601 protein, partial cds | |
| 3128 | 8732 | 13730 | 1.26 | 2.0E-70 | AL133207.2 NT | Novel human gene mapping to chromosome X | |
| 3838 | 8840 | 13847 | 1.17 | 2.0E-70 | AJ246003.1 NT | Homo sapiens Spast gene for spastic protein | |
| 3936 | 8935 | 13928 | 4.94 | 2.0E-70 | M69181.1 NT | Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds | |
| 4069 | 9063 | 14051 | 1.03 | 2.0E-70 | L78810.1 NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds | |
| 4069 | 9063 | 14052 | 1.03 | 2.0E-70 | L78810.1 NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds | |
| 3309 | 8320 | | 3.18 | 1.0E-70 | 4507476 NT | Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGm3) mRNA | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2148 | 7127 | 12244 | 14.02 | 5.0E-71 | AF056322.1 | NT | Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds |
| 4001 | 8997 | 13986 | 0.87 | 5.0E-71 | AW816405.1 | EST_HUMAN | QV4-ST0234-131189-037-055 ST0234 Homo sapiens cDNA |
| 103 | 5180 | 10191 | 0.97 | 4.0E-71 | 4507592 | NT | Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA |
| 348 | 5400 | 10409 | 215.31 | 4.0E-71 | AF157626.1 | NT | Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds |
| 348 | 5400 | 10410 | 215.31 | 4.0E-71 | AF157626.1 | NT | Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds |
| 2816 | 7836 | 12851 | 1.81 | 4.0E-71 | 45058880 | NT | Homo sapiens plasminogen (PLG) mRNA |
| 4304 | 9296 | 14282 | 7.98 | 4.0E-71 | AF056322.1 | NT | Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds |
| 4827 | 9811 | 14792 | 6.12 | 4.0E-71 | 7657602 | NT | Homo sapiens putative heme-binding protein (SOUL) mRNA |
| 1210 | 6210 | 11250 | 16.61 | 2.0E-71 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| | | | | | | | oy15603.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to |
| 632 | 5660 | 10665 | 1.87 | 1.0E-71 | AJ077927.1 | EST_HUMAN | contains LOR1 b2 LOR1 repetitive element; |
| 927 | 5944 | 10978 | 6.13 | 1.0E-71 | 7706281 | NT | Homo sapiens neuronal cell death-related protein (LOC51616) mRNA |
| 1083 | 6080 | 11119 | 4.33 | 1.0E-71 | AF205890.1 | NT | Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds |
| 1320 | 6318 | 11366 | 8.38 | 1.0E-71 | AF012872.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds |
| 2029 | 7012 | 12120 | 1.35 | 1.0E-71 | AB017007.1 | NT | Homo sapiens PMS2L16 mRNA, partial cds |
| 2029 | 7012 | 12121 | 1.35 | 1.0E-71 | AB017007.1 | NT | Homo sapiens PMS2L16 mRNA, partial cds |
| 2621 | 7583 | 12693 | 3.09 | 1.0E-71 | 7657153 | NT | Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEY1) mRNA |
| 3422 | 8430 | 13456 | 2.36 | 1.0E-71 | AF119665.1 | NT | Homo sapiens inorganic pyrophosphatase mRNA, complete cds |
| 3516 | 8524 | 13534 | 5.34 | 1.0E-71 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 3516 | 8524 | 13535 | 5.34 | 1.0E-71 | AF246219.1 | NT | Homo sapiens SNARE protein kinase SNAK mRNA, complete cds |
| 3563 | 8570 | 13575 | 0.73 | 1.0E-71 | BE122850.1 | EST_HUMAN | 02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19 |
| 3563 | 8570 | 13576 | 0.73 | 1.0E-71 | BE122850.1 | EST_HUMAN | 02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19 |
| 3656 | 8582 | 13667 | 1.73 | 1.0E-71 | AF218904.1 | NT | Homo sapiens attractin precursor (ATRN) gene, exon 19 |
| 4345 | 9336 | 14319 | 2.05 | 1.0E-71 | D28476.1 | NT | Human mRNA for KIAA045 gene, complete cds |
| 4460 | 9450 | 14431 | 1.19 | 1.0E-71 | H23176.1 | EST_HUMAN | ym56h10.11 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 |
| 405 | 5441 | 10460 | 0.74 | 9.0E-72 | A1857635.1 | EST_HUMAN | wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' contains Alu repetitive element, |
| 405 | 5441 | 10461 | 0.74 | 9.0E-72 | A1857635.1 | EST_HUMAN | wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 |
| 3965 | 8992 | 13977 | 1.54 | 7.0E-72 | 4501866 | NT | Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit No. | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-------------|---|-------------------------|--|
| 3996 8982 | 13978 | 1.54 | 7.0E-72 | 4501866 NT | | | | Homo sapiens acconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA |
| 3996 8992 | 13979 | 1.54 | 7.0E-72 | 4501866 NT | | | | Homo sapiens acconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA |
| 64 5144 | 10148 | 2.81 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA | | |
| 64 5144 | 10149 | 2.81 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA | | |
| 65 5144 | 10148 | 18.08 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA | | |
| 65 5144 | 10149 | 18.08 | 5.0E-72 | BF333707.1 | EST_HUMAN | QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA | | |
| 1122 6128 | | 2.73 | 5.0E-72 | L11645.1 | NT | | | Homo sapiens alpha-tubulin mRNA, complete cds |
| 4676 9661 | | 1.32 | 4.0E-72 | 11034844 NT | | | | Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA |
| 5048 100119 | 14988 | 1.07 | 4.0E-72 | AB033104.1 | NT | | | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 19 5099 | 10082 | 2.48 | 3.0E-72 | 50311976 NT | | | | Homo sapiens pre-B-cell colony-enhancing factor (PBCEF) mRNA |
| 892 5910 | | 1.27 | 3.0E-72 | AA723823.1 | EST_HUMAN | ah63a06.s1 Scares testis_ Homo sapiens cDNA clone 1310290 3' | | |
| 1137 6142 | 11171 | 11.37 | 3.0E-72 | U16306.1 | NT | | | Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds |
| 1137 6142 | 11172 | 11.37 | 3.0E-72 | U16306.1 | NT | | | Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds |
| 1174 6177 | 11211 | 1.12 | 3.0E-72 | U80226.1 | NT | | | Human gamma-aminobutyric acid transaminase mRNA, partial cds |
| 1174 6177 | 11212 | 1.12 | 3.0E-72 | U80226.1 | NT | | | Human gamma-aminobutyric acid transaminase mRNA, partial cds |
| 3001 8019 | 13032 | 12.79 | 3.0E-72 | AJ228043.1 | NT | | | Human segment 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 3205 8220 | 13242 | 2.5 | 3.0E-72 | 8923548 NT | | | | Human hypothetical protein FLJ20585 (FLJ20585), mRNA |
| 3732 8736 | 13734 | 3.01 | 3.0E-72 | S77589.1 | NT | | | TCR V delta 2-C alpha -T-cell receptor delta and C alpha fusion gene [alternatively spliced, splice junction] human, precursor B-cell line REH, mRNA Partial_211 nt] |
| 4414 9404 | 14389 | 3.55 | 3.0E-72 | 11416196 NT | | | | Human hypothetical protein (FLJ11127), mRNA |
| 4621 9606 | 14593 | 1.08 | 3.0E-72 | AF167572.1 | NT | | | Human sapiens protein methyltransferase (JBP-1) mRNA, complete cds |
| 4621 9606 | 14594 | 1.08 | 3.0E-72 | AF167572.1 | NT | | | Human sapiens protein methyltransferase (JBP-1) mRNA, complete cds |
| 2022 7005 | 12110 | 1.03 | 1.0E-72 | AA846225.1 | EST_HUMAN | a183d02.s1 Scares_parathyroid tumor_NBHPA_Homo sapiens cDNA clone IMAGE_1387395 3' | | |
| 1433 6430 | 11486 | 1.25 | 9.0E-73 | AW374988.1 | EST_HUMAN | MRO-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA | | |
| 1021 6030 | | | | | | ws55c08.X11 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE_2501098 3' similar to TR:Q58050 | | |
| 1117 6123 | 11153 | 0.98 | 7.0E-73 | 8923290 NT | | | | Q59050 HYPOTHETICAL PROTEIN MJ1656. ; Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA |
| 3227 8242 | 13284 | 1.64 | 7.0E-73 | AL163206.2 | NT | | | Hom sapiens chromosome 21 segment HS21C008 |
| 4787 9771 | | 1.48 | 7.0E-73 | AL163282.2 | NT | | | Hom sapiens chromosome 21 segment HS21C082 |
| 157 | 5223 | 1.71 | 6.0E-73 | AL163218.2 | NT | | | Hom sapiens chromosome 21 segment HS21C018 |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 1321 | 6319 | 11367 | 1.38 | 3.0E-73 | AW843769.1 | EST_HUMAN | CN0-CN0044-260100-164-f08 CN0044 Homo sapiens cDNA |
| 1825 | 6815 | 11909 | 1.1 | 3.0E-73 | 11435913 | NT | Homo sapiens heme-binding protein (HEBP) mRNA |
| 1825 | 6815 | 11910 | 1.1 | 3.0E-73 | 11435913 | NT | Homo sapiens heme-binding protein (HEBP) mRNA |
| 841 | 5860 | 10900 | 2.37 | 2.0E-73 | AF135897.1 | NT_HUMAN | Homo sapiens BASS1 (BASS1) mRNA, partial cds |
| 1906 | 6893 | | 3.12 | 2.0E-73 | AW898081.1 | EST_HUMAN | RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA |
| 3108 | 8124 | 13143 | 3.99 | 2.0E-73 | 4502582 | NT | Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA |
| 4311 | 9303 | | 1.02 | 2.0E-73 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 1745 | 6740 | 11819 | 2.61 | 1.0E-73 | AU121585 | MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5' | |
| 2413 | 7384 | 12503 | 1.04 | 1.0E-73 | AF198349.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 731 | 5754 | 10775 | 1.76 | 8.0E-74 | 4557426 | NT | Homo sapiens CD39-like 4 (CD39L4) mRNA |
| 1909 | 6895 | 11989 | 2.57 | 7.0E-74 | AJ001689.1 | NT | Homo sapiens NKGD2 gene, exon 10 |
| 3253 | 8266 | 13288 | 1.22 | 7.0E-74 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| | | | | | | | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 1106 | 6112 | 11143 | 4 | 6.0E-74 | AF109967.1 | NT | |
| 1587 | 6584 | 11645 | 0.92 | 6.0E-74 | AW263177.1 | EST_HUMAN | Xn78g07_x1 Spares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3' |
| 2252 | 7229 | 12347 | 63.86 | 6.0E-74 | BE388260.1 | EST_HUMAN | 601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5' |
| 2252 | 7229 | 12348 | 53.86 | 6.0E-74 | BE388260.1 | EST_HUMAN | 601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5' |
| 2793 | 7813 | 12831 | 0.97 | 6.0E-74 | AW014039.1 | EST_HUMAN | U1-H-B10-aaH-h-03-0-U1_s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3' |
| 2793 | 7813 | 12832 | 0.97 | 6.0E-74 | AW014039.1 | EST_HUMAN | U1-H-B10-aaH-h-03-0-U1_s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3' |
| 3631 | 8637 | 13642 | 1.37 | 6.0E-74 | BE048846.1 | EST_HUMAN | hr54a11_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3' |
| 3631 | 8637 | 13643 | 1.37 | 6.0E-74 | BE048846.1 | EST_HUMAN | hr54a11_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3' |
| 4866 | 9846 | 14821 | 1.55 | 6.0E-74 | 4758135 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA |
| 4866 | 9846 | 14822 | 1.55 | 6.0E-74 | 4758135 | NT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA |
| 894 | 5912 | 10951 | 2.15 | 5.0E-74 | AW020986.1 | EST_HUMAN | df17g09_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5' |
| 2630 | 7590 | | 6.51 | 5.0E-74 | AW362756.1 | EST_HUMAN | PM0-CT028t-271089-001-h07 CT0289 Homo sapiens cDNA |
| 2777 | 5335 | 10349 | 5.48 | 4.0E-74 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 842 | 5861 | 10901 | 5.8 | 4.0E-74 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 1922 | 6908 | 12002 | 1.42 | 4.0E-74 | AB026898.1 | NT | Homo sapiens DNA, DLEc1 to ORCTL4 gene region, section 1/2 (DLEc1, ORCTL3, ORCTL4 genes, complete cds) |
| 1922 | 6908 | 12003 | 1.42 | 4.0E-74 | AB026898.1 | NT | Homo sapiens DNA, DLEc1 to ORCTL4 gene region, section 1/2 (DLEc1, ORCTL3, ORCTL4 genes, complete cds) |
| 2019 | 7002 | 12106 | 5.12 | 4.0E-74 | 4506192 | NT | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2019 | 7002 | 12107 | 5.12 | 4.0E-74 | 4506192 | NT | Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA |
| 2074 | 7056 | 12166 | 1.18 | 4.0E-74 | AB032984.1 | NT | Homo sapiens mRNA for KIAA1168 protein, partial cds |
| 3017 | 8034 | 13045 | 5.03 | 4.0E-74 | AJ006976.1 | NT | Homo sapiens PLP gene |
| 3449 | 8457 | 13483 | 0.81 | 4.0E-74 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3950 | 8948 | 13937 | 1.22 | 4.0E-74 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 4425 | 9415 | 14402 | 1.86 | 4.0E-74 | 76621183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 4481 | 9471 | 14452 | 1.19 | 4.0E-74 | Z17227.1 | NT | Homo sapiens mRNA for transmembrane receptor protein |
| 4902 | 9881 | 14850 | 1.02 | 4.0E-74 | 4504326 | NT | Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoady-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (if functional protein), beta subunit (HADHB) mRNA |
| 4902 | 9881 | 14851 | 1.02 | 4.0E-74 | 4504328 | NT | Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoady-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (if functional protein), beta subunit (HADHB) mRNA |
| 5011 | 9882 | 14957 | 0.91 | 4.0E-74 | AB037863.1 | NT | Homo sapiens mRNA for KIAA1442 protein, partial cds |
| 943 | 5980 | 10993 | 263.61 | 2.0E-74 | 7669491 | NT | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA |
| 943 | 5980 | 10994 | 263.61 | 2.0E-74 | 7669491 | NT | Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA |
| 1156 | 6160 | 11194 | 1.2 | 2.0E-74 | AF020092.1 | NT | Human endogenous retrovirus HERV-K-T47D |
| 1225 | 6224 | 11270 | 2.76 | 2.0E-74 | AI950528.1 | EST_HUMAN | wx51e07.X1\CI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN_95 .contains element MER22 repetitive element ; Homo sapiens epidermal growth factor receptor (avian erythroblastotic leukemia viral (v-erb-b) oncogene homolog) (ECFR) mRNA |
| 1560 | 6557 | 11618 | 3.33 | 2.0E-74 | 4885198 | NT | Homo sapiens epidermal growth factor receptor (avian erythroblastotic leukemia viral (v-erb-b) oncogene homolog) (ECFR) mRNA |
| 1560 | 6557 | 11619 | 3.33 | 2.0E-74 | 4885198 | NT | Homo sapiens epidermal growth factor receptor (avian erythroblastotic leukemia viral (v-erb-b) oncogene homolog) (ECFR) mRNA |
| 2526 | 7492 | 12612 | 3.89 | 2.0E-74 | AI557280.1 | EST_HUMAN | PT2.15_G11.1 tumor2 Homo sapiens cDNA 3' |
| 4846 | 9828 | 14802 | 2.77 | 2.0E-74 | AL355092.1 | NT | Novel human gene mapping to chromosome 22 |
| 4846 | 9828 | 14803 | 2.77 | 2.0E-74 | AL355092.1 | NT | Novel human gene mapping to chromosome 22 |
| 4850 | 9832 | 14807 | 3.98 | 2.0E-74 | J02963.1 | NT | Human platelet glycoprotein IIb mRNA, 3' end |
| 54 | 5135 | 10132 | 2.92 | 1.0E-74 | 7657334 | NT | Homo sapiens Misshepar/NIK-related kinase (MINK), mRNA |
| 335 | 5387 | 10394 | 4.23 | 1.0E-74 | AW816405.1 | EST_HUMAN | QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA |
| 496 | 5532 | 10539 | 1.19 | 1.0E-74 | 89222829 | NT | Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA |
| 503 | 5538 | 10544 | 29.7 | 1.0E-74 | X02344.1 | NT | Homo sapiens beta 2 gene |
| 596 | 5627 | 10623 | 2.36 | 1.0E-74 | 4508020 | NT | Homo sapiens zinc finger protein 259 (ZNF259) mRNA |
| 984 | 5999 | 11030 | 2.04 | 1.0E-74 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 2165 | 7144 | 12262 | 5 | 1.0E-74 | AB002059.1 | NT | Homo sapiens DNA for Human P2XIV, complete cds |
| 3066 | 8082 | 13096 | 3.19 | 1.0E-74 | 4758697 | NT | Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA |
| 3822 | 8824 | 13831 | 0.67 | 1.0E-74 | 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3822 | 8824 | 13832 | 0.67 | 1.0E-74 | 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 3861 | 8853 | 13868 | 4.97 | 1.0E-74 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 4145 | 9140 | 14124 | 1.12 | 1.0E-74 | BE467769.1 | EST_HUMAN | In273h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:BO511.12 |
| 2573 | 7536 | | 3.52 | 8.0E-75 | AF176228.1 | NT | Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds CE17351 ; wk38a08.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4 |
| 2257 | 7234 | 12352 | 0.98 | 6.0E-75 | AI817415.1 | EST_HUMAN | RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); |
| 1112 | 5184 | 10193 | 3.57 | 4.0E-75 | BE081333.1 | EST_HUMAN | QV1-BT0632-21 02020-076-802_BT0632 Homo sapiens cDNA |
| 456 | 5493 | | 0.99 | 4.0E-75 | N36757.1 | EST_HUMAN | ys0n08.r1 Soes melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2659055 5' |
| 1728 | 6723 | 11801 | 1.27 | 4.0E-75 | AW897230.1 | EST_HUMAN | CMD-NN0057-15040-335-a11 NN0057 Homo sapiens cDNA |
| 2776 | 7797 | 12816 | 5.17 | 4.0E-75 | BE409464.1 | EST_HUMAN | MGCC_21 Homo sapiens cDNA clone IMAGE:3638344 5' |
| 3421 | 8428 | 13455 | 0.97 | 4.0E-75 | 8922637 | NT | Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA |
| 987 | 6002 | 11033 | 2.28 | 3.0E-75 | AF157623.1 | NT | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |
| 988 | 6002 | 11033 | 2.29 | 3.0E-75 | AF157623.1 | NT | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |
| 1800 | 6791 | 11881 | 1.84 | 3.0E-75 | AB011153.1 | NT | Homo sapiens mRNA for KIAA0581 protein, partial cds |
| 1837 | 6876 | 11966 | 2.26 | 3.0E-75 | 5453871 | NT | Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA |
| 2053 | 7035 | 12147 | 0.92 | 3.0E-75 | 4507334 | NT | Homo sapiens synaptotagmin 1 (SYN1), mRNA |
| 2356 | 7330 | 12446 | 3.59 | 3.0E-75 | 4759153 | NT | Homo sapiens synaptosomal-associated protein, 25kD (SNAP29) mRNA |
| 2955 | 7974 | 12989 | 0.8 | 3.0E-75 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3116 | 8132 | 13151 | 1.01 | 3.0E-75 | AB011153.1 | NT | Homo sapiens mRNA for KIAA0581 protein, partial cds |
| 3273 | 8285 | 13308 | 0.75 | 3.0E-75 | M72393.1 | NT | Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds |
| 3273 | 8285 | 13309 | 0.75 | 3.0E-75 | M72393.1 | NT | Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds |
| 4044 | 9040 | 14031 | 1.58 | 3.0E-75 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4314 | 9306 | 14290 | 0.82 | 3.0E-75 | 7662421 | NT | Homo sapiens KIAA0977 protein (KIAA0977), mRNA |
| 4996 | 9968 | | 0.82 | 3.0E-75 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C069 |
| 2239 | 7216 | 12334 | 30.85 | 1.0E-75 | AW168135.1 | EST_HUMAN | xg60d02.x1 NCI_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11 PTR7 repetitive element; |
| 2876 | 7895 | 12819 | 3.35 | 1.0E-75 | X52221.1 | NT | H sapiens ERCC2 gene, exons 1 & 2 (partial) |
| 4552 | 9540 | 14525 | 1.71 | 1.0E-75 | BE279301.1 | EST_HUMAN | 6011576331F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5' |
| 4993 | 9965 | 14943 | 1.23 | 1.0E-75 | BE894192.1 | EST_HUMAN | 601437730F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5' |
| 45 | 5126 | 10116 | 3.62 | 9.0E-76 | AI652648.1 | EST_HUMAN | wb630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235_O75235 |
| 45 | 5126 | 10117 | 3.62 | 9.0E-76 | AI652648.1 | EST_HUMAN | TRAP1 ; wb630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235_O75235 |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 924 | 5941 | 10974 | 0.84 | 8.0E-6 | 4504374 | NT | Homo sapiens H factor 1 (complement) (HF1) mRNA |
| 924 | 5941 | 10975 | 0.84 | 8.0E-6 | 4504374 | NT | Homo sapiens H factor 1 (complement) (HF1) mRNA |
| 2839 | 7859 | 12879 | 1.17 | 8.0E-6 | 706724 | NT | Homo sapiens mediator (Sur2) mRNA |
| 767 | 5788 | 10817 | 1.86 | 7.0E-6 | 5016092 | NT | Homo sapiens dihydrodipamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA |
| 3220 | 8235 | 13256 | 3.47 | 7.0E-6 | AF056390.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 3226 | 8241 | 13263 | 7.12 | 7.0E-6 | 4505052 | NT | Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products |
| 4246 | 9240 | 14223 | 4.97 | 7.0E-6 | 4507184 | NT | Homo sapiens sepiapterin reductase [7'-8-dihydrobiopterin:NADP+ oxidoreductase] (SPR) mRNA |
| 4246 | 9240 | 14224 | 4.97 | 7.0E-6 | 4507184 | NT | Homo sapiens sepiapterin reductase [7'-8-dihydrobiopterin:NADP+ oxidoreductase] (SPR) mRNA |
| 1214 | 6213 | | | 16.64 | 6.0E-76 | BE396253.1 | EST_HUMAN |
| 1903 | 6890 | 11983 | 15.24 | 5.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 1903 | 6890 | 11984 | 15.24 | 5.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 1903 | 6890 | 11985 | 15.24 | 5.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 3134 | 8150 | 13172 | 0.8 | 4.0E-76 | BE814096.1 | EST_HUMAN | QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA IMAGE:3083862 3' |
| 623 | 5650 | 10653 | 1.54 | 3.0E-76 | BF516262.1 | EST_HUMAN | U1-H-BW7-tanz-b-04-0-U1,s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3' |
| 623 | 5650 | 10654 | 1.54 | 3.0E-76 | BF516262.1 | EST_HUMAN | U1-H-BW7-tanz-b-04-0-U1,s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3' |
| 1564 | 6561 | 11623 | 21.41 | 3.0E-76 | 4503476 | NT | Homo sapiens: eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA |
| 1564 | 6561 | 11624 | 21.41 | 3.0E-76 | 4503476 | NT | Homo sapiens: eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA |
| 3344 | 8353 | 13370 | 6.25 | 3.0E-76 | BF375689.1 | EST_HUMAN | RC5-ST0300-180100-033-A03 S10300 Homo sapiens cDNA |
| 3344 | 8353 | 13371 | 6.25 | 3.0E-76 | BF375689.1 | EST_HUMAN | RC5-ST0300-180100-033-A03 S10300 Homo sapiens cDNA |
| 279 | 5337 | 10351 | 1 | 2.0E-76 | D84295.1 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 340 | 5392 | 10398 | 1.94 | 2.0E-76 | D84295.1 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 340 | 5392 | 10399 | 1.94 | 2.0E-76 | D84295.1 | NT | Human mRNA for possible protein TPRDII, complete cds |
| 458 | 5495 | | 1.42 | 2.0E-76 | 4557662 | NT | Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA |
| 585 | 5616 | 10615 | 1.68 | 2.0E-76 | 4503944 | NT | Human sapiens glucagon (GCG) mRNA |
| 1014 | 6024 | 11056 | 1.16 | 2.0E-76 | 4758053 | NT | Human sapiens cAMP responsive element binding protein 1 (CREB1) mRNA |
| 1504 | 6502 | 11558 | 2.34 | 2.0E-76 | 4504028 | NT | Human sapiens GM2 ganglioside activator protein (GM2A) mRNA |
| 1504 | 6502 | 11559 | 2.34 | 2.0E-76 | 4504028 | NT | Human sapiens GM2 ganglioside activator protein (GM2A) mRNA |
| 2768 | 7789 | 12811 | 3.35 | 2.0E-76 | P23266 | SWISSPROT | OLFACCTOR RECEPTOR-LIKE PROTEIN FG |
| 3223 | 8238 | 13260 | 1.89 | 2.0E-76 | AA445992.1 | EST_HUMAN | ZM64e02_s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.; |
| 3223 | 8238 | 13261 | 1.89 | 2.0E-76 | AA445992.1 | EST_HUMAN | ZM64e02_s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.; |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 3396 | 8404 | 13430 | 1.04 | 2.0E-76 | AI821149.1 | EST_HUMAN | ae83b02.y5 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:743396 5' similar to TR:O14591 O14591 SIMILARITY TO P22059 ; |
| 3682 | 8656 | 13688 | 7.33 | 2.0E-76 | AA40700.1 | EST_HUMAN | ZU70g11.1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:743396 5' similar to WP:R05D3.2 CE00281 ; |
| 4400 | 8391 | 14975 | 1 | 2.0E-76 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 4790 | 9774 | 14758 | 6.31 | 2.0E-76 | AW879618.1 | EST_HUMAN | QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA |
| 4173 | 9168 | 14755 | 5.78 | 1.0E-76 | D63874.1 | NT | Human mRNA for HMG-1, complete cds |
| 4173 | 9168 | 14156 | 5.78 | 1.0E-76 | D63874.1 | NT | Human mRNA, for HMG-1, complete cds |
| 187 | 5250 | 10261 | 3.03 | 8.0E-77 | R83144.1 | EST_HUMAN | Yp11h02.11 Scares_breast_3NbHBst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP_ANKB_HUMAN Q01484 ANKYRN BRAIN VARIANT 1 ; |
| 4391 | 9382 | 14364 | 1.16 | 8.0E-77 | BF205181.1 | EST_HUMAN | 6018866926F1 NIH_MGC_C_17 Homo sapiens cDNA clone IMAGE:4109503 5' |
| 1889 | 6878 | 11988 | 1.52 | 7.0E-77 | AA625755.1 | EST_HUMAN | ZU91g01.s1 Scares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3' |
| 2345 | 7319 | 12459 | 9.62 | 7.0E-77 | 4505944 NT | Hom sapiens: polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA | |
| 250 | 5319 | 10329 | 5.1 | 6.0E-77 | 4505944 NT | Hom sapiens: polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA | |
| 1511 | 6509 | 11566 | 2.09 | 6.0E-77 | A1204066.1 | EST_HUMAN | Homo sapiens: interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA |
| 4772 | 9756 | 14743 | 0.98 | 6.0E-77 | 4557752 NT | Hom sapiens: midline 1 (Optiz/BBB syndrome) (MID1) mRNA | |
| 4772 | 9756 | 14744 | 0.98 | 6.0E-77 | 4557752 NT | Hom sapiens: midline 1 (Optiz/BBB syndrome) (MID1) mRNA | |
| 1216 | 6215 | 11255 | 1.5 | 5.0E-77 | AF041015.1 | NT | 7 Homo sapiens glucokinase (GCK) gene, exon 2 |
| 1343 | 6340 | 11391 | 2.76 | 5.0E-77 | 4557250 NT | Hom sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA | |
| 2613 | 7575 | 12689 | 1.11 | 5.0E-77 | AF16266.1 | NT | Hom sapiens lysed-like kinase 1 (TLK1) mRNA, complete cds |
| 2690 | 7848 | 12762 | 1.24 | 5.0E-77 | 4503160 NT | Hom sapiens cullin 1 (CUL1) mRNA | |
| 3443 | 8451 | 13478 | 1.75 | 5.0E-77 | 8394518 NT | Hom sapiens ubiquitin specific protease 18 (USP18) mRNA | |
| 4565 | 9553 | 14539 | 0.99 | 5.0E-77 | 5031660 NT | Hom sapiens EGF-like repeats and discoidin like domains 3 (EDIL3) mRNA | |
| 4565 | 9553 | 14540 | 0.99 | 5.0E-77 | 5031660 NT | Hom sapiens EGF-like repeats and discoidin like domains 3 (EDIL3) mRNA | |
| 4780 | 9764 | 14749 | 2.68 | 5.0E-77 | AL043953.1 | EST_HUMAN | DKFZp43TG1728_r1_434 (synonym: lites3) Homo sapiens cDNA clone DKFZp43TG1728 5' |
| 3620 | 8627 | 13634 | 1.93 | 4.0E-77 | AL449758.1 | EST_HUMAN | AL449758 Homo sapiens fetal brain (Slavkides GS) Homo sapiens cDNA RC3-BN0053-170200-011-h01 BN0053 |
| 1928 | 6914 | 12010 | 1.57 | 3.0E-77 | 5730038 NT | Hom sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA | |
| 1928 | 6914 | 12011 | 1.57 | 3.0E-77 | 5730038 NT | Hom sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA | |
| 1334 | 6332 | 11380 | 2.09 | 2.0E-77 | AV764617.1 | EST_HUMAN | AV764617 MDS Homo sapiens cDNA clone MDSBTf10 5' |
| 1407 | 6405 | 11464 | 7.17 | 2.0E-77 | AW897712.1 | EST_HUMAN | RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA |
| 2045 | 7027 | 12138 | 5.42 | 2.0E-77 | 7706315 NT | Hom sapiens CGI-79 protein (LOC51634) mRNA | |
| 2518 | 7773 | 12602 | 2.22 | 2.0E-77 | AB037836.1 | NT | Hom sapiens mRNA for KIAA1415 protein, partial cds |
| 2518 | 7773 | 12603 | 2.22 | 2.0E-77 | AB037836.1 | NT | Hom sapiens mRNA for KIAA1415 protein, partial cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--|
| 3922 | 8922 | 13913 | 1.53 | 2.0E-77 | BE044316.1 | EST_HUMAN | hs43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN : |
| 4288 | 9280 | 14268 | 0.82 | 2.0E-77 | AI613519.1 | EST_HUMAN | tw22g02.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN ; |
| 4288 | 9280 | 14269 | 0.82 | 2.0E-77 | AI613519.1 | EST_HUMAN | tw22g02.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN ; |
| 4465 | 9455 | | 1.29 | 2.0E-77 | | | Homo sapiens: glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA |
| 4623 | 9608 | 14596 | 6.49 | 2.0E-77 | AA653025.1 | EST_HUMAN | ns68g12.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914_60S RIBOSOMAL PROTEIN L29. [1] contains element MSR1 repetitive element; |
| 44 | 5124 | 10112 | 0.89 | 1.0E-77 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 44 | 5124 | 10113 | 0.89 | 1.0E-77 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 270 | 5329 | 10340 | 3.11 | 1.0E-77 | | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 270 | 5329 | 10341 | 3.11 | 1.0E-77 | | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 864 | 7733 | 10925 | 6.08 | 1.0E-77 | | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 864 | 7733 | 10926 | 6.08 | 1.0E-77 | | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 1875 | 6864 | 11953 | 1.58 | 1.0E-77 | AW058119.1 | EST_HUMAN | wn83e05.x1 Soares_thymus_NHFT1 Homo sapiens cDNA clone IMAGE:2538160 3' |
| 2376 | 7348 | 12469 | 1.33 | 1.0E-77 | AB028024.1 | NT | Homo sapiens mRNA for KIAA1101 protein, complete cds |
| 2971 | 7989 | 13002 | 2.25 | 1.0E-77 | | | Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA |
| 4227 | 9221 | 14201 | 4.08 | 1.0E-77 | | | Homologous protein (LOC51626), mRNA |
| 4393 | 9384 | 14366 | 17.29 | 1.0E-77 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4516 | 9506 | 14486 | 2.27 | 1.0E-77 | | | Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA |
| 4554 | 9542 | 14527 | 0.74 | 1.0E-77 | A1273014.1 | EST_HUMAN | q109g01.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3' |
| 4728 | 9713 | 14698 | 1.24 | 1.0E-77 | | | Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA |
| 4898 | 9877 | 14845 | 1.42 | 1.0E-77 | | | Homo sapiens KIAA0005 gene product (KIAA0005), mRNA |
| 4898 | 9877 | 14846 | 1.42 | 1.0E-77 | | | Homo sapiens KIAA0005 gene product (KIAA0005), mRNA |
| 4989 | 9361 | 14341 | 0.68 | 1.0E-77 | | | Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA |
| 84 | 5161 | 10172 | 2.26 | 6.0E-78 | AU118789.1 | EST_HUMAN | AU118789_HEMBA1_Homo sapiens cDNA clone HEMBA1004354 5' |
| 84 | 5161 | 10173 | 2.26 | 6.0E-78 | AU118789.1 | EST_HUMAN | AU118789_HEMBA1_Homo sapiens cDNA clone HEMBA1004354 5' |

Table 4
Single Exon Probes Expressed in HBL 100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3240 | 8253 | 13274 | 0.88 | 6.0E-78 | BF344101.1 | EST_HUMAN | 602016926F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152511 5' |
| 217 | 5280 | 10291 | 1.01 | 5.0E-78 | 114224861 | NT | Homo sapiens hypothetical protein FLJ1316 (FLJ1316), mRNA be54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to W:P:Y48B6A.6 |
| 2491 | 7459 | 12574 | 4.77 | 5.0E-78 | AW673424.1 | EST_HUMAN | CE22121 ; |
| 3301 | 8312 | 13339 | 4.18 | 5.0E-78 | M55586.1 | NT | Human collagenase type IV (COL4A1) gene, exon 6 |
| 1120 | 6126 | 11156 | 1.66 | 4.0E-78 | AL043314.2 | EST_HUMAN | DKFZp434N0323 r1 434 (synonym: h1es3) Homo sapiens cDNA clone DKFZp434N0323 5' |
| 1487 | 6484 | 11539 | 1.28 | 4.0E-78 | AL355841.1 | NT | Novel human gene mapping to chromosome 22 |
| 2254 | 7231 | 12350 | 20.59 | 4.0E-78 | AF107405.1 | NT | Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds |
| 4195 | 9188 | 14168 | 1.87 | 4.0E-78 | 7656876 | NT | Homo sapiens syncytin (LOC30816), mRNA |
| 4628 | 9613 | 14602 | 1.75 | 4.0E-78 | 4505806 | NT | Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA |
| 4628 | 9613 | 14603 | 1.75 | 4.0E-78 | 4505806 | NT | Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA |
| 1160 | 5226 | 10235 | 3.27 | 3.0E-78 | AF05901.1 | NT | Homo sapiens eRF1 gene, complete cds |
| 1160 | 5226 | 10236 | 3.27 | 3.0E-78 | AF05901.1 | NT | Homo sapiens eRF1 gene, complete cds |
| 2240 | 7217 | 12335 | 1.06 | 3.0E-78 | 4502142 | NT | Homo sapiens apoptosis inhibitor 3 (API3) mRNA |
| 3142 | 8158 | 13180 | 1.34 | 3.0E-78 | 4507164 | NT | Homo sapiens nuclear antigen Spi100 (SP100) mRNA |
| 3178 | 8683 | | 1.23 | 3.0E-78 | AU140604.1 | EST_HUMAN | AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5' |
| 3048 | 8065 | | 2.47 | 2.0E-78 | U04489.1 | NT | Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20 |
| 3907 | 8907 | | 1.51 | 2.0E-78 | AA311872.1 | EST_HUMAN | EST182533 ,lukrat T-cells VI Homo sapiens cDNA 5' end |
| 5007 | 9973 | 14953 | 1.22 | 1.0E-78 | 4758843 | NT | Homo sapiens nucleoporin 155kD (NUP155) mRNA |
| 4560 | 9548 | 14533 | 3.65 | 9.0E-79 | 111525891 | NT | Homo sapiens peptide YY (PYY), mRNA |
| 4714 | 9690 | 14684 | 5.64 | 9.0E-79 | BE000837.1 | EST_HUMAN | RC2-BN0074-090300-014-012 BN0074 Homo sapiens cDNA |
| 3657 | 8663 | 13656 | 0.91 | 8.0E-79 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 4366 | 9357 | 14337 | 1.57 | 8.0E-79 | D28478.1 | NT | Human mRNA for KIAA0045 gene, complete cds |
| 4366 | 9357 | 14338 | 1.57 | 8.0E-79 | D28478.1 | NT | Human mRNA for KIAA0045 gene, complete cds |
| 3179 | 8185 | 13218 | 19.1 | 7.0E-79 | BE619648.1 | EST_HUMAN | 60147276F1 NIH_MGC_68 Homo sapiens cDNA clone FLJ10283 (FLJ10283), mRNA |
| 3103 | 8119 | | 0.99 | 4.0E-79 | 8922325 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 311 | 5366 | 10377 | 1.61 | 3.0E-79 | AF114488.1 | NT | Homo sapiens cell-line tsA201 a chloride ion current inducer protein (IClin) gene, complete cds |
| 963 | 5978 | 11012 | 5.56 | 3.0E-79 | AF222708.1 | NT | Human zinc finger protein ZNF131 mRNA, partial cds |
| 3025 | 8042 | 13051 | 2.52 | 3.0E-79 | U09410.1 | NT | Human zinc finger protein ZNF131 mRNA, partial cds |
| 285 | 5343 | | 1.02 | 2.0E-79 | HE3129.1 | EST_HUMAN | yr48f03.s1 Shares fetal liver spleen NFLS Homo sapiens cDNA clone IMAGE:2085413 |
| 628 | 5656 | 10661 | 1.22 | 2.0E-79 | BE319926.1 | EST_HUMAN | 601153415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5' |
| 915 | 5931 | 10966 | 1.47 | 2.0E-79 | 4757841 | NT | Homo sapiens BCL2-like 2 (BCL2L2) mRNA |
| 1018 | 6028 | | 1.10 | 2.0E-79 | A1523747.1 | EST_HUMAN | th18h10.1 NT NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2118885 3' |
| 11751 | 6745 | 11824 | 0.92 | 2.0E-79 | 7657024 | NT | Homo sapiens Dickkopf gene 4 (DKK4), mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1751 | 6745 | 11825 | 0.92 | 2.0E-79 | 7657024 | NT | Homo sapiens Dickkopf gene 4 (DKK4). mRNA |
| 2087 | 7068 | 12180 | 3.3 | 2.0E-79 | 4585663 | NT | Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 2087 | 7068 | 12181 | 3.3 | 2.0E-79 | 4585663 | NT | Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 2130 | 7110 | 12223 | 2.05 | 2.0E-79 | AJ271408.1 | NT | Homo sapiens for Fas-associated factor, FAF1 (Faf1 gene) |
| 2249 | 7226 | 12346 | 2.65 | 2.0E-79 | AF244138.1 | NT | Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds |
| 4041 | 9037 | 14027 | 1.34 | 2.0E-79 | AJ271408.1 | NT | Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene) |
| 3073 | 8089 | 13102 | 18.41 | 9.0E-80 | AA725848.1 | EST_HUMAN | ai23ed5.s1_Scares_testis_NHT Homo sapiens cDNA clone 1343648 3' |
| 3073 | 8089 | 13103 | 18.41 | 9.0E-80 | AA725848.1 | EST_HUMAN | ai23ed5.s1_Scares_testis_NHT Homo sapiens cDNA clone 1343648 3' |
| 3521 | 8528 | | 1.06 | 8.0E-80 | U94387.1 | NT | Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds |
| 4797 | 9781 | 14764 | 1.67 | 7.0E-80 | HO4619.1 | EST_HUMAN | Y49d02.r1_Scares_placenta Nb24P Homo sapiens cDNA clone IMAGE:1520675' |
| 889 | 5907 | 10947 | | 2.22 | 6.0E-80 | AI422197.1 | EST_HUMAN |
| 1604 | 6600 | 11661 | 2.05 | 6.0E-80 | U64898.1 | NT | tt58d02.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NALH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ; |
| 2234 | 7211 | 12327 | 4.78 | 6.0E-80 | 6631094 | NT | Homo sapiens NRD convertase mRNA, complete cds |
| 2234 | 7211 | 12328 | 4.78 | 6.0E-80 | 6631094 | NT | Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA |
| 4162 | 9157 | 14142 | 1.33 | 6.0E-80 | AB032981.1 | NT | Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA |
| 4162 | 9157 | 14143 | 1.33 | 6.0E-80 | AB032981.1 | NT | Homo sapiens mRNA for KIAA1155 protein, partial cds |
| 583 | 5614 | 10614 | 5.48 | 5.0E-80 | 4506228 | NT | Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA |
| 825 | 5845 | 10882 | 1.83 | 5.0E-80 | AF108830.1 | NT | Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 825 | 5845 | 10883 | 1.83 | 5.0E-80 | AF108830.1 | NT | Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 1169 | 6172 | | 1.23 | 5.0E-80 | X91647.1 | NT | H.sapiens ncx1 gene (exon 12) |
| 1429 | 6426 | | 1.63 | 5.0E-80 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21TC083 |
| 2300 | 7275 | 12394 | 1.18 | 5.0E-80 | U89358.1 | NT | Human Ig3mbt protein homolog mRNA, complete cds |
| 2363 | 7337 | 12454 | 8.73 | 5.0E-80 | AB037555.1 | NT | Homo sapiens mRNA for KIAA1434 protein, partial cds |
| 2722 | 7679 | 12792 | 6.29 | 5.0E-80 | 4504292 | NT | Homo sapiens histone family, member J (H3FJ) mRNA |
| 4796 | 9780 | 14763 | 1.24 | 5.0E-80 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 216 | 5279 | | 15.21 | 3.0E-80 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21TC010 |
| 4571 | 9559 | 14548 | 1.41 | 3.0E-80 | BF085509.1 | EST_HUMAN | PM0-GN0013-04900-002-E03 Homo sapiens cDNA |
| 4753 | 9738 | | 7.56 | 3.0E-80 | BE817465.1 | EST_HUMAN | QV4-BN0263-04900-241-g10 BN0263 Homo sapiens cDNA |
| 1762 | 6754 | 11839 | 3.95 | 2.0E-80 | R35321.1 | EST_HUMAN | yg65a08.1 Scares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5' |
| 1823 | 6813 | 11907 | 1.48 | 2.0E-80 | AI444821.1 | EST_HUMAN | RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7 |
| 2002 | 6985 | 12089 | 3.58 | 2.0E-80 | AL043116.2 | EST_HUMAN | DKFZp43D1323_1144 (synonym: hts3) Homo sapiens cDNA clone DKFZp43D1323 5' |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 338 5390 | 791 5812 | 10842 | 1.79 | 1.0E-80 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 1914 6900 | | | 1.53 | 1.0E-80 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 4674 9659 | 14642 | | 2.27 | 1.0E-80 | AI732656.1 | EST_HUMAN | mn01f12.x5 NCI CGAP_Co8 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.H1 OFR repetitive element ; z23sg07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains Alu repetitive element |
| 2144 7123 | 12239 | | 0.95 | 7.0E-81 | AA011080.1 | EST_HUMAN | z221d10.r1 Soares_fetal_heart_NbhH119W Homo sapiens cDNA clone IMAGE:359635 5' similar to contains SW:KRHA_FABIT Q02857 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1];contains element MER22 repetitive element ; |
| 4262 9255 | 14244 | | 6.63 | 6.0E-81 | BE256829.1 | EST_HUMAN | 601111970F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5' |
| 4262 9255 | 14245 | | 6.63 | 6.0E-81 | BE256829.1 | EST_HUMAN | 601111970F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5' |
| 2155 7134 | 12253 | | 5.16 | 5.0E-81 | BE268042.1 | EST_HUMAN | 601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3352840 5' |
| 1786 6778 | 11870 | | 1.6 | 4.0E-81 | AW779612.1 | EST_HUMAN | hmb8d02.x1 NCI CGAP_Co4 Homo sapiens cDNA clone IMAGE:3345480 5' |
| 3097 8113 | 13131 | | 3.66 | 4.0E-81 | AB037766.1 | NT | P53620 COATOMER GAMMA SUBUNIT ; ws80h03.x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:CGP_BOVIN |
| 3544 85551 | 13558 | | 0.78 | 4.0E-81 | AW004608.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1345 protein, partial cds |
| 4036 8032 | 14019 | | 2.04 | 4.0E-81 | AF263306.1 | EST_HUMAN | STRIATIN ; |
| 4036 9032 | 14020 | | 2.04 | 4.0E-81 | AF263306.1 | NT | Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds |
| 4268 9261 | 14251 | | 0.99 | 4.0E-81 | 89923209 | NT | Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds |
| 1248 6246 | 11285 | | 12.27 | 3.0E-81 | Y18000.1 | NT | Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA |
| 1248 6246 | 11286 | | 12.27 | 3.0E-81 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 2310 7285 | 12405 | | 1.5 | 3.0E-81 | AF077188.1 | NT | Homo sapiens NF2 gene |
| 2922 7941 | 12957 | | 5.68 | 3.0E-81 | 4506280 | NT | Homo sapiens cullin 4A (CUL4A) mRNA, complete cds |
| 2922 7941 | 12958 | | 5.68 | 3.0E-81 | 4506280 | NT | Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA |
| 2759 7780 | 12804 | | 2.23 | 2.0E-81 | BE784636.1 | EST_HUMAN | 601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5' |
| 2759 7780 | 12805 | | 2.23 | 2.0E-81 | BE784636.1 | EST_HUMAN | 601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5' |
| 3686 8690 | 13693 | | 0.93 | 2.0E-81 | AW611542.1 | EST_HUMAN | 11g85c01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3877121 5' |
| 3568 8575 | 13581 | | 1.35 | 1.0E-81 | AW960658.1 | EST_HUMAN | ES1737279 IMAGE sequences, MAGF Homo sapiens cDNA |
| 4384 9375 | 14354 | | 2.11 | 1.0E-81 | AA040370.1 | EST_HUMAN | 2k45h09.r1 Soares_pregnant_uterus NbHPU Homo sapiens cDNA synthase - fruit fly ; PIR:S52437 SS2437 CDP-diacetylglucosid synthase |
| 4510 9500 | 14479 | | 10.97 | 1.0E-81 | BE047896.1 | EST_HUMAN | b245cc04.y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291526 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 13 | 5093 | 10077 | 4.69 | 8.0E-82 | AF161406.1 | NT | Homo sapiens HSPC28S mRNA, partial cds |
| 107 | 5093 | 10077 | 5.26 | 8.0E-82 | AF161406.1 | NT | Homo sapiens HSPC28B mRNA, partial cds |
| 261 | 5320 | 10330 | 2.55 | 8.0E-82 | U08988.1 | NT | Human CRFβ14 gene, partial cds |
| 804 | 5625 | 10855 | 2.38 | 8.0E-82 | U08988.1 | NT | Human CRFβ14 gene, partial cds |
| 876 | 5694 | 10935 | 1.93 | 8.0E-82 | U08988.1 | NT | Human CRFβ4 gene, partial cds |
| 1459 | 6456 | 11515 | 1.39 | 8.0E-82 | AB037748.1 | NT | Homo sapiens mRNA for KIAA1327 protein, partial cds |
| 1617 | 6614 | 11681 | 1.23 | 8.0E-82 | 6715601 | NT | Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA |
| 4121 | 9115 | 14102 | 0.84 | 8.0E-82 | 8923432 | NT | Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA |
| 1424 | 6421 | | 1.04 | 7.0E-82 | BF035527.1 | EST_HUMAN | 60145853 F NIH_MGC_C_66 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 2693 | 7651 | 12765 | 1.55 | 7.0E-82 | AU144050 | HOMBA1 Homo sapiens cDNA clone HEMBA1 0007852 3' | AU144050 HEMBA1 Isoform 1 mRNA, complete cds |
| 1632 | 6629 | 11698 | 100.34 | 4.0E-82 | AF081484.1 | NT | Homo sapiens alpha-tubulin |
| 275 | 5334 | 10347 | 16.31 | 3.0E-82 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 693 | 5717 | 10734 | 3.55 | 3.0E-82 | BE005705.1 | EST_HUMAN | RC2-BN0120-010400-013-f02 BN0120 Homo sapiens cDNA |
| 779 | 5800 | 10830 | 5.3 | 3.0E-82 | 5174702 | NT | Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA |
| 859 | 5878 | 10919 | 8.88 | 3.0E-82 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 1044 | 8054 | | 90.59 | 3.0E-82 | AA725848.1 | EST_HUMAN | ai23e05_si_Scares_testis_NHT Homo sapiens cDNA clone 134364B 3' |
| 1337 | 6335 | 11385 | 0.96 | 3.0E-82 | AW875073.1 | EST_HUMAN | RC6-PT001-190100-021-B02 PT001 Homo sapiens cDNA |
| 1438 | 6435 | 11492 | 2.02 | 3.0E-82 | AI163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1860 | 6849 | 11837 | 1.66 | 3.0E-82 | BER13232.1 | EST_HUMAN | RC1-BN0005-260700-018-904 BN0005 Homo sapiens cDNA |
| 3198 | 8214 | | 2.15 | 3.0E-82 | 5453811 | NT | Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA |
| 592 | 5623 | 10621 | 1.39 | 2.0E-82 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 592 | 5623 | 10622 | 1.39 | 2.0E-82 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 1647 | 6843 | 11715 | 1.78 | 2.0E-82 | AL046300.1 | EST_HUMAN | DKFZp43M117_11434 (synonym: h1es2) Homo sapiens cDNA clone DKFZp43M117 5' |
| 3756 | 8759 | 13758 | 0.85 | 2.0E-82 | D87675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4112 | 9106 | 14092 | 0.83 | 2.0E-82 | 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 4426 | 9416 | 14403 | 1.06 | 2.0E-82 | AB029019.1 | NT | Homo sapiens mRNA for KIAA1096 protein, partial cds |
| 4426 | 9416 | 14404 | 1.06 | 2.0E-82 | AB029019.1 | NT | Homo sapiens mRNA for KIAA1096 protein, partial cds |
| 4720 | 9705 | 14691 | 2.77 | 2.0E-82 | AF045555.1 | NT | Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds |
| 4908 | 9887 | 14859 | 1.58 | 2.0E-82 | 4507580 | NT | Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA |
| 4908 | 9887 | 14860 | 1.58 | 2.0E-82 | 4507580 | NT | Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA |

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 587 | 5618 | 10616 | 1.67 | 1.0E-82 | 11545921 | NT | Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA |
| 1189 | 6190 | | 1.57 | 1.0E-82 | BE885106.1 | EST_HUMAN | 60151085F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5' |
| 1266 | 6284 | 11305 | 3.2 | 1.0E-82 | BE064386.1 | EST_HUMAN | RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA |
| 1267 | 6265 | 11306 | 1.14 | 1.0E-82 | AB011110.2 | NT | Homo sapiens mRNA for KIAA0538 protein, partial cds |
| 1389 | 6386 | 11438 | 4.62 | 8.0E-83 | BE383973.1 | EST_HUMAN | 601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5' |
| 1642 | 7700 | 11709 | 4.3 | 8.0E-83 | N66951.1 | EST_HUMAN | 2448f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:3614362 5' |
| 1339 | 6337 | 11386 | 1.67 | 7.0E-83 | AW385529.1 | EST_HUMAN | QV4-L-T0016-271298-068-H11 LT0016 Homo sapiens cDNA |
| 2794 | 7814 | | 1.62 | 7.0E-83 | AA58465.1 | EST_HUMAN | nt12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element |
| 4670 | 9655 | | 6.92 | 7.0E-83 | BF221813.1 | EST_HUMAN | Tp37a07.X1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316 |
| 5036 | 10007 | | 1.51 | 7.0E-83 | BF221813.1 | EST_HUMAN | Tp37a07.X1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316 |
| 401 | 5437 | 10456 | 1.97 | 6.0E-83 | M33520.1 | NT | Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29 |
| 1749 | 6743 | 11822 | 7.97 | 6.0E-83 | AW573088.1 | EST_HUMAN | hf31h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HKEIN P44471 HYPOTHETICAL PROTEIN HI0034.; |
| 2977 | 7995 | | 1.02 | 6.0E-83 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 2996 | 8014 | 13026 | 1.01 | 6.0E-83 | AA701457.1 | EST_HUMAN | zif8c05.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:4365080 3' |
| 3483 | 8491 | 13507 | 0.82 | 6.0E-83 | 11430241 | NT | [Homo sapiens hypothetical protein FLJ10379] (FLJ10379), mRNA |
| 932 | 5949 | | 1.95 | 5.0E-83 | U17883.1 | NT | [Human succinate dehydrogenase iron-protein subunit (sdhb) gene, exon 5 |
| 1997 | 7704 | | 2.85 | 5.0E-83 | AF006305.1 | NT | Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds |
| 3553 | 8560 | 13566 | 1.13 | 5.0E-83 | AL133207.2 | NT | Novel human gene mapping to chromosome X |
| 3810 | 8813 | 13819 | 0.89 | 5.0E-83 | 4885190 | NT | Homo sapiens deoxyribonuclease I (DNASE1), mRNA |
| 4907 | 9886 | 14857 | 14.02 | 5.0E-83 | 4557013 | NT | Homo sapiens catalase (CAT) mRNA |
| 4907 | 9886 | 14858 | 14.02 | 5.0E-83 | 4557013 | NT | Homo sapiens catalase (CAT) mRNA |
| 634 | 5662 | 10667 | 1.76 | 4.0E-83 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 3435 | 8443 | 13469 | 1.08 | 4.0E-83 | BE888078.1 | EST_HUMAN | 601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5' |
| 982 | 5997 | | 3.79 | 3.0E-83 | AA3668311.1 | EST_HUMAN | EST79842 Facienta Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9 np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133282 similar to contains THR.12 THR repetitive element; |
| 2705 | 7662 | | 1.44 | 3.0E-83 | AA632854.1 | EST_HUMAN | np64g05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 |
| 1764 | 6756 | 11841 | 1.7 | 2.0E-83 | AA993492.1 | EST_HUMAN | Q92614 MYELOBLAST KIAA0216.; |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit No. | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-------------|-----------------------|---|--------------------|
| 1764 | 8756 | 11842 | 1.7 | 2.0E-83 | AA993492.1 | EST_HUMAN | 0f64905_s1 Scareas testis NIH Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 | |
| 1884 | 6873 | 11962 | 3.01 | 2.0E-83 | N66951.1 | EST_HUMAN | Q92614 MYEOBLAST KIAA0216 ; | |
| 2779 | 7800 | 12818 | 2.73 | 2.0E-83 | BE82694.1 | EST_HUMAN | 2e48f12_s1 Scareas fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3' | |
| 3195 | 82111 | | 2.22 | 2.0E-83 | 11430834 | NT | RC6-ET0046-280600-013-112 ET0046 Homo sapiens cDNA | |
| 3687 | 8691 | | 0.74 | 2.0E-83 | AL163202.2 | NT | Homo sapiens: sal (<i>Drosophila</i>)-like 1 (SALL1). mRNA | |
| 4210 | 9203 | 14185 | 4.16 | 2.0E-83 | AF202879.1 | NT | Homo sapiens: chromosome 21 segment HS21C002 | |
| 4517 | 9507 | 14487 | 6.32 | 2.0E-83 | 7706398 | NT | Homo sapiens: hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds | |
| 4517 | 9507 | 14488 | 6.32 | 2.0E-83 | 7706398 | NT | Homo sapiens: ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA | |
| 1387 | 6384 | 11435 | 2.31 | 1.0E-83 | 4504326 | NT | Homo sapiens: ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA | |
| 1387 | 6384 | 11436 | 2.31 | 1.0E-83 | 4504326 | NT | Homo sapiens: hydroxacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydrolase (trifunctional protein), beta subunit (HADHB) mRNA | |
| 2585 | 7548 | 12663 | 1.22 | 1.0E-83 | BE883690.1 | EST_HUMAN | Homo sapiens: hydroxacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydrolase (trifunctional protein), beta subunit (HADHB) mRNA | |
| 3777 | 8780 | 13783 | 5.31 | 1.0E-83 | AF053788.1 | NT | 601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808754 5' | |
| 4122 | 9116 | 14103 | 3.74 | 1.0E-83 | 225822.1 | NT | Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds | |
| 4733 | 9718 | 14703 | 2.36 | 1.0E-83 | 4502166 | NT | H.sapiens gene for mitochondrial docosanol-CoA delta-isomerase, exon 3 | |
| 3107 | 8711 | 13714 | 4.14 | 7.0E-84 | BE901209.1 | EST_HUMAN | Homo sapiens: amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA | |
| 1276 | 6274 | 11313 | 2.87 | 6.0E-84 | BE838864.1 | EST_HUMAN | 601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858853 5' | |
| 1276 | 6274 | 11314 | 2.87 | 6.0E-84 | BE838864.1 | EST_HUMAN | RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA | |
| 2334 | 7308 | 12429 | 3.11 | 6.0E-84 | AA776574.1 | EST_HUMAN | RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA | |
| 5044 | 10015 | 14984 | 0.98 | 8.0E-84 | RO5859.1 | EST_HUMAN | aa66a03_s1 Stratagene Schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3' | |
| 704 | 5728 | 10745 | 0.8 | 5.0E-84 | AA382811.1 | EST_HUMAN | ye83a04_r1 Scareas fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125262 5' | |
| 2945 | 7964 | | 1.24 | 5.0E-84 | AF108718.1 | NT | Homo sapiens chromosome 3 subtelomeric region | |
| 1386 | 8383 | 11434 | 2.71 | 4.0E-84 | AI685321.1 | EST_HUMAN | wa76c04_x1 Scareas NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN_O43847 NARDILYSIN PRECURSOR ; | |
| 4792 | 9776 | 14760 | 1.93 | 4.0E-84 | 4505928 | NT | Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA | |
| 4793 | 9777 | 14761 | 1.73 | 4.0E-84 | AF069601.2 | NT | Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds | |
| 314 | 5369 | 10380 | 1.77 | 3.0E-84 | AF026200.1 | NT | Homo sapiens Bach1 protein homolog mRNA, partial cds | |
| 1920 | 6906 | 12000 | 1.89 | 3.0E-84 | 5453855 | NT | Novel human mRNA containing Zinc finger C2H2 type domains | |
| 1953 | 6944 | 12048 | 3.98 | 3.0E-84 | AL096880.1 | NT | Homo sapiens DNA, DLECT1 to ORC1L4 genes, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds) | |
| 3510 | 8518 | 13529 | 0.97 | 3.0E-84 | AB026898.1 | NT | | |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3662 | 8667 | 13673 | 5.61 | 3.0E-84 | AF014459.1 | NT | Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds |
| 2047 | 7029 | 12141 | 4.68 | 2.0E-84 | BE953397.1 | EST_HUMAN | CMI-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA |
| 2047 | 7029 | 12142 | 4.68 | 2.0E-84 | BE953397.1 | EST_HUMAN | CMI-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA |
| 2873 | 7892 | 12915 | 8.93 | 2.0E-84 | AF036943.1 | NT | Homo sapiens myelin transcription factor 1-like (MYT1-) mRNA, complete cds |
| 2892 | 7911 | 12932 | 1.41 | 2.0E-84 | X89211.1 | NT | H.sapiens DNA for endogenous retroviral like element |
| 310 | 5365 | 10376 | 1.21 | 1.0E-84 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 545 | 5579 | 10583 | 16.96 | 1.0E-84 | 4507952 | NT | Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA |
| 710 | 5734 | | 1.23 | 1.0E-84 | 11427631 | NT | Homo sapiens complement component 5 (C5), mRNA |
| 1274 | 6272 | 11311 | 2.76 | 1.0E-84 | AA984379.1 | EST_HUMAN | am85bi11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3' |
| 2001 | 6984 | 12088 | 1.8 | 1.0E-84 | BE392137.1 | EST_HUMAN | 601308006f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5' |
| 2162 | 7141 | 12258 | 1.8 | 1.0E-84 | 11427197 | NT | Homo sapiens pericentriolar material 1 (PCM1), mRNA |
| 3665 | 8670 | 13675 | 2.55 | 1.0E-84 | AA720851.1 | EST_HUMAN | nw12s06.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3' |
| 4292 | 9284 | 14271 | 4.33 | 1.0E-84 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4561 | 9549 | 14534 | 2.93 | 1.0E-84 | AL043314.2 | EST_HUMAN | DKFZp434N0323_1 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323_5' |
| 4561 | 9549 | 14535 | 2.93 | 1.0E-84 | AL043314.2 | EST_HUMAN | DKFZp434N0323_1 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323_5' |
| 4756 | 9284 | 14271 | 2.67 | 1.0E-84 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 |
| 4952 | 9929 | 14907 | 0.71 | 1.0E-84 | AW371947.1 | EST_HUMAN | RC4-BT0311-141299-012-q06 BT0311 Homo sapiens cDNA |
| 4952 | 9929 | 14908 | 0.71 | 1.0E-84 | AW371947.1 | EST_HUMAN | RC4-BT0311-141299-012-q06 BT0311 Homo sapiens cDNA |
| 952 | 5968 | | 2.75 | 9.0E-85 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1056 | 6065 | 11094 | 10.8 | 9.0E-85 | U51432.1 | NT | Homo sapiens nuclear protein Skip mRNA, complete cds |
| 1056 | 6065 | 11095 | 10.8 | 9.0E-85 | U51432.1 | NT | Homo sapiens nuclear protein Skip mRNA, complete cds |
| 1543 | 6541 | 11598 | 1.1 | 9.0E-85 | M33282.1 | NT | Human plasminogen gene, exon 7 |
| 1543 | 6541 | 11599 | 1.1 | 9.0E-85 | M33282.1 | NT | Human plasminogen gene, exon 7 |
| 1635 | 6632 | 11702 | 2.05 | 9.0E-85 | 7657020 | NT | Homo sapiens Dkfp434P211 protein (DKFZp434P211), mRNA |
| 3711 | 8715 | 13717 | 0.91 | 9.0E-85 | 7019418 | NT | Homo sapiens nucleolar GTPase (HUMAUANTG), mRNA |
| 4130 | 9125 | 14109 | 1.08 | 9.0E-85 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4639 | 9624 | 14615 | 1.44 | 9.0E-85 | M33764.1 | NT | Human ornithine decarboxylase gene, complete cds |
| 4639 | 9624 | 14616 | 1.44 | 9.0E-85 | M33764.1 | NT | Human ornithine decarboxylase gene, complete cds |
| 4757 | 9741 | 14726 | 1.1 | 9.0E-85 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C088 |
| 1119 | 6125 | 11155 | 34.29 | 7.0E-85 | L05094.1 | NT | Homo sapiens ribosomal protein L27 mRNA, complete cds |
| 2271 | 7247 | 12364 | 2.11 | 5.0E-85 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1280 | 6279 | 11320 | 0.77 | 3.0E-85 | AF096157.1 | NT | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6 |
| 1742 | 6737 | 11813 | 6.32 | 3.0E-85 | T97495.1 | EST_HUMAN | ye53g08.11 Shares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121604 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4188 | 9181 | 14164 | 1.26 | 3.0E-85 | BE267189.1 | EST_HUMAN | 601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5' |
| 4743 | 9728 | 14714 | 1.48 | 3.0E-85 | 11024695 | NT | Homo sapiens F-box only protein 24 (FBXO24), mRNA |
| 4743 | 9728 | 14715 | 1.48 | 3.0E-85 | 11024695 | NT | Homo sapiens F-box only protein 24 (FBXO24), mRNA |
| 4809 | 9793 | 14775 | 1 | 3.0E-85 | 7363442 | NT | Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA |
| 948 | 5964 | 10998 | 0.72 | 2.0E-85 | 7657266 | NT | Homo sapiens KIAA0929 protein Ms2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 1023 | 6033 | 11064 | 1.96 | 2.0E-85 | AF248540.1 | NT | Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds |
| 1380 | 6377 | 11425 | 1.33 | 2.0E-85 | 7706205 | NT | Homo sapiens CGI-201 protein (LOC51340), mRNA |
| 1395 | 6392 | 11445 | 7.52 | 2.0E-85 | 5174776 | NT | Homo sapiens apolipoprotein C-II (APOC2) mRNA |
| 1395 | 6392 | 11446 | 7.52 | 2.0E-85 | 5174775 | NT | Homo sapiens apolipoprotein C-II (APOC2) mRNA |
| 2169 | 7148 | 12265 | 1.4 | 2.0E-85 | U10525.1 | NT | Human DNA polymerase beta gene, exons 12 and 13 |
| 2750 | 63115 | 1024 | 2.24 | 2.0E-85 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 2856 | 7975 | 12290 | 2.18 | 2.0E-85 | M30938.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 4207 | 9200 | 14182 | 5.76 | 2.0E-85 | 4505680 | NT | Homo sapiens plasminogen (PLG) mRNA |
| 4755 | 9740 | 14725 | 0.97 | 2.0E-85 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 2223 | 7200 | | 3.19 | 1.0E-85 | BE794306.1 | EST_HUMAN | 601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5' |
| 2329 | 7303 | 12423 | 5.67 | 1.0E-85 | BE618392.1 | EST_HUMAN | 601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5' |
| 2329 | 7303 | 12424 | 5.67 | 1.0E-85 | BE618392.1 | EST_HUMAN | 601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5' |
| 1404 | 6401 | | 54.78 | 9.0E-86 | BE274217.1 | EST_HUMAN | 601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5' |
| 923 | 5940 | 10972 | 0.75 | 7.0E-86 | AA850801.1 | EST_HUMAN | aj88f08.s1 Scores_perathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1403559 3' |
| 923 | 5940 | 10973 | 0.75 | 7.0E-86 | AA850801.1 | EST_HUMAN | aj88f08.s1 Scores_perathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1403559 3' |
| 1275 | 6273 | 11312 | 2.27 | 6.0E-86 | 4505492 | NT | Homo sapiens oxoglutarate dehydrogenase (lipoyamide) (OGDH) mRNA |
| 5001 | 9972 | 14948 | 1.8 | 6.0E-86 | 6005833 | NT | Homo sapiens 24 kDa intrinsic membrane protein (PMF24), mRNA |
| 211 | 5274 | 10283 | 1.35 | 4.0E-86 | BE547173.1 | EST_HUMAN | 601072584F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5' |
| 284 | 5323 | 10332 | 2.04 | 2.0E-86 | AA306264.1 | EST_HUMAN | EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end |
| 411 | 5448 | | 2.83 | 2.0E-86 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 1170 | 6173 | 11207 | 1.94 | 2.0E-86 | N58977.1 | EST_HUMAN | yZ19a08.s1 Scores_multiple_sclerosis_2NBHMSP_Homo sapiens cDNA clone IMAGE:2833478 5' |
| 2128 | 7108 | 12222 | 3.37 | 2.0E-86 | 9635487 | NT | Human endogenous retrovirus, complete genome |
| 2207 | 7184 | 12307 | 1.08 | 2.0E-86 | AB033103.1 | NT | Homo sapiens mRNA for KIAA1277 protein, partial cds |
| 3331 | 8341 | 13359 | 1.19 | 2.0E-86 | AW986142.1 | EST_HUMAN | EST37821f MAGE ressequences, MAGI Homo sapiens cDNA |
| 3661 | 8666 | 13671 | 2.64 | 2.0E-86 | AF156776.1 | NT | Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAA1-delta) mRNA, complete cds |
| 3681 | 8686 | 13672 | 2.64 | 2.0E-86 | AF156776.1 | NT | Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAA1-delta) mRNA, complete cds |
| 3927 | 8927 | | 2.69 | 2.0E-86 | AW515742.1 | EST_HUMAN | hd87908Jx1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2816542 3' |
| 4645 | 9630 | 14625 | 3.42 | 2.0E-86 | AF056490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 1562 6559 | 11621 | 2.08 | 1.0E-86 | | 4826855 | NT | Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA |
| 3089 8105 | 13120 | 1.45 | 1.0E-86 | | 5453649 | NT | Homo sapiens fibulin 5 (FBN5) mRNA |
| 3164 8180 | 13202 | 2.68 | 1.0E-86 | L20492.1 | NT | Human gamma-glutamyl transpeptidase mRNA, complete cds | |
| 3222 8237 | 13258 | 1.17 | 1.0E-86 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 | |
| 3222 8237 | 13259 | 1.17 | 1.0E-86 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 | |
| 3842 8844 | 13852 | 1.22 | 1.0E-86 | | 7706161 | NT | Homo sapien's hypothetical protein (LOC51318), mRNA |
| 3842 8844 | 13853 | 1.22 | 1.0E-86 | | 7706161 | NT | Homo sapien's hypothetical protein (LOC51318), mRNA |
| 4142 9137 | 14121 | 5.37 | 1.0E-86 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 | |
| 476 5512 | 10525 | 131.14 | 8.0E-87 | X62245.1 | NT | O.cuniculus mRNA for elongation factor 1 alpha | |
| 2233 7210 | 12325 | 1.99 | 7.0E-87 | BF063211.1 | EST_HUMAN | 788502.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779.3' | |
| 2233 7210 | 12326 | 1.99 | 7.0E-87 | BF063211.1 | EST_HUMAN | 788502.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779.3' | |
| 3448 8456 | 13482 | 0.78 | 6.0E-87 | | 7657213 | NT | Homo sapien's hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 1140 6145 | 11176 | 2.38 | 5.0E-87 | AA382811.1 | EST_HUMAN | EST198094 Testis I Homo sapiens cDNA 5' end | |
| 951 5967 | 11000 | 1.12 | 4.0E-87 | AL163210.2 | NT | Homo sapien's chromosome 21 segment HS21C010 | |
| 1153 6157 | 11190 | 18.02 | 4.0E-87 | AB037835.1 | NT | Homo sapien's mRNA for KIAA1414 protein, partial cds | |
| 1980 6965 | 12071 | 1.85 | 4.0E-87 | AB007925.1 | NT | Homo sapien's mRNA for KIAA0456 protein, partial cds | |
| 2355 7329 | 12444 | 1.2 | 4.0E-87 | | 7706299 | NT | Homo sapien's CGI-60 protein (LOC51826), mRNA |
| 2355 7329 | 12445 | 1.2 | 4.0E-87 | | 7706299 | NT | Homo sapien's myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA |
| 3383 8391 | 13444 | 1.88 | 4.0E-87 | | 5174574 | NT | Homo sapien's high-mobility group (nonhistone chromosomal) protein 4 (HMGA4) mRNA |
| 2704 7661 | 12773 | 5.54 | 2.0E-87 | .4885420 | NT | Q92-BN0143-050600-254-a03 BN0148 Homo sapiens cDNA | |
| 2878 7897 | | 1.17 | 2.0E-87 | BF327920.1 | EST_HUMAN | AU116935-1 Homo sapiens cDNA clone HEMBA1003037 5' | |
| 3696 8700 | 13703 | 0.88 | 2.0E-87 | AU116935.1 | EST_HUMAN | CW0-TN033-150900-552-h08 TN038 Homo sapiens cDNA | |
| 4758 9742 | 14727 | 0.66 | 2.0E-87 | BF376311.1 | EST_HUMAN | Homo sapien's putative glycolipid transfer protein (LOC51054), mRNA | |
| 1163 7693 | | 1.89 | 1.0E-87 | | 7705683 | NT | PM2-CT0263-141098-301-904 CT0265 Homo sapiens cDNA |
| 1406 6403 | 11460 | 1.69 | 1.0E-87 | AW361977.1 | EST_HUMAN | PM2-CT0263-141098-301-904 CT0265 Homo sapiens cDNA | |
| 1406 6403 | 11461 | 1.69 | 1.0E-87 | AW361977.1 | EST_HUMAN | PM2-CT0263-141098-301-904 CT0265 Homo sapiens cDNA | |
| 3628 8635 | 13640 | 13.27 | 1.0E-87 | Y00052.1 | NT | Human mRNA for T-cell cyclophilin | |
| 3649 8655 | 13661 | 2.3 | 1.0E-87 | | 4758827 | NT | Homo sapien's neurexin III (NRXN3) mRNA |
| 909 5926 | 10961 | 0.7 | 9.0E-88 | | 5453887 | NT | Homo sapien's protease inhibitor 4 (nailatin) (PI4) mRNA |
| 1089 6096 | 11126 | 6.3 | 9.0E-88 | AF167465.1 | NT | Homo sapien's double stranded RNA activated protein kinase (PKR) gene, exon 12 | |
| 1331 6329 | 11377 | 2.48 | 9.0E-88 | AB037820.1 | NT | Homo sapien's mRNA for KIAA1399 protein, partial cds | |
| 1331 6329 | 11378 | 2.48 | 9.0E-88 | AB037820.1 | NT | Homo sapien's mRNA for KIAA1399 protein, partial cds | |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID No. | Exon SEQ ID No. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 3542 | 8549 | 13557 | 0.89 | 9.0E-88 | AL163209.2 | NT | Homo sapiens: chromosome 21 segment HS21C009 |
| 4147 | 9142 | 14126 | 3.04 | 9.0E-88 | X91929.1 | NT | H. sapiens: ECE-1 gene (exon 9) |
| 4147 | 9142 | 14127 | 3.04 | 9.0E-88 | X91929.1 | NT | H. sapiens: ECE-1 gene (exon 9) |
| 1792 | 6783 | | 1.98 | 5.0E-88 | 7661887 | NT | Homo sapiens: KIAA0063 gene product (KIAA0063), mRNA |
| 2568 | 7531 | 12650 | 4.62 | 5.0E-88 | N89399.1 | EST_HUMAN | K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1 |
| 2931 | 7950 | 12957 | 0.71 | 5.0E-88 | AF114488.1 | NT | Homo sapiens: intersectin short isoform (ITSN) mRNA, complete cds |
| 2941 | 7960 | 12979 | 0.76 | 5.0E-88 | AF114488.1 | NT | Homo sapiens: intersectin short isoform (ITSN) mRNA, complete cds |
| 2941 | 7960 | 12980 | 0.76 | 5.0E-88 | AF114488.1 | NT | Homo sapiens: intersectin short isoform (ITSN) mRNA, complete cds |
| 3305 | 8316 | | 2.56 | 5.0E-88 | AI693217.1 | EST_HUMAN | wd68h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element;contains element MER22 MER22 repetitive element; |
| 3458 | 8466 | 13493 | 0.7 | 5.0E-88 | AF114488.1 | NT | Homo sapiens: intersectin short isoform (ITSN) mRNA, complete cds |
| 1309 | 6307 | 11355 | 1.13 | 4.0E-88 | BF091229.1 | EST_HUMAN | PM1-TN0028-050900-004-110 TN0028 Homo sapiens cDNA |
| 1309 | 6309 | 11356 | 1.13 | 4.0E-88 | BF091229.1 | EST_HUMAN | PM1-TN0028-050900-004-110 TN0028 Homo sapiens cDNA |
| 722 | 5745 | 10764 | 1.4 | 3.0E-88 | 11545800 | NT | Homo sapiens: hypothetical protein FLJ21634 (FLJ21634), mRNA |
| 1776 | 6768 | 226 | 3.0E-88 | 4508020 | NT | Homo sapiens: zinc finger protein 259 (ZNF259) mRNA | |
| 2877 | 7896 | 12920 | 4.85 | 3.0E-88 | N66951.1 | EST_HUMAN | ZB48f12.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3' |
| 4118 | 9112 | 14096 | 0.69 | 3.0E-88 | 4501912 | NT | Homo sapiens: a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA |
| 4118 | 9112 | 14097 | 0.69 | 3.0E-88 | 4501912 | NT | Homo sapiens: a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA |
| 4351 | 9342 | 364 | 3.0E-88 | 11429300 | NT | Homo sapiens: hypothetical protein FLJ20220 (FLJ20220), mRNA | |
| 1019 | 6029 | 11058 | 1.27 | 2.0E-88 | 7305198 | NT | Homo sapiens: Calseinilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA |
| 1585 | 6582 | 11644 | 1.92 | 2.0E-88 | AF246219.1 | NT | Homo sapiens: SNARE protein kinase SNAK mRNA, complete cds |
| 1711 | 6706 | 11782 | 4.8 | 2.0E-88 | AF246219.1 | NT | Homo sapiens: SNARE protein kinase SNAK mRNA, complete cds |
| 3384 | 8392 | 13415 | 0.99 | 2.0E-88 | AF246219.1 | NT | Homo sapiens: SNARE protein kinase SNAK mRNA, complete cds |
| 4301 | 9293 | 14280 | 2.35 | 2.0E-88 | 5031668 | NT | Homo sapiens: dynein, axonemal, presenilin-binding protein 4 (DNAL4), mRNA |
| 2661 | 7620 | 12732 | 1.49 | 8.0E-89 | BE31157.1 | EST_HUMAN | 601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5' |
| 430 | 5468 | 10496 | 1.24 | 7.0E-89 | 7657213 | NT | Homo sapiens: hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 430 | 5468 | 10497 | 1.24 | 7.0E-89 | 7657213 | NT | Homo sapiens: hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 4730 | 9715 | 14700 | 3.49 | 7.0E-89 | 4557390 | NT | Homo sapiens: complement component 8, beta polypeptide (C8B) mRNA |
| 4774 | 9753 | 14746 | 5.7 | 7.0E-89 | AL045748.1 | EST_HUMAN | DKFZp434E246_1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434E246 5' |
| 1007 | 6017 | 11047 | 2.12 | 6.0E-89 | 5803114 | NT | Homo sapiens: inner membrane protein, mitochondrial (mitofillin) (IMMT), mRNA |
| 2151 | 7130 | 12247 | 1.98 | 6.0E-89 | 4506124 | NT | Homo sapiens: serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA |
| 2366 | 7340 | 12456 | 5.05 | 6.0E-89 | 4507798 | NT | Homo sapiens: ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA |
| 2366 | 7340 | 12457 | 5.05 | 6.0E-89 | 4507798 | NT | Homo sapiens: ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3446 | 8454 | 13480 | 0.75 | 6.0E-89 | 7661817 | NT | Homo sapiens HSPC159 protein (HSPC159) mRNA |
| 4354 | 9345 | 14324 | 0.91 | 6.0E-89 | 7661737 | NT | Homo sapiens HSPC019 protein (HSPC019) mRNA |
| 4503 | 9493 | 14470 | 3.9 | 6.0E-89 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 4503 | 9493 | 14471 | 3.9 | 6.0E-89 | AB007866.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 4903 | 9882 | 14852 | 3.31 | 5.0E-89 | BE244323.1 | EST_HUMAN | TCBAP2EU0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP2EU0383 cDNA clone TCBAP0383 |
| 4903 | 9882 | 14853 | 3.31 | 5.0E-89 | BE244323.1 | EST_HUMAN | TCBAP2EU0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP0383 cDNA clone TCBAP0383 |
| 2807 | 7827 | 12843 | 0.95 | 3.0E-89 | AW976181.1 | EST_HUMAN | EST388290 MAGE resequences, MAGN Homo sapiens cDNA |
| 127 | 5442 | 10462 | 0.87 | 2.0E-89 | 7706670 | NT | Homo sapiens PXR26 protein (PXR26), mRNA |
| 127 | 5442 | 10463 | 0.87 | 2.0E-89 | 7706670 | NT | Homo sapiens PXR26 protein (PXR26), mRNA |
| 526 | 5561 | 10564 | 0.68 | 2.0E-89 | AB037763.1 | NT | Homo sapiens mRNA for KIAA1342 protein, partial cds |
| 2811 | 7831 | 12847 | 1.44 | 2.0E-89 | AI222095.1 | EST_HUMAN | q96c08.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GammaUTAMY TRANSEPTIDASE 1 PRECURSOR (HUMAN); contains AUU repetitive element |
| 4022 | 9018 | 14005 | 1.18 | 2.0E-89 | AF089897.1 | NT | Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds |
| 4030 | 9026 | 14014 | 4.76 | 2.0E-89 | X58742.1 | NT | H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11 |
| 4030 | 9026 | 14015 | 4.76 | 2.0E-89 | X58742.1 | NT | H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11 |
| 4223 | 9217 | 14196 | 1.09 | 2.0E-89 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4367 | 9359 | 14339 | 1.05 | 2.0E-89 | AJ007378.1 | NT | Homo sapiens GGT gene, exon 5 |
| 1046 | 6056 | 11084 | 3.19 | 8.0E-90 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1047 | 6056 | 11084 | 2.72 | 8.0E-90 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1310 | 7744 | 11357 | 3.66 | 8.0E-90 | BE670561.1 | EST_HUMAN | 766f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3' |
| 1310 | 7744 | 11358 | 3.66 | 8.0E-90 | BE670561.1 | EST_HUMAN | 766f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3' |
| 826 | 5846 | | 4.22 | 7.0E-90 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced |
| 2994 | 8012 | 13024 | 1.08 | 6.0E-90 | X91926.1 | NT | H.sapiens FCE-1 gene (exon 6) |
| 2994 | 8012 | 13025 | 1.08 | 6.0E-90 | X91926.1 | NT | H.sapiens FCE-1 gene (exon 6) |
| 4105 | 9099 | 14085 | 9.58 | 6.0E-90 | 8922398 | NT | Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA |
| 4105 | 9099 | 14083 | 9.58 | 6.0E-90 | 8922398 | NT | Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA |
| 154 | 5220 | | 78.69 | 5.0E-90 | AB035344.1 | NT | Homo sapiens TCL6 gene, exon 1-10b |
| 1173 | 6176 | 11210 | 2.39 | 5.0E-90 | U80226.1 | NT | Human gamma-aminobutyric acid transaminase mRNA, partial cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID No. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1784 6776 | 11867 | 1.48 | 5.0E-90 | A1222095.1 | EST_HUMAN | | q9g6c08_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element |
| 1784 6776 | 11868 | 1.48 | 5.0E-90 | A1222095.1 | EST_HUMAN | | q9g6c08_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element; |
| 2484 7452 | 12566 | 1.82 | 5.0E-90 | AF114487.1 | NT | | Homo sapiens intersectin long isoform (IISN) mRNA, complete cds |
| 300 5357 | 10369 | 2.4 | 4.0E-80 | AF231920.1 | NT | | Homo sapiens chromosome 21 unknown mRNA |
| 300 5357 | 10370 | 2.4 | 4.0E-80 | AF231920.1 | NT | | Homo sapiens chromosome 21 unknown mRNA |
| 1070 6078 | 11109 | 3.28 | 4.0E-90 | 4505316 | NT | | Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA |
| 1650 6646 | 11719 | 9.18 | 4.0E-90 | X39033.1 | NT | | H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16 |
| 4522 9512 | 14497 | 4.85 | 4.0E-90 | D87675.1 | NT | | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4653 9638 | 14629 | 1.95 | 4.0E-90 | AB033070.1 | NT | | Homo sapiens mRNA for KIAA1244 protein, partial cds |
| 4673 9658 | 14641 | 1.82 | 4.0E-90 | M95867.1 | NT | | Human prohormone converting enzyme (NEC2) gene, exon 8 |
| 5010 9981 | 14956 | 0.92 | 4.0E-90 | 5729777 | NT | | Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA |
| 213 5276 | 10290 | 4.2 | 2.0E-90 | BE537913.1 | EST_HUMAN | | 601067378F NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5' |
| 1154 6158 | 11191 | 71.49 | 2.0E-90 | 5031748 | NT | | Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA |
| 1154 6158 | 11192 | 71.49 | 2.0E-90 | 5031748 | NT | | Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA |
| 3755 8758 | 13757 | 1.88 | 2.0E-90 | A1138213.1 | EST_HUMAN | | q5j4c02_x1 Soares_qbacteria_8t9eweeks_2NbHf8t9W Homo sapiens cDNA clone IMAGE:1713410 3' |
| 4550 9538 | 14524 | 0.97 | 2.0E-90 | AB006627.1 | NT | | Similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.; |
| 4754 9739 | 14724 | 8.45 | 2.0E-90 | 5729835 | NT | | Homo sapiens mRNA for KIAA0289 gene, partial cds |
| 274 5333 | 10346 | 5.3 | 1.0E-90 | 4502168 | NT | | Homo sapiens GRB2-related adaptor protein (GRAF) mRNA |
| 373 7693 | 10436 | 1.98 | 1.0E-90 | AF231920.1 | NT | | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 374 7693 | 10436 | 1.9 | 1.0E-90 | AF231920.1 | NT | | Homo sapiens chromosome 21 unknown mRNA |
| 686 5710 | 10723 | 1.73 | 1.0E-90 | A1237589.1 | NT | | Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial |
| 686 5710 | 10724 | 1.73 | 1.0E-90 | A1237589.1 | NT | | Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial |
| 720 5743 | 10761 | 11.11 | 1.0E-90 | AF264750.1 | NT | | Homo sapiens ALR-like protein mRNA, partial cds |
| 720 5743 | 10762 | 11.11 | 1.0E-90 | AF264750.1 | NT | | Homo sapiens ALR-like protein mRNA, partial cds |
| 1093 6100 | | 3 | 1.0E-90 | 4507828 | NT | | Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA |
| 1287 6286 | 11329 | 2.29 | 1.0E-90 | AF098154.1 | NT | | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3 |
| 1287 6286 | 11330 | 2.29 | 1.0E-90 | AF098154.1 | NT | | Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3 |
| 1628 6625 | | 4.57 | 1.0E-90 | BE37984.1 | EST_HUMAN | | 601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1861 | 6850 | 11938 | 2.56 | 1.0E-90 | 11420514 | NT | Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA |
| 2780 | 7801 | 12819 | 9.3 | 1.0E-90 | 6005720 | NT | Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA |
| 3761 | 8764 | 13765 | 0.99 | 1.0E-90 | AB020710.1 | NT | Homo sapiens mRNA for KIAA08903 protein, partial cds |
| 3761 | 8764 | 13766 | 0.99 | 1.0E-90 | AB020710.1 | NT | Homo sapiens mRNA for KIAA08903 protein, partial cds |
| | | | | | | | Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced |
| 4299 | 9291 | 14278 | 1.62 | 1.0E-90 | AF167340.1 | NT | HUM0005381 Liver HepG2 cell line. 1-Homo sapiens cDNA clone s381 3' |
| 4073 | 9067 | 14057 | 6.67 | 8.0E-91 | D12234.1 | EST_HUMAN | Z90604.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3' |
| 3394 | 8402 | 13428 | 2.26 | 5.0E-91 | AA702794.1 | EST_HUMAN | AU149539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5' |
| 4385 | 9376 | 14355 | 1.19 | 5.0E-91 | AU145639.1 | EST_HUMAN | AU149539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5' |
| 4385 | 9376 | 14356 | 1.19 | 5.0E-91 | AU145639.1 | EST_HUMAN | Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA |
| 4664 | 9649 | 14636 | 1.09 | 5.0E-91 | 7110634 | NT | Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA |
| 4664 | 9649 | 14637 | 1.09 | 5.0E-91 | 7110634 | NT | Homo sapiens: lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds |
| 3129 | 8145 | 13165 | 1.87 | 4.0E-91 | AF156776.1 | NT | Homo sapiens: lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds |
| 3129 | 8145 | 13166 | 1.67 | 4.0E-91 | AF156776.1 | NT | Homo sapiens: solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA |
| 1578 | 6575 | 11637 | 1.86 | 3.0E-91 | 11430193 | NT | Homo sapiens: solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA |
| 1578 | 6575 | 11638 | 1.86 | 3.0E-91 | 11430193 | NT | Homo sapiens: ubiquitin-conjugating BIR-domain enzyme APOLION mRNA, complete cds |
| 1754 | 7701 | 11830 | 1.4 | 3.0E-91 | AF265555.1 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3265 | 8278 | 13301 | 1.55 | 3.0E-91 | AI163293.2 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3380 | 8388 | 13410 | 3.62 | 3.0E-91 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3380 | 8388 | 13411 | 3.62 | 3.0E-91 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3699 | 8703 | 13706 | 1.57 | 3.0E-91 | AF084530.1 | NT | Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds |
| 4458 | 9448 | 14428 | 6.17 | 3.0E-91 | M30938.1 | NT | Human Ku (F70/p80) subunit mRNA, complete cds |
| 4820 | 9804 | 14785 | 1.2 | 3.0E-91 | AL163285.2 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 4820 | 9804 | 14786 | 1.2 | 3.0E-91 | AL163285.2 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 49 | 5130 | 10124 | 2.61 | 1.0E-91 | AL163284.2 | NT | Homo sapiens randomly primed sublibrary Homo sapiens cDNA clone IMAGE:2735280 3' |
| 1226 | 6225 | 11271 | 5.11 | 1.0E-91 | AW449746.1 | EST_HUMAN | U+H-B13-akts-d-01-0-U1 s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3' |
| 1222 | 6222 | 11265 | 7.33 | 9.0E-92 | AJ001689.1 | NT | Homo sapiens NK2D gene, exon 10 |
| 1222 | 6222 | 11266 | 7.33 | 9.0E-92 | AJ001689.1 | NT | Homo sapiens NK2D gene, exon 10 |
| 91 | 5168 | 10178 | 6.58 | 8.0E-92 | W26367.1 | EST_HUMAN | 26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA clone IMAGE:3614687 5' |
| 283 | 5341 | 10354 | 7.99 | 8.0E-92 | BE38663.1 | EST_HUMAN | 601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5' |
| 25 | 5105 | 10089 | 2.65 | 7.0E-92 | AB031007.1 | NT | Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype |
| 235 | 7716 | 10307 | 1 | 7.0E-92 | AB018301.1 | NT | Homo sapiens mRNA for KIAA0758 protein, partial cds |
| 235 | 7716 | 10308 | 1 | 7.0E-92 | AB018301.1 | NT | Homo sapiens mRNA for KIAA0758 protein, partial cds |
| 586 | 5617 | | 0.93 | 7.0E-92 | AF007822.1 | NT | Homo sapiens cytoplasmic Sepsase truncated isoform mRNA, complete cds |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1261 | 6259 | 11302 | 2.83 | 7.0E-92 | 4502384 | NT | Homo sapiens: B-cell CLL/lymphoma 7b (BCL7B) mRNA |
| 2123 | 7103 | 12215 | 8.39 | 7.0E-92 | 5031570 | NT | Homo sapiens: ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA |
| 2123 | 7103 | 12216 | 8.39 | 7.0E-92 | 5031570 | NT | Homo sapiens: ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA |
| 2493 | 7461 | 12576 | 2.56 | 7.0E-92 | AF167706_1 | NT | Homo sapiens: cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds |
| 2653 | 7613 | 12723 | 5.83 | 7.0E-92 | 6005738 | NT | Homo sapiens: NRAS-related gene (DIS155E), mRNA |
| 2679 | 76317 | 12752 | 0.93 | 7.0E-92 | AB031007_1 | NT | Homo sapiens: DNA, MHC class I region, 7.1 ancestral haplotype |
| 32270 | 10047 | 13304 | 0.67 | 7.0E-92 | 4507500 | NT | Homo sapiens: T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA |
| 32270 | 10047 | 13305 | 0.67 | 7.0E-92 | 4507500 | NT | Homo sapiens: T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA |
| 4455 | 9445 | 14425 | 1.24 | 7.0E-92 | S71824_1 | NT | N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt] |
| 4455 | 9445 | 14426 | 1.24 | 7.0E-92 | S71824_1 | NT | N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt] |
| 4844 | 9B26 | 14801 | 0.94 | 7.0E-92 | AL163281_2 | NT | Homo sapiens: chromosome 21 segment HS21C081 |
| 1552 | 6549 | | 1.37 | 5.0E-92 | BE3908B2_1 | EST_HUMAN | 601283012F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606018 5' |
| 2892 | 7650 | 12764 | 2.21 | 3.0E-92 | BE3909714_1 | EST_HUMAN | 601501242F NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5' |
| 26 | 5106 | 10090 | 1.42 | 2.0E-92 | 4501868 | NT | Homo sapiens: activin A receptor, type IIb (ACVR2B), mRNA |
| 178 | 5241 | 10251 | 3.37 | 2.0E-92 | 11422946 | NT | Homo sapiens: hypothetical protein dj462O23_2 (DJ462O23_2), mRNA |
| 178 | 5241 | 10252 | 3.37 | 2.0E-92 | 11422946 | NT | Homo sapiens: hypothetical protein dj462O23_2 (DJ462O23_2), mRNA |
| 740 | 5763 | 10787 | 2.34 | 2.0E-92 | BE299190_1 | EST_HUMAN | 6011183337F NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5' |
| 740 | 5763 | 10788 | 2.34 | 2.0E-92 | BE299190_1 | EST_HUMAN | 6011183337F NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5' |
| 1676 | 6672 | | 1.45 | 2.0E-92 | ST8653_1 | NT | mrg=mus-related [human, Genomic, 2416 nt] |
| 1896 | 6884 | 11976 | 1.59 | 2.0E-92 | AL818119_1 | EST_HUMAN | wk27d07_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 |
| 1896 | 6884 | 11977 | 1.59 | 2.0E-92 | AL818119_1 | EST_HUMAN | Q12844 BREAKPOINT CLUSTER REGION PROTEIN; |
| 1995 | 6979 | 12084 | 8.59 | 2.0E-92 | 4506860 | NT | Q12844 BREAKPOINT CLUSTER REGION PROTEIN; |
| 2588 | 7551 | 12666 | 15.93 | 2.0E-92 | 6912457 | NT | Homo sapien's syndecan 4 (amphibiglycan, ruydoseen) (SDC4), mRNA |
| 2756 | 6611 | 11676 | 3.99 | 2.0E-92 | 11418424 | NT | Homo sapien's calcineurin binding protein 1 (KIAA0330), mRNA |
| 2756 | 6611 | 11677 | 3.99 | 2.0E-92 | 11418424 | NT | Homo sapien's collagen, type XII, alpha 1 (COL12A1), mRNA |
| 3532 | 8538 | 13543 | 1.16 | 2.0E-92 | AF231919_1 | NT | Homo sapien's collagen, type XII, alpha 1 (COL12A1), mRNA |
| 3532 | 8538 | 13544 | 1.16 | 2.0E-92 | AF231919_1 | NT | Homo sapien's syndecan 2 (unknown), mRNA |
| 3602 | 8609 | 13617 | 5.87 | 2.0E-92 | 5803180 | NT | Homo sapiens stress-induced phosphoprotein 1 (Hsp70/Hsp80-organizing protein) (STIP1), mRNA |
| 4165 | 9160 | 14147 | 1.16 | 2.0E-92 | M10976_1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4835 | 9819 | | 2.79 | 2.0E-92 | AL040437.1 | EST_HUMAN | DKF7p434C0414_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5' |
| 1813 | 6803 | 11895 | 2.03 | 1.0E-92 | R78078.1 | EST_HUMAN | y80e08_r1 Scates placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5' |
| 1813 | 6803 | 11896 | 2.03 | 1.0E-92 | R78078.1 | EST_HUMAN | y80e08_r1 Scates placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5' |
| 2020 | 7003 | 12103 | 40.93 | 1.0E-92 | 45066668 | NT | Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA |
| 1979 | 6964 | 12070 | 2.63 | 9.0E-93 | AU121681.1 | EST_HUMAN | AU121681MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5' |
| 1991 | 6976 | | 27.81 | 9.0E-93 | AA316723.1 | EST_HUMAN | EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29 |
| 3534 | 8540 | 13546 | 1.75 | 9.0E-93 | BE38857.1 | EST_HUMAN | 601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5' |
| 4209 | 9202 | 14184 | 1.1 | 9.0E-93 | AU121681.1 | EST_HUMAN | AU121681MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5' |
| 244 | 5304 | 10314 | 8.34 | 7.0E-93 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 1362 | 6359 | 11409 | 2.07 | 5.0E-93 | AB014511.1 | NT | Homo sapiens mRNA for KIAA0671 protein, partial cds |
| 1383 | 6380 | 11429 | 8.53 | 5.0E-93 | AJ674184.1 | EST_HUMAN | wcd09c08_x1_NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3' |
| 1383 | 6380 | 11430 | 8.53 | 5.0E-93 | AJ674184.1 | EST_HUMAN | wcd09c08_x1_NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3' |
| 3162 | 8178 | 13200 | 4.58 | 5.0E-93 | X04201.1 | NT | Human skeletal muscle 1.3 kb mRNA for tropomyosin |
| 86 | 5163 | | 5.69 | 4.0E-93 | AA459933.1 | EST_HUMAN | ZX5049_s1 Scates testis_NIH Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM : |
| 442 | 5479 | 10496 | 1.62 | 4.0E-93 | | 4557879 | Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA |
| 442 | 5479 | 10497 | 1.62 | 4.0E-93 | | 4557879 | Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA |
| 763 | 5784 | 10812 | 4.03 | 4.0E-93 | | 7657454 | Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| 763 | 5784 | 10813 | 4.03 | 4.0E-93 | | 7657454 | Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA |
| 1164 | 6167 | 11201 | 1.25 | 4.0E-93 | | 8923658 | Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA |
| 1932 | 6918 | 12017 | 3.59 | 4.0E-93 | AF047677.1 | NT | Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5 |
| 2183 | 7162 | 12282 | 0.93 | 4.0E-93 | AF157476.1 | NT | Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds |
| 2533 | 7498 | 12618 | 1.01 | 4.0E-93 | | 7556972 | Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA |
| 3487 | 8495 | 13512 | 0.79 | 4.0E-93 | | 7705396 | Homo sapiens tumor antigen SL-P-8p (HCC8), mRNA |
| 3935 | 8934 | 13927 | 5.14 | 4.0E-93 | | 4504654 | Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA |
| 4863 | 8495 | 13512 | 0.83 | 4.0E-93 | | 7705396 | Homo sapiens tumor antigen SL-P-8p (HCC8), mRNA |
| 3567 | 8574 | 13579 | 19.66 | 3.0E-93 | Bf680630.1 | EST_HUMAN | 602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5' |
| 3567 | 8574 | 13580 | 19.66 | 3.0E-93 | Bf680630.1 | EST_HUMAN | 602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5' |
| 190 | 5254 | 10265 | 31.68 | 2.0E-93 | AB015610.1 | NT | Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds |
| 190 | 5254 | 10266 | 31.68 | 2.0E-93 | AB015610.1 | NT | Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds |
| 321 | 5376 | 10386 | 9.39 | 2.0E-93 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 322 | 5376 | 10386 | 6.39 | 2.0E-93 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 2072 | 7054 | 12164 | 1.96 | 2.0E-93 | U40763.1 | NT | Human Clik-associated RS cyclophilin CARs-Cyp mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2416 | 7387 | 12507 | 1.74 | 2.0E-93 | BE252982.1 | EST_HUMAN | 601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5' |
| 4986 | 9943 | 14920 | 1.01 | 2.0E-93 | BE263201.1 | EST_HUMAN | 601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5' |
| 102 | 5179 | 10189 | 2.66 | 1.0E-93 | AF238997.1 | NT | Homo sapiens CTR1 pseudogene |
| 102 | 5179 | 10190 | 2.66 | 1.0E-93 | AF238997.1 | NT | Homo sapiens CTR1 pseudogene |
| 514 | 5549 | 10554 | 17.48 | 1.0E-93 | 7657016 | NT | Homo sapiens hypothetical protein D3328E19.C1.1, mRNA oy84b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 |
| 595 | 5626 | 10675 | 3.67 | 1.0E-93 | AI146755.1 | EST_HUMAN | ZINC FINGER PROTEIN_; |
| 861 | 5880 | 10921 | 7.39 | 1.0E-93 | DB7675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 1217 | 6216 | 11256 | 8.15 | 1.0E-93 | 8923270 | NT | Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA |
| 1217 | 6216 | 11257 | 8.15 | 1.0E-93 | 8923270 | NT | Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA |
| 1325 | 6323 | 11370 | 1.13 | 1.0E-93 | AB046783.1 | NT | Homo sapiens mRNA for KIAA1563 protein, partial cds |
| 1327 | 6325 | 11372 | 3.03 | 1.0E-93 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds |
| 2276 | 7252 | 12370 | 5.14 | 1.0E-93 | AF231981.1 | NT | Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds |
| 2394 | 7365 | 12487 | 12.91 | 1.0E-93 | AF055066.1 | NT | Homo sapiens NHC class 1 region |
| 2435 | 7406 | | 1.31 | 1.0E-93 | AL137200.1 | NT | Novel human gene mapping to chromosome 1 |
| 2749 | 6275 | 11315 | 1.39 | 1.0E-93 | BE297369.1 | EST_HUMAN | 601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5' |
| 2749 | 6275 | 11316 | 1.39 | 1.0E-93 | BE297369.1 | EST_HUMAN | 601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5' |
| 2863 | 7883 | 12803 | 3.34 | 1.0E-93 | DB7675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 3144 | 8160 | | 1.76 | 1.0E-93 | AF231981.1 | NT | Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds |
| 4305 | 9297 | 14283 | 2.36 | 1.0E-93 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3836 | 8858 | 13864 | 3.44 | 6.0E-94 | AF142482.1 | NT | Homo sapiens transcription enhancer factor-5 mRNA, complete cds |
| 1806 | 6797 | | 38.53 | 4.0E-94 | LO5094.1 | NT | Homo sapiens ribosomal protein L27 mRNA, complete cds |
| 2656 | 7549 | 12664 | 1.13 | 4.0E-94 | 4506008 | NT | Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA |
| 3567 | 8594 | 13598 | 1.02 | 4.0E-94 | AW197851.1 | EST_HUMAN | xn89f12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3' |
| 3667 | 8594 | 13599 | 1.02 | 4.0E-94 | AW197851.1 | EST_HUMAN | xn89f12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3' |
| 4579 | 9567 | 14556 | 3.55 | 4.0E-94 | AI591312.1 | EST_HUMAN | PROTEIN TYROSINE PHOSPHATASE : |
| 607 | 5634 | 10535 | 3.13 | 3.0E-94 | AB022785.1 | NT | Homo sapiens ASH2L gene, complete cds, similar to <i>Drosophila</i> ash2 gene |
| 711 | 5735 | 10751 | 1.52 | 3.0E-94 | 4502506 | NT | Homo sapiens complement component 5 (C5) mRNA |
| 1701 | 6636 | 11772 | 3.56 | 3.0E-94 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds |
| 1701 | 6636 | 11773 | 3.56 | 3.0E-94 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds |
| 1735 | 6730 | 11807 | 6.42 | 3.0E-94 | 4557556 | NT | Homo sapiens ET1 binding protein p300 (EP300) mRNA |

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Table 4

Single Exon Probes Expressed in HBL 100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 4065 | 9059 | 14046 | 0.67 | 3.0E-94 | AA464805.1 | EST_HUMAN | zw63g08.r1 Soares_total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5' |
| 5051 | 10022 | 14991 | 0.7 | 3.0E-94 | 4507848 | NT | Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA |
| 148 | 5214 | 10228 | 2.88 | 1.0E-94 | BE295714.1 | EST_HUMAN | 601175762f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5' |
| 3015 | 8032 | 13042 | 2.59 | 1.0E-94 | BE253433.1 | EST_HUMAN | 60111696f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5' |
| 3015 | 8032 | 13043 | 2.59 | 1.0E-94 | BE253433.1 | EST_HUMAN | 60111696f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5' |
| 4233 | 9227 | 14211 | 1.7 | 1.0E-94 | 9506692 | NT | Homo sapiens hypothetical protein (FLJ20746), mRNA |
| 1441 | 6444 | 11503 | 5.95 | 9.0E-95 | AF021302.1 | NT | Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds |
| 3082 | 8098 | 13112 | 1.09 | 9.0E-95 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 3082 | 8098 | 13113 | 1.09 | 9.0E-95 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 4406 | 9397 | 14380 | 3.37 | 8.0E-95 | A1700998.1 | EST_HUMAN | w609d4.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 4406 | 9397 | 14381 | 3.37 | 8.0E-95 | A1700998.1 | EST_HUMAN | w609d4.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN); |
| 273 | 5332 | 10344 | 10.53 | 7.0E-95 | D877675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 273 | 5332 | 10345 | 10.53 | 7.0E-95 | D877675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 4241 | 9235 | 14219 | 5.66 | 7.0E-95 | M95708.1 | NT | Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds |
| 4289 | 9281 | | | 1.4 | 7.0E-95 | AL163246.2 | NT |
| 1605 | 6601 | 11662 | 3.13 | 2.0E-95 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 1605 | 6601 | 11663 | 3.13 | 2.0E-95 | 7662027 | NT | Homo sapiens KIAA0255 gene product (KIAA0255), mRNA |
| 1901 | 6888 | 11982 | 3.11 | 2.0E-95 | 4607512 | NT | Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA |
| 1904 | 6891 | 11986 | 1.74 | 2.0E-95 | BE393873.1 | EST_HUMAN | 60131216.f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5' |
| 2359 | 7333 | 12449 | 1.55 | 2.0E-95 | 5453665 | NT | Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA |
| 2359 | 7333 | 12450 | 1.55 | 2.0E-95 | 5453665 | NT | Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA |
| 2396 | 7367 | 12488 | 2.79 | 2.0E-95 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 2442 | 7412 | 12528 | 1.84 | 2.0E-95 | 4756423 | NT | Homo sapiens glycine cleavage system protein H (carbamoyl carrier) (GCSH) mRNA |
| 3084 | 8100 | 13115 | 1.95 | 2.0E-95 | AF015452.1 | NT | Homo sapiens Usurpin-gamma mRNA, complete cds |
| 3484 | 8492 | 13508 | 2.78 | 2.0E-95 | 7705900 | NT | Homo sapiens unconventional myosin-15 (LOC51168), mRNA |
| 3484 | 8492 | 13509 | 2.78 | 2.0E-95 | 7705900 | NT | Homo sapiens unconventional myosin-15 (LOC51168), mRNA |
| 3537 | 8543 | 13549 | 1.17 | 2.0E-95 | AB037807.1 | NT | Homo sapiens mRNA for KIAA1386 protein, partial cds |
| 3664 | 8669 | 13674 | 1 | 2.0E-95 | A1290264.1 | EST_HUMAN | qm01cd2.x1 Soares_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 |
| 4236 | 9230 | 14213 | 1.61 | 2.0E-95 | 7657185 | NT | Homo sapiens hypothetical protein (HS322B1A), mRNA |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4873 | 9852 | 14827 | 2.65 | 2.0E-95 | 7661979 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 4917 | 9895 | 14859 | 0.92 | 2.0E-95 | AA447931.1 | EST_HUMAN | zv11007_r1_Soares_total_fetus_Nb2HFB_9w_Homo_sapiens cDNA clone IMAGE:786157 5' |
| 4917 | 9895 | 14870 | 0.92 | 2.0E-95 | AA447931.1 | EST_HUMAN | zv11007_r1_Soares_total_fetus_Nb2HFB_9w_Homo_sapiens cDNA clone IMAGE:786157 5' |
| 439 | 7720 | 10493 | 3.42 | 8.0E-96 | BE907607.1 | EST_HUMAN | 6011497608F1NH_MGC_70_Homo_sapiens cDNA clone IMAGE:3899761 5' |
| 439 | 7720 | 10494 | 3.42 | 8.0E-96 | BE907607.1 | EST_HUMAN | 6011497608F1NH_MGC_70_Homo_sapiens cDNA clone IMAGE:3899761 5' |
| 3813 | 8816 | 13822 | 1.16 | 7.0E-96 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 2198 | 7176 | 12299 | 2.4 | 6.0E-96 | BE171984.1 | EST_HUMAN | MR0-HT0559-2b0200-002-3b7 HT0559 Homo sapiens cDNA |
| 3244 | 8257 | 13278 | 0.86 | 6.0E-96 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3402 | 8411 | 13437 | 37.31 | 6.0E-96 | M26873.1 | NT | Human glyceratehyde-3-phosphate dehydrogenase pseudogene 3' end |
| 3118 | 5373 | 10382 | 3.23 | 5.0E-96 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 832 | 5851 | 10889 | 3.33 | 5.0E-96 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 832 | 5851 | 10890 | 3.33 | 5.0E-96 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 2545 | 7510 | | 2.15 | 5.0E-96 | 11416767 | NT | Homo sapiens Phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA |
| 4748 | 9733 | | 1.28 | 5.0E-96 | X60812.1 | NT | H. sapiens DNA for monooamine oxidase type A(7) (partial) |
| 4067 | 9061 | | 10.55 | 3.0E-96 | H68656.1 | EST_HUMAN | y87h12_r1_Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5' |
| 4112 | 5449 | | 4.94 | 2.0E-96 | 4_503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 738 | 5761 | 10784 | 1.2 | 2.0E-96 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C043 |
| 1756 | 6749 | 11832 | 1.81 | 2.0E-96 | 7706205 | NT | Homo sapiens CGI-201 protein (LOC51340), mRNA |
| 4613 | 9599 | 14585 | 2.68 | 2.0E-96 | BE148074.1 | EST_HUMAN | RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA |
| 663 | 5669 | 10698 | 2.97 | 1.0E-96 | Y18890.1 | NT | Human endogenous retrovirus type K (HERV-K), gag, pol and env genes |
| 1743 | 6738 | 111814 | 4.56 | 1.0E-96 | AW955054.1 | EST_HUMAN | EST367124 IMAGE sequences, MAGC Homo sapiens cDNA |
| 1743 | 6738 | 111815 | 4.56 | 1.0E-96 | AW955054.1 | EST_HUMAN | EST367124 IMAGE sequences, MAGC Homo sapiens cDNA |
| 2204 | 7705 | 12305 | 1.95 | 1.0E-96 | U51472.2 | NT | Felis catus superfast myosin heavy chain (sMHC) mRNA, complete cds |
| 925 | 5942 | 10976 | 3.84 | 4.0E-97 | BE004436.1 | EST_HUMAN | CMD-BN0106-170300-283-a06 BN0106 Homo sapiens cDNA |
| 1867 | 6856 | 11944 | 1.34 | 4.0E-97 | 5453572 | NT | Homo sapiens briefein A-inhibited guanine nucleotide-exchange protein 2 (BiG2), mRNA |
| 241 | 5302 | 10312 | 2.28 | 3.0E-97 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 863 | 5882 | 10923 | 9.5 | 3.0E-97 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 863 | 5882 | 10924 | 9.5 | 3.0E-97 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 1415 | 7747 | 11473 | 1.64 | 3.0E-97 | 4758813 | NT | Homo sapiens N-myco (and STATA) interactor (NM), mRNA |
| 2371 | 7706 | 12462 | 2.66 | 3.0E-97 | U36255.1 | NT | Human beta-prime-adipin (BAM22) gene, exon 7 |
| 3186 | 8202 | 13224 | 1.14 | 3.0E-97 | 5174478 | NT | Homo sapiens pericentrin (PCNT) mRNA |
| 4635 | 9620 | 14612 | 35.24 | 1.0E-97 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 890 | 5908 | 10948 | 6.71 | 9.0E-98 | BE090973.1 | EST_HUMAN | PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA |
| 1257 | 6225 | 11297 | 1.1 | 9.0E-98 | 8393692 | NT | Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA |
| 5021 | 9982 | 14966 | 1.03 | 9.0E-98 | 11419594 | NT | Homo sapiens F5H1 primary response (LRRPR1, rat) homolog 1 (F5HPR1), mRNA |
| 24 | 5104 | | | 8.0E-98 | AJ251158.1 | NT | Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS |
| 1529 | 6526 | 11584 | 1.06 | 8.0E-98 | 5031810 | NT | Homo sapiens II.2-inducible T-cell kinase (ITK), mRNA |
| 1529 | 6526 | 11585 | 1.06 | 8.0E-98 | 5031810 | NT | Homo sapiens II.2-inducible T-cell kinase (ITK), mRNA |
| 1688 | 6684 | 11759 | 3.31 | 8.0E-98 | AB017007.1 | NT | Homo sapiens FMS2L_16 mRNA, partial cds |
| 1688 | 6684 | 11760 | 3.31 | 8.0E-98 | AB017007.1 | NT | Homo sapiens FMS2L_16 mRNA, partial cds |
| 3706 | 8710 | 13713 | 6.04 | 8.0E-98 | J04469.1 | NT | Human mitochrondrial creatine kinase (CKMT) gene, complete cds |
| 2113 | 7093 | 12207 | 1.06 | 3.0E-98 | JA03124.1 | EST_HUMAN | AAJ403124_3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18 |
| 2534 | 7499 | 12619 | 1.4 | 3.0E-98 | AB014607.1 | NT | Homo sapiens mRNA for KIAA0707 protein, partial cds |
| 2676 | 7634 | 12775 | 2.13 | 3.0E-98 | AA077498.1 | EST_HUMAN | 781BH01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01 |
| 726 | 5749 | 10770 | 2.43 | 2.0E-98 | BE261694.1 | EST_HUMAN | 601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE3502245_5 |
| 2026 | 7009 | 12115 | 2.25 | 2.0E-98 | BE291281.1 | EST_HUMAN | 601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE3528134_5 |
| 2176 | 7155 | 12275 | 2.4 | 2.0E-98 | AL165202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 3989 | 8987 | 13973 | 0.94 | 2.0E-98 | 8923308 | NT | Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA |
| 4172 | 9167 | 14154 | 0.68 | 2.0E-98 | AF032597.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 4214 | 9207 | 14186 | 3.27 | 2.0E-98 | 4758331 | NT | Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA |
| 4680 | 9665 | 14646 | 1.61 | 2.0E-98 | AF218902.1 | NT | Homo sapiens attractin precursor (ATRIN) gene, exon 18 |
| 4680 | 9665 | 14647 | 1.61 | 2.0E-98 | AF218902.1 | NT | Homo sapiens attractin precursor (ATRIN) gene, exon 16 |
| 403 | 5439 | 10459 | 91.85 | 1.0E-98 | AB62007.1 | EST_HUMAN | W26504_x1_NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE2261743' similar to SW:RL2B_HUMAN |
| 452 | 5489 | 10504 | 2.47 | 1.0E-98 | AW998611.1 | EST_HUMAN | P29316_60S RIBOSOMAL PROTEIN L23A_ |
| 1761 | 6753 | 11838 | 68.95 | 1.0E-98 | N49818.1 | EST_HUMAN | y23f05.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE243585_5' similar to SW:RL2B_HUMAN |
| 2069 | 7051 | 12159 | 1.5 | 6.0E-99 | 11430555 | NT | PIR:S54204_S64204 ribosomal protein L29 - human ; |
| 2069 | 7051 | 12160 | 1.5 | 6.0E-99 | 11430555 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA |
| 4605 | 9593 | 14579 | 1.1 | 6.0E-99 | 4502660 | NT | Homo sapiens CD34 antigen (CD34) mRNA |
| 1924 | 6910 | 12005 | 0.92 | 5.0E-99 | Y11365.1 | NT | H.sapiens IMPA gene, exon 8 |
| 4432 | 9422 | 14408 | 1.25 | 5.0E-99 | AF008660.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV7S2 region |
| 4586 | 9574 | 14584 | 1.82 | 5.0E-99 | AF265555.1 | NT | Homo sapiens ubiquitin-conjugating B1R-domain enzyme APOLLON mRNA, complete cds |
| 4586 | 9574 | 14585 | 1.82 | 5.0E-99 | AF265555.1 | NT | Homo sapiens ubiquitin-conjugating B1R-domain enzyme APOLLON mRNA, complete cds |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1220 | 6220 | | 21.29 | 2.0E-99 | AW274792.1 | EST_HUMAN | xp0960521 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI_NON-MUSCLE ISOFORM (HUMAN); |
| 3184 | 8200 | 13223 | 2.08 | 2.0E-99 | M309383.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 4412 | 9402 | 14387 | 2.65 | 2.0E-99 | AF095703.1 | NT | Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds |
| 313 | 5368 | 10379 | 1.21 | 1.0E-99 | AF114487.1 | NT | Homo sapiens intersect long isoform (ITSN) mRNA, complete cds |
| 378 | 5425 | 10440 | 1.23 | 1.0E-99 | 11526150 | NT | Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA |
| 1396 | 6393 | 11447 | 8.91 | 1.0E-99 | M309383.1 | NT | Human Ku (p70/p80) subunit mRNA, complete cds |
| 1525 | 6522 | 11578 | 3.27 | 1.0E-99 | AF192523.1 | NT | Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds |
| 1525 | 6522 | 11579 | 3.27 | 1.0E-99 | AF192523.1 | NT | Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds |
| 1886 | 6875 | 11964 | 1.12 | 1.0E-99 | 4503730 | NT | Homo sapiens FK506-binding protein 8 (35kD) (FKBP8) mRNA, and translated products |
| 1886 | 6875 | 11965 | 1.12 | 1.0E-99 | 4503730 | NT | Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products |
| 3011 | 8028 | 13039 | 1.27 | 1.0E-99 | J03171.1 | NT | Human intereron-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds |
| 4255 | 9249 | 14233 | 2.45 | 1.0E-99 | AF098018.1 | NT | Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14 |
| 4255 | 9249 | 14234 | 2.45 | 1.0E-99 | AF098018.1 | NT | Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14 |
| 1 | 5083 | 10067 | 1.69 | 1.0E-100 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 2 | 5083 | 10067 | 1.64 | 1.0E-100 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 67 | 5146 | 10151 | 1.24 | 1.0E-100 | 11418230 | NT | Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA |
| 67 | 5146 | 10152 | 1.24 | 1.0E-100 | 11418230 | NT | Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA |
| 85 | 5162 | 10174 | 2.54 | 1.0E-100 | AW275237.1 | EST_HUMAN | x77861.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3' |
| 168 | 5233 | 10243 | 0.69 | 1.0E-100 | AL163206.2 | NT | Homo sapiens chromosomes 21 segment HS21C006 |
| 315 | 5370 | 10381 | 1.05 | 1.0E-100 | AL163249.2 | NT | Homo sapiens chromosomes 21 segment HS21C049 |
| 341 | 5393 | 10400 | 1.8 | 1.0E-100 | T05087.1 | EST_HUMAN | ES10287 fetal brain, Stratagene (cat#38206) Homo sapiens cDNA clone HFBCR32 |
| 434 | 5472 | | 1.98 | 1.0E-100 | AF003528.1 | NT | Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 486 | 5523 | | 19.01 | 1.0E-100 | X89631.1 | NT | G gorilla DNA for ZNF80 gene homolog |
| 506 | 5541 | 10547 | 1.38 | 1.0E-100 | BE180609.1 | EST_HUMAN | RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA |
| 1003 | 6013 | 11042 | 2.46 | 1.0E-100 | 7661685 | NT | Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA |
| 1003 | 6013 | 11043 | 2.48 | 1.0E-100 | 7661685 | NT | Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA |
| 1514 | 6512 | | 1.64 | 1.0E-100 | AW207555.1 | EST_HUMAN | U1-H-B1-aff-c-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3' |
| 1519 | 6516 | 11573 | 1.15 | 1.0E-100 | AI200857.1 | EST_HUMAN | qf62109.x1 Socares testis_NHT Homo sapiens cDNA clone IMAGE:1754635 3' similar to SW:CYT_COTJA P81061 CYSTATIN; |
| 1827 | 6817 | 11911 | 1.44 | 1.0E-100 | AB032994.1 | NT | Homo sapiens mRNA for KIAA1168 protein, partial cds |
| 2634 | 7594 | 12707 | 1.52 | 1.0E-100 | 11418976 | NT | Homo sapiens KIAA0957 protein (KIAA0957), mRNA |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2952 | 7971 | | 4.15 | 1.0E-100 | D11078.1 | NT | Homo sapiens RGH2 gene, retrovirus-like element |
| 4089 | 9083 | 14074 | 1.57 | 1.0E-100 | AF057354.1 | NT | Homo sapiens myotubularin-related protein 1a mRNA, partial cds |
| 4114 | 9108 | 14093 | 2.28 | 1.0E-100 | 45037922 | NT | Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA |
| 4920 | 9898 | 14872 | 3.82 | 1.0E-100 | 5032104 | NT | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 4920 | 9898 | 14873 | 3.82 | 1.0E-100 | 5032104 | NT | Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA |
| 76 | 5154 | 10164 | 1.88 | 1.0E-101 | 7110714 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 76 | 5154 | 10165 | 1.88 | 1.0E-101 | 7110714 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 677 | 5702 | 10710 | 2.59 | 1.0E-101 | AB007915.2 | NT | Homo sapiens mRNA for KIAA0446 protein, partial cds |
| 694 | 5718 | 10735 | 6.32 | 1.0E-101 | 7110734 | NT | Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA |
| 694 | 5718 | 10736 | 6.32 | 1.0E-101 | 7110734 | NT | Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA |
| 762 | 5783 | 10811 | 4.64 | 1.0E-101 | 7657454 | NT | Homo sapiens pescadillo (zebrafish) homolog 1 containing BRCT domain (PES1), mRNA |
| 843 | 5862 | 10902 | 3.85 | 1.0E-101 | 4503914 | NT | Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA |
| 970 | 5985 | 11020 | 34.36 | 1.0E-101 | BF68128.1 | EST_HUMAN | 602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5' |
| 1035 | 6045 | 11074 | 1.9 | 1.0E-101 | AI221878.1 | EST_HUMAN | q999e09.x1 Shares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:4297291 5' |
| 1548 | 6546 | 11606 | 2.07 | 1.0E-101 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 1548 | 6546 | 11607 | 2.07 | 1.0E-101 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 1707 | 6702 | 11779 | 1 | 1.0E-101 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1707 | 6702 | 11780 | 1 | 1.0E-101 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1905 | 6892 | 11987 | 1.32 | 1.0E-101 | 4502996 | NT | Homo sapiens carboxypeptidase A1 (pancreatic) CPA1 mRNA |
| 2003 | 6986 | 12090 | 2.61 | 1.0E-101 | BEE43070.1 | EST_HUMAN | RC3-ST0281-160600-016-h09 ST0281 Homo sapiens cDNA |
| 2288 | 7767 | 12381 | 0.97 | 1.0E-101 | 5729892 | NT | Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA |
| 2541 | 7506 | 12625 | 6.73 | 1.0E-101 | X72893.1 | NT | H.sapiens EW/S gene, exon 5 |
| 2670 | 7628 | 12741 | 5.15 | 1.0E-101 | A237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 2670 | 7628 | 12742 | 5.15 | 1.0E-101 | A237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 2884 | 7903 | | 1251 | 1.0E-101 | A252312.1 | NT | Homo sapiens genomic downstream Rhesus box |
| 3130 | 8146 | 13167 | 2.4 | 1.0E-101 | 4885270 | NT | Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA |
| 3167 | 8183 | | 2.76 | 1.0E-101 | BF035327.1 | EST_HUMAN | 60145853TF1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 3296 | 8307 | 13332 | 2.01 | 1.0E-101 | AW985566.1 | EST_HUMAN | EST377629 MAGE sequences, Homo sapiens cDNA |
| 3316 | 7628 | 12741 | 3.42 | 1.0E-101 | A237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 3316 | 7628 | 12742 | 3.42 | 1.0E-101 | A237744.1 | NT | Homo sapiens RIBIIR gene (partial), exon 12 |
| 3785 | 8788 | 13792 | 5.05 | 1.0E-101 | AB022785.1 | NT | Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene |
| 4668 | 9847 | 14823 | 1.61 | 1.0E-101 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 4668 | 9847 | 14824 | 1.61 | 1.0E-101 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | Top Hit Accession No. | Top-Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|-----------------------|-------------------------|--|
| 40 | 5120 | 10108 | 0.96 | 1.0E-102 | AF012872.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 [pI4K230] mRNA, complete cds |
| 339 | 5391 | 10397 | 4.55 | 1.0E-102 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 615 | 5642 | 10645 | 0.83 | 1.0E-102 | BE252470.1 | EST_HUMAN | 601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5' |
| 766 | 5787 | 10816 | 0.81 | 1.0E-102 | 4557534 | NT | Homo sapiens down-regulated in adenoma (DRA) mRNA |
| 1100 | 6107 | 11137 | 3.79 | 1.0E-102 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 1249 | 6247 | 11287 | 1.82 | 1.0E-102 | 11437146 | NT | Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA |
| 1249 | 6247 | 11288 | 1.82 | 1.0E-102 | 11437146 | NT | Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA |
| 1394 | 6391 | 11444 | 373.13 | 1.0E-102 | BE408447.1 | EST_HUMAN | 601299882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5' |
| 2246 | 7223 | 12342 | 3.39 | 1.0E-102 | AI124669.1 | EST_HUMAN | am60c10_x1 Johnston frontal cortex Homo sapiens cDNA clone SW:GC95 HUMAN Q08379 GOLGIN-95. |
| 2246 | 7223 | 12343 | 3.39 | 1.0E-102 | AI124669.1 | EST_HUMAN | am60c10_x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG85 HUMAN Q08379 GOLGIN-95. |
| 2786 | 7807 | 12824 | 0.69 | 1.0E-102 | 11419442 | NT | Homo sapiens peroxisome biogenesis factor 1 (PEX1), mRNA |
| 2991 | 8009 | 13022 | 1.4 | 1.0E-102 | 7661979 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 3060 | 8077 | 13089 | 2.88 | 1.0E-102 | AU141005.1 | EST_HUMAN | AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5' |
| 3060 | 8077 | 13090 | 2.88 | 1.0E-102 | AU141005.1 | EST_HUMAN | AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5' |
| 4111 | 9105 | 14091 | 1.63 | 1.0E-102 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 4287 | 9219 | 14267 | 2.09 | 1.0E-102 | BE251310.1 | EST_HUMAN | 60110784F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5' |
| 4948 | 9925 | 14903 | 1.17 | 1.0E-102 | R66488.1 | EST_HUMAN | y32G04.11 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5' |
| 68 | 5147 | 10153 | 1.86 | 1.0E-103 | BE808158.1 | EST_HUMAN | 601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5' |
| 68 | 5147 | 10154 | 1.86 | 1.0E-103 | BE808158.1 | EST_HUMAN | 601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5' |
| 99 | 5176 | 10186 | 7.11 | 1.0E-103 | D87078.2 | NT | Homo sapiens mRNA for KIAA0235 protein, partial cds |
| 208 | 5272 | 10284 | 9 | 1.0E-103 | 5453793 | NT | Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA |
| 966 | 5981 | 11013 | 0.87 | 1.0E-103 | A1278348.1 | NT | Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPP-E gene) |
| 1224 | 6223 | 11269 | 8.76 | 1.0E-103 | BE877541.1 | EST_HUMAN | 60148538F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5' |
| 1561 | 6558 | 11620 | 3.06 | 1.0E-103 | AF012872.1 | NT | Homo sapiens phosphatidylinositol 4-kinase 230 [pI4K230] mRNA, complete cds |
| 1870 | 6859 | 11947 | 0.99 | 1.0E-103 | 7657532 | NT | Homo sapiens sing GDS-ASSOCIATED PROTEIN (SMAP), mRNA |
| 1930 | 6916 | 12013 | 1.28 | 1.0E-103 | 4502428 | NT | Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA |
| 1930 | 6916 | 12014 | 1.28 | 1.0E-103 | 4502428 | NT | Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA |
| 2242 | 7219 | 12338 | 2.16 | 1.0E-103 | AU134991.1 | EST_HUMAN | AU134991 PLACE1 Homo sapiens cDNA clone PLACE100065 5' |
| 2383 | 7354 | 12476 | 1.58 | 1.0E-103 | AF060568.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 2547 | 7512 | 12630 | 1.26 | 1.0E-103 | N32770.1 | EST_HUMAN | yw91d08.s1 Soares_placenta_8to9weeks_2NbHP80&W Homo sapiens cDNA clone IMAGE:259598 3' |
| 2995 | 8013 | | 2.58 | 1.0E-103 | BE744722.1 | EST_HUMAN | 60157113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:383431 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Acession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|----------------------|-------------------------|--|
| 3295 | 8306 | 13331 | 4.02 | 1.0E-103 | AW298245.1 | EST_HUMAN | U1-H-BW0- <i>glt-h-11-0-U1</i> .s1 NCI_CGGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3' |
| 3555 | 8363 | 13379 | 1.23 | 1.0E-103 | AB040892.1 | NT | Homo sapiens mRNA for KIAA1459 protein, partial cds |
| 3669 | 8674 | | 9 | 1.0E-103 | AF023861.1 | NT | Macaca mulatta cyclophilin A mRNA, complete cds |
| 3704 | 8708 | 13711 | 1.2 | 1.0E-103 | AA485663.1 | EST_HUMAN | ab10d12.s1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element; |
| 3739 | 8743 | 13743 | 1.26 | 1.0E-103 | 11430876 | NT | Homo sapiens neuropilin 1 (NRP1) mRNA |
| 3897 | 8895 | 13895 | 2.44 | 1.0E-103 | T23683.1 | EST_HUMAN | seq340 b4HB3MA-Cot109+10-Bio H Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-73' |
| 4646 | 9631 | 14626 | 3.54 | 1.0E-103 | AL163228.2 | NT | Homo sapien's chromosome 21 segment HS21C078 |
| 233 | 5296 | 10305 | 4.73 | 1.0E-104 | AL037549.3 | EST_HUMAN | DKFZp564H1072_r1_564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072_5' |
| 233 | 5296 | 10306 | 4.73 | 1.0E-104 | AL037549.3 | EST_HUMAN | DKFZp564H1072_r1_564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072_5' |
| 1849 | 6838 | 11927 | 1.93 | 1.0E-104 | 4502428 | NT | Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA |
| 2131 | 7111 | 12224 | 5.4 | 1.0E-104 | AA132975.1 | EST_HUMAN | gb:T14116_mna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN); |
| 2141 | 7120 | 12236 | 5.95 | 1.0E-104 | BE744628.1 | EST_HUMAN | 6015774601 NIH MGIC_9 Homo sapiens cDNA clone IMAGE:3926438 5' |
| 2308 | 7283 | 12402 | 3.55 | 1.0E-104 | BF334221.1 | EST_HUMAN | RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA |
| 2308 | 7283 | 12403 | 3.55 | 1.0E-104 | BF334221.1 | EST_HUMAN | RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA |
| 2370 | 7343 | 12461 | 6.02 | 1.0E-104 | 5031570 | NT | Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA |
| 2430 | 7401 | 12519 | 1.36 | 1.0E-104 | 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 2430 | 7401 | 12520 | 1.36 | 1.0E-104 | 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 2800 | 7820 | 12837 | 6.92 | 1.0E-104 | M34671.1 | NT | Human lymphocytic antigen CD59/MEM43 mRNA, complete cds |
| 2846 | 7866 | | 2.57 | 1.0E-104 | Y11151.1 | NT | H. sapiens gene encoding phenylpyruvate lautomerase II |
| 3189 | 8205 | 13227 | 0.95 | 1.0E-104 | AU133296.1 | EST_HUMAN | AU133296 OVARC1 Homo sapiens cDNA clone OVARC1000936 5' |
| 3307 | 8318 | | 1.84 | 1.0E-104 | AA319436.1 | EST_HUMAN | EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end |
| 3639 | 8841 | 13848 | 1.14 | 1.0E-104 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 4008 | 9004 | 13992 | 1.24 | 1.0E-104 | F11745.1 | EST_HUMAN | HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07 |
| 4252 | 9246 | 14230 | 4.98 | 1.0E-104 | X02761.1 | NT | Human mRNA for fibronectin (FN precursor) |
| 4477 | 9467 | 14446 | 1.5 | 1.0E-104 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 4477 | 9467 | 14447 | 1.5 | 1.0E-104 | AF231920.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 276 | 7691 | 10348 | 3.85 | 1.0E-105 | 4502166 | NT | Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA |
| 422 | 5080 | 10064 | 19.42 | 1.0E-105 | 4505150 | NT | Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA |
| 589 | 5620 | 10618 | 6.63 | 1.0E-105 | AF032897.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 589 | 5620 | 10619 | 6.63 | 1.0E-105 | AF032897.1 | NT | Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds |
| 1640 | 6637 | | 5.46 | 1.0E-105 | AB020981.1 | NT | Homo sapiens mRNA for cyclin B2, complete cds |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--------------------|
| 1667 6663 | 11738 | 1.04 | 1.0E-105 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 | |
| 1785 6777 | 11869 | 1.78 | 1.0E-105 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 | |
| 1885 6874 | 11963 | 1.62 | 1.0E-105 | D50918.1 | NT | Human mRNA for KIAA0128 gene, partial cds | |
| 2126 7106 | 12220 | 5.92 | 1.0E-105 | AA318389.1 | EST_HUMAN | EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit | |
| 2260 7237 | | 1.56 | 1.0E-105 | BE891786.1 | EST_HUMAN | 601434491F_ NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5' | |
| 2649 7609 | | 0.96 | 1.0E-105 | AA584808.1 | EST_HUMAN | no10dd05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3' | |
| 2937 7956 | | 3.39 | 1.0E-105 | AJ229041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3 | |
| 3252 8265 | 13286 | 1.32 | 1.0E-105 | BF347753.1 | EST_HUMAN | 602022595F_1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158143 5' | |
| 3252 8265 | 13287 | 1.32 | 1.0E-105 | BF347753.1 | EST_HUMAN | 602022595F_1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158143 5' | |
| 3981 8979 | 13964 | 6.06 | 1.0E-105 | AW961688.1 | EST_HUMAN | EST373761 MAGE sequences, MAGG Homo sapiens cDNA | |
| 4781 9765 | | 4.42 | 1.0E-105 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 | |
| 4934 9911 | 14889 | 0.92 | 1.0E-105 | AB018339.1 | NT | Homo sapiens mRNA for KIAA0796 protein, partial cds | |
| 4974 9950 | 14928 | 1.08 | 1.0E-105 | AB020673.1 | NT | Homo sapiens mRNA for KIAA0866 protein, complete cds | |
| 4987 9961 | 14938 | 0.67 | 1.0E-105 | AW966015.1 | EST_HUMAN | EST378088 MAGE sequences, MAGI Homo sapiens cDNA | |
| 150 5216 | | 1.69 | 1.0E-105 | AW503208.1 | EST_HUMAN | UHF-BN0-ek-g-07-0-U_1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5' | |
| 205 5269 | 10282 | 2.72 | 1.0E-105 | AJ565005.1 | EST_HUMAN | Iq78e01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2215008 3' | |
| 537 5572 | 10576 | 1.61 | 1.0E-105 | AW965556.1 | EST_HUMAN | EST377628 MAGE sequences, MAGI Homo sapiens cDNA | |
| 602 5631 | 10631 | 8.07 | 1.0E-105 | J00146.1 | NT | Human dihydrofolate reductase pseudogene (pshd1) | |
| 603 5631 | 10631 | 6.16 | 1.0E-105 | J00146.1 | NT | Human dihydrofolate reductase pseudogene (pshd1) | |
| 1492 6490 | 11545 | 1.76 | 1.0E-106 | AF145712.1 | NT | Homo sapiens soluble neuropilin-1 mRNA, complete cds | |
| 1662 6658 | 11732 | 3.2 | 1.0E-106 | U48724.1 | NT | Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds | |
| 1681 6677 | 11751 | 2.79 | 1.0E-106 | U04510.1 | NT | Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41 | |
| 1767 6759 | 11845 | 3.22 | 1.0E-106 | AA527446.1 | EST_HUMAN | ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element; | |
| 1767 6759 | 11846 | 3.22 | 1.0E-106 | AA527446.1 | EST_HUMAN | ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element; | |
| 2063 7045 | 12153 | 1.25 | 1.0E-106 | BE144286.1 | EST_HUMAN | MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA | |
| 2253 7230 | 12349 | 10.26 | 1.0E-106 | 4504184 | NT | Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA | |
| 2432 7403 | 12522 | 1.47 | 1.0E-106 | AF003528.1 | NT | Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions | |
| 2525 7491 | 12611 | 1 | 1.0E-106 | U64675.2 | NT | Homo sapiens sperm membrane protein BS-63 mRNA, complete cds | |
| 2527 7493 | 12613 | 1.49 | 1.0E-106 | BE260201.1 | EST_HUMAN | 601149783F_1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5' | |
| 2683 7641 | 12757 | 10 | 1.0E-106 | A1276526.1 | EST_HUMAN | q176h10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3' | |
| 2752 6404 | 11462 | 7.19 | 1.0E-106 | 4504184 | NT | Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA | |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--|
| 2752 | 6404 | 11463 | 7.19 | 1.0E-106 | 4504184 | NT | Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA |
| 2805 | 7825 | 12840 | 1.79 | 1.0E-106 | BE384296.1 | EST_HUMAN | 601272675F1 NIH MGCC_20 Homo sapiens cDNA clone IMAGE:3613818 5' |
| 2870 | 7889 | 12910 | 4.45 | 1.0E-106 | AB037747.1 | NT | Homo sapiens mRNA for KIAA1326 protein, partial cds |
| 2870 | 7889 | 12911 | 4.45 | 1.0E-106 | AB037747.1 | NT | Homo sapiens mRNA for KIAA1326 protein, partial cds |
| 3107 | 8123 | 13141 | 2.41 | 1.0E-106 | 8922965 | NT | Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA |
| 3107 | 8123 | 13142 | 2.41 | 1.0E-106 | 8922965 | NT | Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA |
| 3356 | 8364 | 13380 | 0.99 | 1.0E-106 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3356 | 8364 | 13381 | 0.99 | 1.0E-106 | AB033104.1 | NT | Homo sapiens mRNA for KIAA1278 protein, partial cds |
| 3714 | 8718 | 13719 | 0.92 | 1.0E-106 | AF001445.1 | NT | Homo sapiens core binding factor alpha 1 subunit (CBFA1) gene, exon 2 |
| 3926 | 8926 | 13916 | 10.11 | 1.0E-106 | AW974650.1 | EST_HUMAN | EST386875 MAGE sequences, MAGN Homo sapiens cDNA |
| 3926 | 8926 | 13917 | 10.11 | 1.0E-106 | AW974650.1 | EST_HUMAN | EST386875 MAGE sequences, MAGN Homo sapiens cDNA |
| 3944 | 8942 | 13932 | 1.74 | 1.0E-106 | 5729729 | NT | Homo sapiens AP15-like 1 (AP15L1), mRNA |
| 4470 | 9460 | 14439 | 0.67 | 1.0E-106 | BE144286.1 | EST_HUMAN | MRO-HT0165-140200-008-d10 H10165 Homo sapiens cDNA |
| 4741 | 9726 | 14711 | 1.39 | 1.0E-106 | U31520.1 | NT | Human alphamannosidase II mRNA, complete cds |
| 234 | 5297 | 234 | 3.3 | 1.0E-107 | AJ271735.1 | NT | Homo sapiens Xq pseudoadultosomal region; segment 1/2 |
| 262 | 5321 | 1.47 | 1.0E-107 | X60459.1 | NT | Human IFN- α R gene for interferon alpha/beta receptor | |
| 624 | 5651 | 10655 | 2.22 | 1.0E-107 | AF155103.1 | NT | Homo sapiens NY-REN-25 antigen mRNA, partial cds |
| 803 | 5824 | 10854 | 1.94 | 1.0E-107 | X60459.1 | NT | Human IFN- α R gene for interferon alpha/beta receptor |
| 875 | 5893 | 10934 | 1.25 | 1.0E-107 | X60459.1 | NT | Human IFN- α R gene for interferon alpha/beta receptor |
| 954 | 5970 | 11003 | 8.1 | 1.0E-107 | AF154121.1 | NT | Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds |
| 1259 | 6257 | 11300 | 2.22 | 1.0E-107 | AB032253.1 | NT | Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds |
| 1536 | 6534 | 11593 | 8.86 | 1.0E-107 | BF087405.1 | EST_HUMAN | QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA |
| 1713 | 6708 | 11784 | 4.61 | 1.0E-107 | AF136275.1 | NT | Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3 |
| 1804 | 6795 | 11885 | 2.87 | 1.0E-107 | AB001922.2 | NT | Homo sapiens mRNA for KIAA0453 protein, partial cds |
| 1804 | 6795 | 11886 | 2.87 | 1.0E-107 | AB001922.2 | NT | Homo sapiens mRNA for KIAA0453 protein, partial cds |
| 2146 | 7125 | 12242 | 1.06 | 1.0E-107 | U13729.1 | NT | Human dipeptidyl peptidase IV (CD26) gene, exon 20 |
| 2301 | 7276 | 12395 | 4.22 | 1.0E-107 | AW842451.1 | EST_HUMAN | PM1-CN0031-1-190100-001-d03 CN0031 Homo sapiens cDNA |
| 2301 | 7276 | 12396 | 4.22 | 1.0E-107 | AW842451.1 | EST_HUMAN | PM1-CN0031-1-190100-001-d03 CN0031 Homo sapiens cDNA |
| 2463 | 7432 | 12550 | 1.65 | 1.0E-107 | BE732460.1 | EST_HUMAN | 601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5' |
| 2463 | 7432 | 12551 | 1.65 | 1.0E-107 | BE732460.1 | EST_HUMAN | 601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5' |
| 2938 | 7957 | 12974 | 3.71 | 1.0E-107 | AW842451.1 | EST_HUMAN | PM1-CN0031-1-190100-001-d03 CN0031 Homo sapiens cDNA |
| 2938 | 7957 | 12975 | 3.71 | 1.0E-107 | AW842451.1 | EST_HUMAN | PM1-CN0031-1-190100-001-d03 CN0031 Homo sapiens cDNA |
| 3026 | 8043 | 13052 | 7.53 | 1.0E-107 | 5902097 | NT | Homo sapiens SMT3 (suppressor of mlf two 3, yeast) homolog 2 (SMT3H2), mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 3736 | 8740 | 13739 | 5.33 | 1.0E-107 | AF020671.1 | NT | Homo sapiens myobubularin (MTM1) gene, exon 9 |
| 940 | 5957 | 10990 | 2.88 | 1.0E-108 | BE286042.1 | EST_HUMAN | 60117018 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3552348 5' |
| 1246 | 6244 | 11284 | 5.83 | 1.0E-108 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 2025 | 7008 | 12114 | 1.65 | 1.0E-108 | BF026728.1 | EST_HUMAN | 601671914 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5' |
| | | | | | | | bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S |
| 2360 | 7334 | 12451 | 12.25 | 1.0E-108 | BE206694.1 | EST_HUMAN | RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse heokine mRNA, complete cds (MOUSE); |
| 4033 | 9029 | 14017 | 1.15 | 1.0E-108 | AW664438.1 | EST_HUMAN | hir2a11.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE |
| 4394 | 9385 | 14367 | 3.04 | 1.0E-108 | U72961.1 | NT | Human hepatocyte nuclear factor 4-alpha gene, exon 2 |
| 4394 | 9385 | 14368 | 3.04 | 1.0E-108 | U72961.1 | NT | Human hepatocyte nuclear factor 4-alpha gene, exon 2 |
| 4659 | 9644 | 14632 | 3.68 | 1.0E-108 | 7661979 | NT | Homo sapiens KIAA0187 gene product (KIAA0187), mRNA |
| 4765 | 9749 | 14737 | 0.88 | 1.0E-108 | AW504799.1 | EST_HUMAN | U1-HF-BN0-sin-e-04-O-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5' |
| 4791 | 9775 | 14759 | 2.91 | 1.0E-108 | AJ008005.1 | NT | Homo sapiens PSN1 gene, alternative transcript |
| 4962 | 9939 | 14916 | 0.95 | 1.0E-108 | 5031624 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 4988 | 9962 | 14939 | 0.72 | 1.0E-108 | Y12490.1 | NT | Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210) |
| 43 | 5123 | 10111 | 2.46 | 1.0E-109 | AW803116.1 | EST_HUMAN | IL2-UM0077-260400-079-D06 UM0077 Homo sapiens cDNA |
| 66 | 5145 | 10150 | 3.94 | 1.0E-109 | D86974.1 | NT | Human mRNA for KIAA0220 gene, partial cds |
| 218 | 5281 | 10292 | 0.76 | 1.0E-109 | 11422486 | NT | Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA |
| 226 | 5288 | 10296 | 7.69 | 1.0E-109 | 11438391 | NT | Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA |
| 484 | 5501 | 10511 | 9.2 | 1.0E-109 | 4507712 | NT | Homo sapiens leucine-rich repeat domain 2 (TTC2), mRNA |
| 593 | 5624 | 10623 | 15.28 | 1.0E-109 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 593 | 5624 | 10624 | 15.28 | 1.0E-109 | AB023216.1 | NT | Homo sapiens mRNA for KIAA0999 protein, partial cds |
| 1183 | 6185 | 11222 | 93.77 | 1.0E-109 | M28699.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NP23) mRNA, complete cds |
| 1184 | 6185 | 11222 | 72.21 | 1.0E-109 | M28699.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NP23) mRNA, complete cds |
| 1510 | 6508 | 11564 | 1.52 | 1.0E-109 | BE293673.1 | EST_HUMAN | 601186922E2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5' |
| 1510 | 6508 | 11565 | 1.52 | 1.0E-109 | BE293673.1 | EST_HUMAN | 601186922E2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5' |
| 1836 | 6826 | 11914 | 5.54 | 1.0E-109 | D13643.2 | NT | Homo sapiens mRNA for KIAA0018 protein, partial cds |
| 2181 | 7160 | 12280 | 2.32 | 1.0E-109 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 2189 | 7168 | 12288 | 4.31 | 1.0E-109 | Y17123.1 | NT | Homo sapiens SNF6/INI1 gene, exon 6 |
| 2549 | 7514 | 12632 | 4.09 | 1.0E-109 | A1022328.1 | EST_HUMAN | ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 002197 CIRCULATING CATHODIC ANTIGEN; |
| 2549 | 7514 | 12633 | 4.09 | 1.0E-109 | A1022328.1 | EST_HUMAN | ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 002197 CIRCULATING CATHODIC ANTIGEN; |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 2550 7515 | 126534 | 241 | 1.0E-109 | 4504206 | NT | Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA | J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43 |
| 2984 8002 | 13014 | 1.32 | 1.0E-109 | NB5190.1 | EST_HUMAN | CN8-NN0009-190400-750-410 NN0009 Homo sapiens cDNA | CN8-NN0009-190400-750-410 NN0009 Homo sapiens cDNA |
| 3304 8315 | 13341 | 1.43 | 1.0E-109 | AW893192.1 | EST_HUMAN | Homo sapiens retinohydrogenase homolog isoform-1 (RDH) mRNA, complete cds | Homo sapiens retinohydrogenase homolog isoform-1 (RDH) mRNA, complete cds |
| 3304 8315 | 13342 | 1.43 | 1.0E-109 | AW893192.1 | EST_HUMAN | MRO-HT0204-110400-108-a04 HT0208 Homo sapiens cDNA | MRO-HT0204-110400-108-a04 HT0208 Homo sapiens cDNA |
| 3440 8448 | 13474 | 1 | 1.0E-109 | AF240638.1 | NT | ts89e06_x1_NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 | ts89e06_x1_NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 |
| 3751 8755 | | 2.78 | 1.0E-109 | BE146144.1 | EST_HUMAN | nug3c12.s1_NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN | nug3c12.s1_NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN |
| 4023 9019 | 14006 | 4.42 | 1.0E-109 | AI655417.1 | EST_HUMAN | P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ; | P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ; |
| 4038 9034 | 14022 | 0.94 | 1.0E-109 | AA662274.1 | EST_HUMAN | nug3c12.s1_NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN | nug3c12.s1_NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN |
| 4038 9034 | 14023 | 0.94 | 1.0E-109 | AA662274.1 | EST_HUMAN | P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ; | P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ; |
| 4280 9273 | 14262 | 2.85 | 1.0E-109 | 4504206 | NT | Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA | Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA |
| 4469 9459 | 14438 | 1.07 | 1.0E-109 | 7662083 | NT | Homo sapiens KIAA0377 gene product (KIAA0377) mRNA | Homo sapiens KIAA0377 gene product (KIAA0377) mRNA |
| 3 5084 | 10068 | 0.8 | 1.0E-110 | 7549804 | NT | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA |
| 38 5118 | 10105 | 3.85 | 1.0E-110 | 5803073 | NT | Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA | Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA |
| 38 5118 | 10106 | 3.85 | 1.0E-110 | 5803073 | NT | Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA | Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA |
| 109 5084 | 10068 | 0.79 | 1.0E-110 | 7549804 | NT | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA |
| 292 5349 | 10362 | 0.83 | 1.0E-110 | D67291.1 | NT | Human mRNA for inward rectifier potassium channel, complete cds | Human mRNA for inward rectifier potassium channel, complete cds |
| 523 5558 | 10561 | 0.78 | 1.0E-110 | UB4550.1 | NT | Human dystrobrevin (DTN) gene, exon 20 | Human dystrobrevin (DTN) gene, exon 20 |
| 1761 6165 | 11199 | 0.8 | 1.0E-110 | 5031620 | NT | Homo sapiens calcitonin receptor-like (CALCR) mRNA | Homo sapiens calcitonin receptor-like (CALCR) mRNA |
| 1250 6258 | 11301 | 1.42 | 1.0E-110 | AB032253.1 | NT | Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds | Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds |
| 1819 6868 | 11957 | 0.92 | 1.0E-110 | BE379477.1 | EST_HUMAN | 601237545F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5' | 601237545F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5' |
| 2005 6988 | | 1.45 | 1.0E-110 | BF508896.1 | EST_HUMAN | UI-H-B14-eos-b-05-0-JI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3' | UI-H-B14-eos-b-05-0-JI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3' |
| 2767 7788 | | 2 | 1.0E-110 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 2961 6258 | 11301 | 1.29 | 1.0E-110 | AB032253.1 | NT | Homo sapiens BaZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds | Homo sapiens BaZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds |
| 3013 8030 | | 1.07 | 1.0E-110 | U78027.1 | EST_HUMAN | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein L44L and FTP3 (FTP3) genes, complete cds | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein L44L and FTP3 (FTP3) genes, complete cds |
| 4080 9074 | 14062 | 2.55 | 1.0E-110 | M15918.1 | NT | Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene | Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene |
| 4500 9490 | 14466 | 2.09 | 1.0E-110 | AI017213.1 | EST_HUMAN | ou32b10_x1_Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591_NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ; | ou32b10_x1_Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591_NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ; |
| 4520 9510 | 14494 | 3.28 | 1.0E-110 | AU117812 | EST_HUMAN | AU117812_HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5' | AU117812_HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5' |
| 4814 9798 | | 2.3 | 1.0E-110 | 7662441 | NT | Homo sapiens KIAA1002 protein (KIAA1002), mRNA | Homo sapiens KIAA1002 protein (KIAA1002), mRNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|-----------------------|-------------------------|---|
| 174 | 5238 | | | 43.9 | 1.0E-111 U43701.1 | NT | Human ribosomal protein L23a mRNA, complete cds |
| 196 | 5250 | 10273 | | 1.07 | 1.0E-111 4758807 | NT | Homo sapiens ras GTPase activating protein-like (NGAP) mRNA |
| 725 | 5748 | | | 2.71 | 1.0E-111 BF035327.1 | EST_HUMAN | 601458531F11 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5' |
| 734 | 5757 | 10779 | | 3.66 | 1.0E-111 8393092 | NT | Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA |
| 914 | 5930 | 10965 | | 2.29 | 1.0E-111 M25142.1 | NT | Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA |
| 1569 | 6586 | 11648 | | 1.57 | 1.0E-111 7662177 | NT | Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA |
| 4047 | 9043 | 14032 | | 1.17 | 1.0E-111 7661569 | NT | Homo sapiens enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds |
| 4203 | 9196 | 14178 | | 4.64 | 1.0E-111 K02268.1 | NT | Human enkephalin A carboxylase beta (ACACB), mRNA |
| 605 | 5632 | 10632 | | 0.87 | 1.0E-112 4501854 | NT | Homo sapiens acetyl-Coenzyme A carboxylase regulatory protein (S10R) gene, exon 5 |
| 606 | 5633 | 10633 | | 4.82 | 1.0E-112 U29103.1 | NT | Human steroidogenic acute regulatory protein (StAR) gene, exon 5 |
| 606 | 5633 | 10634 | | 4.82 | 1.0E-112 U29103.1 | NT | Human steroidogenic acute regulatory protein (StAR) gene, exon 5 |
| 626 | 5653 | 10657 | | 1.33 | 1.0E-112 BF509039.1 | EST_HUMAN | U1-H-BI4-acid-g-04-U1-s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086023 3' |
| 626 | 5653 | 10658 | | 1.33 | 1.0E-112 BF509039.1 | EST_HUMAN | U1-H-BI4-acid-g-04-U1-s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086023 3' |
| 986 | 6001 | 11032 | | 1.84 | 1.0E-112 AF157623.1 | NT | Homo sapiens HTRA serine protease (PRSS11) gene, complete cds |
| 1045 | 6055 | 11083 | | 2.53 | 1.0E-112 P52742 | SWISSPROT | ZINC FINGER PROTEIN 135 |
| 1645 | 6641 | 11711 | | 3.11 | 1.0E-112 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 1645 | 6641 | 11712 | | 3.11 | 1.0E-112 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 2436 | 7407 | 12524 | | 1.26 | 1.0E-112 BE866859.1 | EST_HUMAN | 601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5' |
| 3004 | 8022 | | | 0.72 | 1.0E-112 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 3171 | 8187 | 13208 | | 1.07 | 1.0E-112 BE083052.1 | EST_HUMAN | RC2-BT0642_030400-021-d09 BT0642 Homo sapiens cDNA |
| 3171 | 8187 | 13209 | | 1.07 | 1.0E-112 BE083052.1 | EST_HUMAN | RC2-BT0642_030400-021-d09 BT0642 Homo sapiens cDNA |
| 3790 | 8793 | 13798 | | 0.71 | 1.0E-112 BE076073.1 | EST_HUMAN | MR2-BT0590_-090300-113-009 BT0590 Homo sapiens cDNA |
| 4603 | 9595 | 14580 | | 5.12 | 1.0E-112 AB037832.1 | NT | Homo sapiens mRNA for KIAA1411 protein, partial cds |
| 4603 | 9595 | 14581 | | 5.12 | 1.0E-112 AB037832.1 | NT | Homo sapiens mRNA for KIAA1411 protein, partial cds |
| 733 | 5756 | 10777 | | 7.13 | 1.0E-113 A1365586.1 | EST_HUMAN | ac8501-x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3' |
| 733 | 5756 | 10778 | | 7.13 | 1.0E-113 A1365586.1 | EST_HUMAN | ac8501-x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3' |
| 928 | 5945 | 10979 | | 7.7 | 1.0E-113 M11985.1 | NT | Human X-linked phosphoglycerate kinase gene, exon 8 |
| 1509 | 6507 | 11563 | | 3.94 | 1.0E-113 A1365586.1 | EST_HUMAN | ac8501-x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3' |
| 1899 | 7702 | 11980 | | 1.45 | 1.0E-113 AF240775.1 | NT | Homo sapiens mRNA for putative RNA helicase, 3' end |
| 3057 | 8074 | 13087 | | 2.19 | 1.0E-113 AJ223948.1 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) |
| 59 | 5139 | 10138 | | 0.76 | 1.0E-114 Y17151.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) |
| 59 | 5139 | 10139 | | 0.76 | 1.0E-114 Y17151.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) |
| 59 | 5139 | 10140 | | 0.76 | 1.0E-114 Y17151.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 637 | 5665 | 10669 | 5.07 | 1.0E-114 | T70551.1 | EST_HUMAN | yd15cd1s1 Scars fetal liver spleen NFLS Homo sapiens cDNA clone IMAGE:1082883' similar to gb:AA21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element; |
| 1054 | 6063 | 11093 | 3.1 | 1.0E-114 | 8923087 | NT | Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA |
| 1294 | 6292 | 11338 | 3.85 | 1.0E-114 | 7657529 | NT | Homo sapiens rhabdoid tumor deletion region protein 1 (RTRD1), mRNA |
| 1602 | 6598 | 11659 | 5.21 | 1.0E-114 | 6631084 | NT | Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA |
| 1633 | 6630 | 11699 | 11.15 | 1.0E-114 | 6679073 | NT | Homo sapiens nucleoprotein-like protein 1 (NLP_1), mRNA |
| 2194 | 7173 | 12294 | 1.31 | 1.0E-114 | AB002374.1 | NT | Human mRNA for KIAA0376 gene, partial cds |
| 2732 | 5125 | 10114 | 1.1 | 1.0E-114 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 2732 | 5125 | 10115 | 1.1 | 1.0E-114 | AB033102.1 | NT | Homo sapiens mRNA for KIAA1276 protein, partial cds |
| 3058 | 8075 | 13088 | 2.52 | 1.0E-114 | X04086.1 | NT | Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13 |
| 3098 | 8114 | 13132 | 1.9 | 1.0E-114 | BT206374.1 | EST_HUMAN | 60186932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5' |
| 3099 | 8909 | 13905 | 1.56 | 1.0E-114 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 4266 | 9259 | 14249 | 1.12 | 1.0E-114 | J03171.1 | NT | Human interferon- α receptor (HuIFN- α -Rec), mRNA, complete cds |
| 4964 | 9941 | 14918 | 1.96 | 1.0E-114 | BE275324.1 | EST_HUMAN | 60112217SF1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346099 5' |
| 22 | 5102 | 10087 | 11.8 | 1.0E-115 | 4758111 | NT | Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA |
| 130 | 5196 | 10211 | 2.72 | 1.0E-115 | 4505938 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA |
| 134 | 5200 | 2176 | 1.0E-115 | | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 290 | 5347 | 10359 | 4.49 | 1.0E-115 | AW804759.1 | EST_HUMAN | QV4-U0394-300300-156-008 UMI0094 Homo sapiens cDNA |
| 778 | 5799 | 10828 | 1.42 | 1.0E-115 | 5174702 | NT | Homo sapien's transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA |
| 778 | 5799 | 10829 | 1.42 | 1.0E-115 | 5174702 | NT | Homo sapien's transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA |
| 780 | 5801 | 10831 | 83.62 | 1.0E-115 | 4503794 | NT | Homo sapien's farnith, heavy polypeptide 1 (FTH1) mRNA |
| 1528 | 6525 | 11582 | 1.41 | 1.0E-115 | AF229180.1 | NT | Homo sapien's alpha-amino adipate semialdehyde synthase mRNA, complete cds |
| 1528 | 6525 | 11583 | 1.41 | 1.0E-115 | AF229180.1 | NT | Homo sapien's alpha-amino adipate semialdehyde synthase mRNA, complete cds |
| 1805 | 6796 | 11887 | 0.93 | 1.0E-115 | U78027.1 | NT | Homo sapien's Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds |
| 2027 | 7010 | 12116 | 1.38 | 1.0E-115 | BE745469.1 | EST_HUMAN | 601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5' |
| 2027 | 7010 | 12117 | 1.38 | 1.0E-115 | BE745469.1 | EST_HUMAN | 601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5' |
| 2236 | 7213 | 12330 | 3.07 | 1.0E-115 | AF231124.1 | NT | Homo sapiens testican-1 mRNA, complete cds |
| 2778 | 7799 | | 2.22 | 1.0E-115 | AW804759.1 | EST_HUMAN | QV4-U0394-300300-156-008 UMI0094 Homo sapiens cDNA |
| 3041 | 8058 | 13067 | 7.57 | 1.0E-115 | AJ245922.1 | NT | Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene) |
| 3041 | 8058 | 13068 | 7.57 | 1.0E-115 | AJ245922.1 | NT | Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene) |
| 3392 | 8400 | 13126 | 2.06 | 1.0E-115 | AJ277892.1 | NT | Homo sapiens partial TTN gene for titin |
| 3929 | 8929 | 13920 | 5.04 | 1.0E-115 | AB002348.2 | NT | Homo sapiens mRNA for KIAA0350 protein, partial cds |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Acession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|----------------------|---|--|
| 4144 9139 | 14123 | 0.96 | 1.0E-116 | AL137163.1 | NT | | Novel human gene mapping to chromosome X |
| 4278 9271 | 14260 | 1.49 | 1.0E-115 | 6912659 | NT | | Homo sapiens str2-like 3 (SIRT3), mRNA |
| 4313 9305 | 14289 | 3.78 | 1.0E-115 | 4758279 | NT | | Homo sapiens EphA4 (EPHA4) mRNA |
| 4459 9449 | 14429 | 0.91 | 1.0E-115 | 8922435 | NT | | Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA |
| 4459 9449 | 14430 | 0.91 | 1.0E-115 | 8922435 | NT | | Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA |
| 4539 9529 | 14515 | 2.4 | 1.0E-115 | AL096857.1 | NT | | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 4539 9529 | 14516 | 2.4 | 1.0E-115 | AL096857.1 | NT | | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 4750 9735 | 14721 | 2.89 | 1.0E-115 | AL163268.2 | NT | | Homo sapiens chromosome 21 segment HS21C068 |
| 4750 9735 | 14722 | 2.89 | 1.0E-115 | AL163268.2 | NT | | Homo sapiens chromosome 21 segment HS21C068 |
| 567 5600 | 10599 | 1.39 | 1.0E-116 | BE275502.1 | EST_HUMAN | AU1121347f NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5' | |
| 792 5813 | 10843 | 1.45 | 1.0E-116 | 4507334 | NT | | Homo sapien's synaptobatinin 1 (SYNU1), mRNA |
| 1951 6937 | 12038 | 2.12 | 1.0E-116 | 5174478 | NT | | Homo sapien's pericentrin (PCNT) mRNA |
| 1951 6937 | 12039 | 2.12 | 1.0E-116 | 5174478 | NT | | Homo sapien's pericentrin (PCNT) mRNA |
| 1975 6960 | 12066 | 1.37 | 1.0E-116 | AU133080.1 | EST_HUMAN | AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5' | |
| 2040 7761 | 12131 | 1 | 1.0E-116 | M19824.1 | NT | | Human apolipoprotein B-100 (apoB) gene, exons 17 and 18 |
| 2040 7761 | 12132 | 1 | 1.0E-116 | M19824.1 | NT | | Human apolipoprotein B-100 (apoB) gene, exons 17 and 18 |
| 2244 7221 | 12340 | 1.16 | 1.0E-116 | 5453941 | NT | | Homo sapien's protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA |
| 2279 7255 | | 1.38 | 1.0E-116 | U78308.1 | NT | | Human olfactory receptor olf17-201-1 (OR17-201-1) gene, olfactory receptor olf17-32 (OR17-32) gene and olfactory receptor pseudo olf17-01 (OR17-01) pseudogene, complete cds |
| 2387 7358 | 12480 | 1.98 | 1.0E-116 | AB018333.1 | NT | | Homo sapiens mRNA for KIAA0790 protein, partial cds |
| 2660 7710 | 12731 | 6 | 1.0E-116 | BE889256.1 | EST_HUMAN | 601513337f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5' | |
| 3101 8117 | 13134 | 5.82 | 1.0E-116 | L77570.1 | NT | | Homo sapien's DiGeorge syndrome critical region, centromeric end |
| 3101 8117 | 13135 | 5.82 | 1.0E-116 | L77570.1 | NT | | Homo sapien's DiGeorge syndrome critical region, centromeric end |
| 4253 9247 | 14231 | 2.06 | 1.0E-116 | 5031954 | NT | | Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA |
| 4707 9692 | 14675 | 1.27 | 1.0E-116 | AI907096.1 | EST_HUMAN | PM-BT135-C70499-016 BT135 Homo sapiens cDNA | |
| 4985 9967 | 14845 | 0.95 | 1.0E-116 | A1243213.1 | NT | | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 554 5588 | 10569 | 1.21 | 1.0E-117 | 4826636 | NT | | Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA |
| 1061 7738 | 11101 | 2.4 | 1.0E-117 | AF124338.1 | NT | | Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15 |
| 1174 6709 | 11785 | 3.05 | 1.0E-117 | AF123320.1 | NT | | Homo sapiens lymphocyte activation-associated protein mRNA, complete cds |
| 1795 6786 | 11876 | 1.83 | 1.0E-117 | M19816.1 | NT | | Human apolipoprotein B-100 (apoB) gene, exon 10 |
| 2149 7128 | 12245 | 1.3 | 1.0E-117 | AW957899.1 | EST_HUMAN | EST369769 MAGE sequences, MAGE Homo sapiens cDNA | |
| 2337 7502 | 12621 | 1.04 | 1.0E-117 | M63468.1 | NT | | Human alpha-5 collagen type IV gene, exon 5 |
| 3194 8210 | 13232 | 1.93 | 1.0E-117 | AA978114.1 | EST_HUMAN | op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3' | |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3884 | 8885 | 13885 | 14.06 | 1.0E-117 | AA316723.1 | EST_HUMAN | EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29 |
| 4218 | 9211 | 14190 | 2.65 | 1.0E-117 | 8669564 | NT | Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA DKFZp434C1120_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120_5' |
| 4444 | 9434 | 14417 | 2.36 | 1.0E-117 | AL042120.1 | EST_HUMAN | H. sapiens mRNA for TPCR16 protein |
| 4584 | 9572 | 14561 | 1.11 | 1.0E-117 | X89670.1 | NT | H. sapiens mRNA for TPCR16 protein |
| 4584 | 9572 | 14562 | 1.11 | 1.0E-117 | X89670.1 | NT | H. sapiens mRNA for TPCR16 protein |
| 4665 | 9650 | 14638 | 11.6 | 1.0E-117 | AF134304.2 | NT | Homo sapiens Scar2 (SCAR2) gene, partial cds |
| 4665 | 9650 | 14639 | 11.6 | 1.0E-117 | AF134304.2 | NT | Homo sapiens Scar2 (SCAR2) gene, partial cds |
| 4782 | 9766 | 14750 | 3.85 | 1.0E-117 | AB020673.1 | NT | Homo sapiens mRNA for KIAA0868 protein, complete cds |
| 69 | 5148 | 10155 | 11.76 | 1.0E-118 | AF161500.1 | NT | Homo sapiens HSPC151 mRNA, complete cds |
| 94 | 5171 | 10181 | 1.94 | 1.0E-118 | AL045854.1 | EST_HUMAN | DKFZp434I056_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I056_5' |
| 513 | 5548 | 10553 | 7.24 | 1.0E-118 | 7657016 | NT | Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA |
| 903 | 7734 | 10957 | 6.59 | 1.0E-118 | 5174680 | NT | Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA |
| 2171 | 7150 | 12267 | 7.75 | 1.0E-118 | BE3889705.1 | EST_HUMAN | 601281947F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3604019_5' |
| 2171 | 7150 | 12268 | 7.75 | 1.0E-118 | BE3889705.1 | EST_HUMAN | 601281947F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3604019_5' |
| 2171 | 7150 | 12269 | 7.75 | 1.0E-118 | BE3889705.1 | EST_HUMAN | 601281947F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3604019_5' |
| 2268 | 7245 | | 1.9 | 1.0E-118 | AW9511729.1 | EST_HUMAN | EST363799 MAGE sequences, MAGB Homo sapiens cDNA |
| 2667 | 7626 | 12738 | 3.94 | 1.0E-118 | U07000.1 | NT | Human breakpoint cluster region (BCR) gene, complete cds |
| 2667 | 7626 | 12739 | 3.94 | 1.0E-118 | U07000.1 | NT | Human breakpoint cluster region (BCR) gene, complete cds |
| 3031 | 8048 | | 4.44 | 1.0E-118 | Y13532.1 | NT | Homo sapiens PRKY exon 7 |
| 3122 | 8138 | 13159 | 4.93 | 1.0E-118 | A1347634.1 | EST_HUMAN | qp01f05.x1 NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1916769_3' |
| 3122 | 8138 | 13160 | 4.93 | 1.0E-118 | A1347634.1 | EST_HUMAN | qp01f05.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769_3' |
| 3972 | 8970 | 13953 | 17.63 | 1.0E-118 | D23660.1 | NT | Human mRNA for ribosomal protein, complete cds |
| 4569 | 9557 | 14545 | 1.42 | 1.0E-118 | 11425793 | NT | Homo sapiens KIAA0478 gene product (KIAA0478), mRNA |
| 748 | 5770 | 10797 | 0.93 | 1.0E-119 | AF170492.1 | NT | Homo sapiens chloride channel CLCA4 (CLCA4) mRNA, complete cds |
| 1020 | 7737 | 11059 | 4.3 | 1.0E-119 | 7705607 | NT | Homo sapiens CGI-105 protein (LOC51011), mRNA |
| 1893 | 6881 | 11972 | 3.42 | 1.0E-119 | AB023147.1 | NT | Homo sapiens mRNA for KIAA0930 protein, partial cds |
| 3029 | 8046 | 13056 | 0.92 | 1.0E-119 | 8922205 | NT | Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA |
| 3847 | 8849 | 13857 | 0.86 | 1.0E-119 | 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 299 | 5356 | 10368 | 1.07 | 1.0E-120 | 4507334 | NT | Homo sapiens synaptotagmin 1 (SYN1), mRNA |
| 1024 | 6034 | 11065 | 2.23 | 1.0E-120 | AF248540.1 | NT | Homo sapiens Integrin 2 (SH3D1B) mRNA, complete cds |
| 1024 | 6034 | 11066 | 2.23 | 1.0E-120 | AF248540.1 | NT | Homo sapiens Integrin 2 (SH3D1B) mRNA, complete cds |
| 1400 | 6397 | 11452 | 6.07 | 1.0E-120 | N44873.1 | EST_HUMAN | Y44012.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273768_5' |
| 1566 | 6563 | 11626 | 4.73 | 1.0E-120 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 17770 | 6762 | 11850 | 3.83 | 1.0E-120 | 4557250 | NT | Homo sapiens disintegrin and metalloproteinase domain 10 (ADAM10) mRNA |
| 2049 | 7031 | 12143 | 1.03 | 1.0E-120 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 2049 | 7031 | 12144 | 1.03 | 1.0E-120 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 3235 | 5355 | 10368 | 0.89 | 1.0E-120 | 4502334 | NT | Homo sapiens synaptolin 1 (SYN1), mRNA |
| 4232 | 9226 | 14209 | 1.43 | 1.0E-120 | AF056490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 4232 | 9226 | 14210 | 1.43 | 1.0E-120 | AF056490.1 | NT | Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds |
| 4527 | 9517 | 14503 | 2.41 | 1.0E-120 | AF098463.1 | NT | Homo sapiens stanniocalcin (STC) gene, partial cds |
| 4527 | 9517 | 14504 | 2.41 | 1.0E-120 | AF098463.1 | NT | Homo sapiens stanniocalcin (STC) gene, partial cds |
| 72 | 5150 | 10159 | 2.65 | 1.0E-121 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 377 | 5424 | 10439 | 1.27 | 1.0E-121 | AU134963.1 | EST_HUMAN | AU134963 PLACE1 Homo sapiens cDNA clone IMAGE1000899 5' |
| 714 | 7728 | 10754 | 1.28 | 1.0E-121 | 5032192 | NT | Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA |
| 2501 | 7469 | 12584 | 1.28 | 1.0E-121 | BF344378.1 | EST_HUMAN | 602014759F NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150286 5' |
| 2501 | 7469 | 12585 | 1.28 | 1.0E-121 | BF344378.1 | EST_HUMAN | 602014759F NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150286 5' |
| 2899 | 7918 | 12939 | 0.89 | 1.0E-121 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 3007 | 8024 | 13036 | 4.04 | 1.0E-121 | Y19208.1 | NT | Homo sapiens hrh3 gene for hair keratin, exons 1 to 9 |
| 3007 | 8024 | 13037 | 4.04 | 1.0E-121 | Y19208.1 | NT | Homo sapiens hrh3 gene for hair keratin, exons 1 to 9 |
| 3459 | 8467 | 13494 | 0.84 | 1.0E-121 | AB037758.1 | NT | Homo sapiens mRNA for KIAA1337 protein, partial cds |
| 3459 | 8467 | 13495 | 0.84 | 1.0E-121 | AB037758.1 | NT | Homo sapiens mRNA for KIAA1337 protein, partial cds |
| 3593 | 8600 | 13607 | 8.01 | 1.0E-121 | AF155156.2 | NT | Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds |
| 4204 | 9197 | 14179 | 1.34 | 1.0E-121 | AI263294.1 | EST_HUMAN | qX57601X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3' |
| 4817 | 9801 | 14781 | 3.38 | 1.0E-121 | X01937.1 | NT | H.sapiens EDE-1 gene (exon 17) |
| 5008 | 9979 | 14954 | 1.26 | 1.0E-121 | AB032481.1 | NT | Homo sapiens HOXD13 gene for homeobox transcription factor, complete cds |
| 265 | 5324 | 10333 | 1.82 | 1.0E-122 | 11526176 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1), mRNA |
| 334 | 5386 | 10363 | 3.2 | 1.0E-122 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 356 | 5406 | 10418 | 1.71 | 1.0E-122 | 11526176 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1), mRNA |
| 871 | 5889 | 10931 | 2.93 | 1.0E-122 | AF114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds |
| 1200 | 6201 | 11238 | 3.95 | 1.0E-122 | M20707.1 | NT | Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II) |
| 1654 | 6650 | 11722 | 3.55 | 1.0E-122 | AF167706.1 | NT | Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds |
| 1674 | 6670 | 11746 | 6.77 | 1.0E-122 | 11418424 | NT | Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA |
| 1674 | 6670 | 11747 | 5.77 | 1.0E-122 | 11418424 | NT | Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA |
| 1778 | 6770 | 11982 | 4.64 | 1.0E-122 | BE906024.1 | EST_HUMAN | 601497032F-1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5' |
| 2420 | 7391 | 12511 | 20.14 | 1.0E-122 | BF316170.1 | EST_HUMAN | 601896173F-1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5' |
| 2420 | 7391 | 12512 | 20.14 | 1.0E-122 | BF316170.1 | EST_HUMAN | 601896173F-1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|--|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| <i>Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds</i> | | | | | | | |
| 2766 | 7787 | 12810 | 0.98 | 1.0E-122 | AF284717.1 | NT | |
| 4699 | 9684 | 14667 | 2.44 | 1.0E-122 | 4502166 NT | | <i>Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1), Alzheimer disease (APP), mRNA</i> |
| 4832 | 9816 | | 1.49 | 1.0E-122 | AW504645.1 | EST_HUMAN | <i>U1-HF-BN0-all-a-03-0-U1 NIH MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'</i> |
| 759 | 5780 | 10807 | 2.05 | 1.0E-123 | BF345274.1 | EST_HUMAN | <i>602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'</i> |
| 759 | 5780 | 10808 | 2.05 | 1.0E-123 | BF345274.1 | EST_HUMAN | <i>602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'</i> |
| 997 | 6009 | 11039 | 5.43 | 1.0E-123 | AL163249.2 | NT | <i>Homo sapiens chromosome 21 segment HS21C049</i> |
| 1006 | 6016 | 11046 | 6.48 | 1.0E-123 | 5803114 NT | | <i>Homo sapiens inner membrane protein, mitochondrial (mitofillin) (IMMT), mRNA</i> |
| 1219 | 6218 | 11260 | 4.18 | 1.0E-123 | 4505818 NT | | <i>Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products</i> |
| 1219 | 6218 | 11261 | 4.18 | 1.0E-123 | 4505818 NT | | <i>Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products</i> |
| 1428 | 6425 | 11484 | 2.56 | 1.0E-123 | AJ388641.1 | NT | <i>Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN012</i> |
| 2042 | 7024 | 12134 | 1.75 | 1.0E-123 | M55419.1 | NT | <i>Human amelogenin (AMELY) gene, 3' end of cds</i> |
| 2042 | 7024 | 12135 | 1.75 | 1.0E-123 | M55419.1 | NT | <i>Human amelogenin (AMELY) gene, 3' end of cds</i> |
| 2042 | 7024 | 12136 | 1.75 | 1.0E-123 | M55419.1 | NT | <i>Human amelogenin (AMELY) gene, 3' end of cds</i> |
| 2042 | 7024 | 12136 | 1.75 | 1.0E-123 | 7705962 NT | | <i>Homo sapiens RAB9-like protein (LOC51209), mRNA</i> |
| 2251 | 7228 | | 2.82 | 1.0E-123 | AL163280.2 | NT | <i>Homo sapiens chromosome 21 segment HS21C080</i> |
| 4326 | 9318 | | 0.93 | 1.0E-123 | AL163280.2 | NT | <i>Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA</i> |
| 266 | 5325 | 10334 | 2.41 | 1.0E-124 | 4507500 NT | | <i>Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA</i> |
| 266 | 5325 | 10335 | 2.41 | 1.0E-124 | 4507500 NT | | <i>Homo sapiens DNA for amyloid precursor protein, complete cds</i> |
| 272 | 5331 | | 1.29 | 1.0E-124 | D87675.1 | NT | <i>Homo sapiens chromosome 21 segment HS21C048</i> |
| 482 | 5619 | 10530 | 2.33 | 1.0E-124 | AL163246.2 | NT | <i>ZB1b04_r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482</i> |
| 682 | 5706 | 10717 | 5.13 | 1.0E-124 | AA397551.1 | EST_HUMAN | <i>G300482_FOL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);</i> |
| 682 | 5706 | 10718 | 5.13 | 1.0E-124 | AA397551.1 | EST_HUMAN | <i>ZB1b04_r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482</i> |
| 749 | 5771 | 10798 | 8.09 | 1.0E-124 | AF155654.1 | NT | <i>Human putative ribosomal protein S11 mRNA</i> |
| 759 | 5820 | 10850 | 1.42 | 1.0E-124 | 4507500 NT | | <i>Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA</i> |
| 853 | 5911 | 10950 | 2.96 | 1.0E-124 | 7705448 NT | | <i>Homo sapiens hypothetical protein (HSPC068), mRNA</i> |
| 1328 | 6326 | 11373 | 4.52 | 1.0E-124 | AF274892.1 | NT | <i>Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds</i> |
| 1328 | 6326 | 11374 | 4.52 | 1.0E-124 | AF274892.1 | NT | <i>Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds</i> |
| 1779 | 6771 | 11863 | 4.44 | 1.0E-124 | AJ31712.1 | NT | <i>Homo sapiens mRNA for nuclear RNA-helicase (nrl61 gene)</i> |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2009 | 6992 | 12096 | 1.32 | 1.0E-124 | BE879524.1 | EST_HUMAN | 601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5' |
| 2388 | 7359 | 12481 | 1.32 | 1.0E-124 | AB024069.1 | NT | Homo sapiens gene for B120, exon 11 |
| 3410 | 8419 | 13447 | 0.74 | 1.0E-124 | S78684.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/B1R1) gene, exon |
| 3410 | 8419 | 13448 | 0.74 | 1.0E-124 | S78684.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/B1R1) gene, exon |
| 3564 | 8571 | 13577 | 1.19 | 1.0E-124 | X13794.1 | NT | H sapiens leucide dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS) |
| 3804 | 8807 | 13873 | 0.88 | 1.0E-124 | 45075600 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 3982 | 8960 | 13950 | 0.81 | 1.0E-124 | 4504116 | NT | Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA |
| 4601 | 9589 | 14576 | 2.01 | 1.0E-124 | AB024069.1 | NT | Homo sapiens gene for B120, exon 11 |
| 4778 | 9762 | | 1.39 | 1.0E-124 | M18778.1 | NT | Human fibronectin gene extra type III repeat (EDII), exon x+1 |
| 3117 | 5372 | 11965 | 11.95 | 1.0E-125 | AB032998.1 | NT | Homo sapiens mRNA for KIAA1172 protein, partial cds |
| 423 | 5081 | 10065 | 4.13 | 1.0E-125 | BE743922.1 | EST_HUMAN | 6015779811F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5' |
| 7118 | 5741 | 10758 | 1.95 | 1.0E-125 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 849 | 5868 | 10909 | 3.29 | 1.0E-125 | AA042813.1 | EST_HUMAN | zK53c07_s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); |
| 983 | 5998 | 11029 | 1.63 | 1.0E-125 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C10 |
| 1136 | 6141 | 11170 | 1.77 | 1.0E-125 | 76672279 | NT | Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744). mRNA |
| 1775 | 6767 | 11858 | 2.36 | 1.0E-125 | AF015450.1 | NT | Homo sapiens Usurpin-alpha mRNA, complete cds |
| 1775 | 6767 | 11859 | 2.36 | 1.0E-125 | AF015450.1 | NT | Homo sapiens Usurpin-alpha mRNA, complete cds |
| 2297 | 7272 | 12389 | 2.15 | 1.0E-125 | AA011278.1 | EST_HUMAN | zK53c07_s1 Soares_fetal liver_spleen_INFSL_S1 Homo sapiens cDNA clone IMAGE:4295688 5' |
| 2431 | 7402 | 12521 | 1.54 | 1.0E-125 | AA042813.1 | EST_HUMAN | gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); |
| 2520 | 7487 | 12605 | 1.74 | 1.0E-125 | 4504696 | NT | Homo sapiens inhibin, alpha (INHA) mRNA |
| 2520 | 7487 | 12606 | 1.74 | 1.0E-125 | 4504696 | NT | Homo sapiens inhibin, alpha (INHA) mRNA |
| 2940 | 10044 | 12978 | 0.98 | 1.0E-125 | BE018009.1 | EST_HUMAN | bb7406.y NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:O95604 O95604 |
| | | | | | | ZINC FINGER PROTEIN_; | zK53c07_s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to |
| 3768 | 8771 | 13776 | 2.21 | 1.0E-125 | AA042813.1 | EST_HUMAN | gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); |
| 4419 | 9409 | 14396 | 2.44 | 1.0E-125 | 11425114 | NT | Homo sapiens zinc finger protein ZNF287 (ZNF287). mRNA |
| 4419 | 9409 | 14397 | 2.44 | 1.0E-125 | 11425114 | NT | Homo sapiens zinc finger protein ZNF287 (ZNF287). mRNA |
| 4484 | 9474 | 14454 | 1.81 | 1.0E-125 | BE315412.1 | EST_HUMAN | 601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5' |
| 765 | 5786 | 10815 | 1.81 | 1.0E-126 | 4758007 | NT | Homo sapiens CDC-like kinase (CLK) mRNA |
| 768 | 5789 | 10818 | 2.59 | 1.0E-126 | M61936.1 | NT | Human laminin B1 chain gene, exon 20 |
| 908 | 5925 | 10960 | 1.36 | 1.0E-126 | X68735.1 | NT | H.sapiens gene for alpha1-antichymotrypsin, exon 3 |
| 2283 | 7259 | 12377 | 1.21 | 1.0E-126 | 8923056 | NT | Homo sapiens hypothetical protein FLJ20048 (FLJ20048). mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|--|
| 2283 | 7259 | 12378 | 1.21 | 1.0E-126 | 8923058 | NT | Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA |
| 2521 | 7488 | 12607 | 2.83 | 1.0E-126 | 6382078 | NT | Homo sapiens RAN binding protein 2 (RANBP2), mRNA |
| 2999 | 8017 | 13030 | 54.41 | 1.0E-126 AA 160709.1 | EST_HUMAN | z072e03_r1 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5' | |
| 2999 | 80117 | 13031 | 54.41 | 1.0E-126 AA 160709.1 | EST_HUMAN | z072e03_r1 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5' | |
| 3545 | 8552 | 13559 | 0.75 | 1.0E-126 X53941.1 | NT | H. sapiens DNA for liver cytochrome b5 pseudogene | |
| 3571 | 8578 | 13584 | 2.04 | 1.0E-126 | 7657038 | NT | Homo sapiens death receptor 6 (DR6), mRNA |
| 4642 | 9627 | 14619 | 0.98 | 1.0E-126 AF 101108.1 | NT | Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63 | |
| 4642 | 9627 | 14620 | 0.98 | 1.0E-126 AF 101108.1 | NT | Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63 | |
| 4687 | 9672 | 14654 | 1.53 | 1.0E-126 N34078.1 | EST_HUMAN | yK78c06_r1 Soares melanocyte 2NbHIM Homo sapiens cDNA clone IMAGE:267850 5' | |
| 171 | 5236 | 10247 | 8.83 | 1.0E-127 AB 024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds | |
| 171 | 5236 | 10248 | 8.83 | 1.0E-127 AB 024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds | |
| 172 | 5236 | 10247 | 8.4 | 1.0E-127 AB 024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds | |
| 172 | 5236 | 10248 | 8.4 | 1.0E-127 AB 024597.1 | NT | Homo sapiens mRNA for casein kinase I epsilon, complete cds | |
| 271 | 5330 | 10342 | 1.45 | 1.0E-127 DB 7675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds | |
| 271 | 5330 | 10343 | 1.45 | 1.0E-127 D8 7675.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds | |
| 870 | 5888 | 10930 | 1.36 | 1.0E-127 AF 114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds | |
| 905 | 5922 | 10959 | 1.51 | 1.0E-127 U72821.2 | NT | Homo sapiens lost on transformation LOT1 mRNA, complete cds | |
| 1652 | 6648 | 11720 | 1.92 | 1.0E-127 4827053 | NT | Homo sapiens ubiquitin specific protease 8 (USP8) mRNA | |
| 2013 | 6996 | 12099 | 2.09 | 1.0E-127 | 5803055 | NT | Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA |
| 2013 | 6996 | 12100 | 2.09 | 1.0E-127 | 5803055 | NT | Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA |
| 2137 | 7117 | 12231 | 38.06 | 1.0E-127 | 4506620 | NT | Homo sapiens ribosomal protein L26 (RPL26) mRNA |
| 2280 | 7256 | 12374 | 2.58 | 1.0E-127 AF 245505.1 | NT | Homo sapiens adican mRNA, complete cds | |
| 2535 | 7500 | 12620 | 16.49 | 1.0E-127 X12881.1 | NT | Human mRNA for cytokeratin 18 | |
| 3606 | 8613 | 13621 | 0.82 | 1.0E-127 AF 114488.1 | NT | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds | |
| 3721 | 8725 | 13725 | 17.44 | 1.0E-127 AW 161297.1 | EST_HUMAN | au80ed6.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170_Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN contains element MEF22 repetitive element; | |
| 4132 | 9127 | 14110 | 22.49 | 1.0E-127 | 7706239 | NT | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA |
| 4132 | 9127 | 14111 | 22.49 | 1.0E-127 | 7706239 | NT | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA |
| 4472 | 9462 | 14441 | 5.1 | 1.0E-127 | 4506384 | NT | Homo sapiens RAD1 (<i>S. pombe</i>) homolog (RAD1) mRNA, and translated products |
| 4498 | 9488 | 14483 | 3.63 | 1.0E-127 AL 163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 | |
| 4537 | 9527 | 14513 | 1.21 | 1.0E-127 | 6912639 | NT | Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 457 | 5494 | 10506 | 4.57 | 1.0E-128 | BE385617.1 | EST_HUMAN | 601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5' |
| 2018 | 7001 | 12104 | 12.06 | 1.0E-128 | U02523.1 | NT | Human FAU1P pseudogene, trinucleotide repeat regions |
| 2018 | 7001 | 12105 | 12.06 | 1.0E-128 | U02523.1 | NT | Human FAU1P pseudogene, trinucleotide repeat regions |
| 2147 | 7126 | 12243 | 127.93 | 1.0E-128 | 4506718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 2377 | 7349 | | 4.72 | 1.0E-128 | 1143745 | NT | Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA |
| 3310 | 8321 | 13344 | 1.28 | 1.0E-128 | AB033073.1 | NT | Homo sapiens mRNA for KIAA1247 protein, partial cds |
| 4529 | 9519 | 14506 | 4.83 | 1.0E-128 | 11426673 | NT | Homo sapiens prospero-related homeobox 1 (PROX1), mRNA |
| 1222 | 5447 | 10469 | 1.18 | 1.0E-129 | S37722.1 | NT | Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4] |
| 410 | 5447 | 10469 | 1.25 | 1.0E-129 | S37722.1 | NT | Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4] |
| 1680 | 6676 | 11750 | 3.33 | 1.0E-129 | AL096880.1 | NT | Novel human mRNA containing Zinc finger C2H2 type domains |
| 1685 | 6681 | 11755 | 1.56 | 1.0E-129 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1685 | 6681 | 11756 | 1.56 | 1.0E-129 | AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1809 | 6799 | 11890 | 5.19 | 1.0E-129 | 11418522 | NT | Homo sapiens zinc finger protein 76 (expressed in testis) (ZNFX6), mRNA |
| 3055 | 8072 | 13082 | 1.71 | 1.0E-129 | Q14585 | SWISSPROT | ZINC FINGER PROTEIN HZF10 |
| 3055 | 8072 | 13083 | 1.71 | 1.0E-129 | Q14585 | SWISSPROT | ZINC FINGER PROTEIN HZF10 |
| 3055 | 8072 | 13084 | 1.71 | 1.0E-129 | Q14585 | SWISSPROT | ZINC FINGER PROTEIN HZF10 |
| 4010 | 9006 | 13994 | 1.03 | 1.0E-129 | 5032230 | NT | Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA |
| 4010 | 9006 | 13995 | 1.03 | 1.0E-129 | 5032230 | NT | Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA |
| 4040 | 9036 | 14026 | 1.96 | 1.0E-129 | AB040892.1 | NT | Homo sapiens mRNA for KIAA1459 protein, partial cds |
| 4158 | 9153 | 14135 | 2.16 | 1.0E-129 | AW755254.1 | EST_HUMAN | CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS Cardiomyopathy associated gene 5 |
| 4158 | 9153 | 14136 | 2.16 | 1.0E-129 | AW755254.1 | EST_HUMAN | CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS Cardiomyopathy associated gene 5 |
| 75 | 5153 | 10163 | 1.96 | 1.0E-129 | 7705530 | NT | Homo sapiens hypothetical protein (HSPC22), mRNA |
| 1627 | 6624 | 11693 | 31.59 | 1.0E-130 | BE275192.1 | EST_HUMAN | 601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5' |
| 1627 | 6624 | 11694 | 31.58 | 1.0E-130 | BE275192.1 | EST_HUMAN | 601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5' |
| 1937 | 6923 | | 2.05 | 1.0E-130 | X04092.1 | NT | Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13 |
| 2698 | 7655 | | 5.31 | 1.0E-130 | AJ010230.1 | NT | Homo sapiens RET finger protein-like 1 antisense transcript, partial |
| 2809 | 7829 | 12844 | 1.17 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' |
| 2809 | 7829 | 12845 | 1.17 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' |
| 3497 | 8505 | 13520 | 0.78 | 1.0E-130 | AF240698.1 | NT | Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--------------------|
| 3681 7829 | 12844 | 5.51 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' | |
| 3681 7829 | 12845 | 5.51 | 1.0E-130 | BE564219.1 | EST_HUMAN | 601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5' | |
| 3833 8835 | 13841 | 1.54 | 1.0E-130 | AW503580.1 | EST_HUMAN | U+HF-BN-akyg-g-06-0-UL71 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5' | |
| 3960 8958 | 13947 | 1.25 | 1.0E-130 | M97710.1 | NT | Human T-cell receptor (V alpha 22-1, J alpha RP/M4265-variant C alpha 1) mRNA | |
| 4408 9399 | 14383 | 9.21 | 1.0E-130 | AW843983.1 | EST_HUMAN | CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA RCO-CT0313-201199-031-a11 C10318 Homo sapiens cDNA | |
| 4926 9903 | 14881 | 1.3 | 1.0E-130 | AW363299.1 | EST_HUMAN | RCO-CT0313-201199-031-a11 C10318 Homo sapiens cDNA RCO-CT0313-201199-031-a11 C10318 Homo sapiens cDNA | |
| 4 5085 | 10069 | 1.8 | 0.0E+00 | AA228126.1 | EST_HUMAN | Z58c04.r1 Scores_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 | |
| 4 5085 | 10070 | 1.8 | 0.0E+00 | AA228126.1 | EST_HUMAN | Z58c04.r1 Scores_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 | |
| 8 5088 | 10074 | 1.14 | 0.0E+00 | 4885136.1 | NT | Homo sapiens checkpoint suppressor 1 (CHES1), mRNA | |
| 21 5101 | 10085 | 5.04 | 0.0E+00 | D833277.1 | NT | Homo sapiens DCRR1 mRNA, partial cds | |
| 21 5101 | 10086 | 5.04 | 0.0E+00 | D833277.1 | NT | Homo sapiens DCRR1 mRNA, partial cds | |
| 27 5107 | 10091 | 107.34 | 0.0E+00 | AF141349.1 | NT | Homo sapiens beta-tubulin mRNA, complete cds | |
| 35 5115 | 10101 | 1.77 | 0.0E+00 | 5802997.1 | NT | Homo sapiens Cd642 effector protein 2 (CEP2), mRNA | |
| 37 5117 | 10104 | 0.74 | 0.0E+00 | M58500.1 | NT | Human heparin cofactor II (HCFC2) gene, exons 1 through 5 | |
| 41 5121 | 10109 | 24.17 | 0.0E+00 | 6857825.1 | NT | Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA | |
| 53 5133 | 10136 | 4.3 | 0.0E+00 | Y71715.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) | |
| 58 5138 | 10137 | 4.3 | 0.0E+00 | Y71715.2 | NT | Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) | |
| 60 5140 | 10141 | 2.89 | 0.0E+00 | D78804.1 | EST_HUMAN | HUM516H0fB Human placenta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-516H08 5' | |
| 60 5140 | 10142 | 2.89 | 0.0E+00 | D78804.1 | EST_HUMAN | HUM516H0fB Human placenta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-516H08 5' | |
| 61 5141 | 10143 | 54.73 | 0.0E+00 | L76558.1 | NT | Human ribosomal protein L7 (RPL7) mRNA, complete cds | |
| 63 5143 | 10146 | 11.31 | 0.0E+00 | AW069534.1 | EST_HUMAN | cr48e07-X1 lila bone marrow stroma Homo sapiens cDNA clone HBMSC_c48e073' | |
| 63 5143 | 10147 | 11.31 | 0.0E+00 | AW069534.1 | EST_HUMAN | cr48e07-X1 lila bone marrow stroma Homo sapiens cDNA clone HBMSC_c48e073' | |
| 74 5152 | 10161 | 2.95 | 0.0E+00 | 4758977.1 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA | |
| 74 5152 | 10162 | 2.95 | 0.0E+00 | 4758977.1 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA | |
| 77 5152 | 10161 | 1.73 | 0.0E+00 | 4758977.1 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA | |
| 77 5152 | 10162 | 1.73 | 0.0E+00 | 4758977.1 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA | |
| 80 5157 | 10168 | 0.7 | 0.0E+00 | 4501850.1 | NT | Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene | |
| 81 5158 | | 50.8 | 0.0E+00 | 4504444.1 | NT | Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA | |
| 90 5167 | 10177 | 77.93 | 0.0E+00 | 5016098.1 | NT | Homo sapiens actin, beta (ACTB) mRNA | |
| 93 5170 | 10180 | 45.78 | 0.0E+00 | U89277.1 | NT | Human polyomaviral 1 homolog (HPV1) mRNA, partial cds | |

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 Table 4
 Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|--|--|
| 100 | 5177 | 10187 | 2.36 | 0.0E+00 A114743.1 | EST_HUMAN | HA1347 Human fetal liver cDNA library Homo sapiens cDNA | |
| 101 | 5178 | 10188 | 1.89 | 0.0E+00 AB037784.1 | NT | Homo sapiens mRNA for KIAA1363 protein, partial cds | |
| 116 | 5188 | 10197 | 0.91 | 0.0E+00 AI623701.1 | EST_HUMAN | ts3805.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 | MITOCHONDRIAL TRANSCRIPTION TERMINATOR PRECURSOR; ; |
| 117 | 5188 | 10197 | 1.65 | 0.0E+00 AI623701.1 | EST_HUMAN | ts3805.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 | MITOCHONDRIAL TRANSCRIPTION TERMINATOR FACTOR PRECURSOR; ; |
| 118 | 7690 | 10198 | 3.4 | 0.0E+00 N36040.1 | EST_HUMAN | yy01h09.r1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2700117 5' | |
| 118 | 7690 | 10199 | 3.4 | 0.0E+00 N36040.1 | EST_HUMAN | yy01h09.r1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2700117 5' | |
| 121 | 5191 | 10204 | 0.7 | 0.0E+00 4505458 | NT | Homo sapiens neuropilin 2 (NRP2) mRNA | |
| 131 | 5197 | 10212 | 4.8 | 0.0E+00 4505938 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA | |
| 131 | 5197 | 10213 | 4.8 | 0.0E+00 4505938 | NT | Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA | |
| 140 | 5205 | 10220 | 1.18 | 0.0E+00 T56945.1 | EST_HUMAN | ya83g04.12 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5' | |
| 140 | 5205 | 10221 | 1.18 | 0.0E+00 T56945.1 | EST_HUMAN | ya83g04.12 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5' | |
| 152 | 5218 | | 70.7 | 0.0E+00 4504444 | NT | Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA | |
| 156 | 5222 | 10234 | 3.22 | 0.0E+00 BE036881.1 | EST_HUMAN | 601460375f1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5' | |
| 158 | 5224 | | 143.39 | 0.0E+00 4504444 | NT | Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA | |
| 161 | 5227 | 10237 | 0.82 | 0.0E+00 AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes | |
| 163 | 5229 | 10238 | 6.28 | 0.0E+00 BE285973.1 | EST_HUMAN | 601174270f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5' | |
| 164 | 5229 | 10238 | 1.45 | 0.0E+00 BE285973.1 | EST_HUMAN | zd62b05.r1 Scares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X162822 :cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN); | |
| 165 | 5230 | 10239 | 6.65 | 0.0E+00 W73973.1 | EST_HUMAN | QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA | |
| 166 | 5231 | 10240 | 2.09 | 0.0E+00 BE162832.1 | EST_HUMAN | QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA | |
| 166 | 5231 | 10241 | 2.09 | 0.0E+00 BE162832.1 | EST_HUMAN | QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA | |
| 167 | 5232 | 10242 | 3.77 | 0.0E+00 AF244088.1 | NT | Homo sapiens zinc finger protein mRNA, complete cds | |
| 170 | 5235 | 10245 | 15.16 | 0.0E+00 AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 | |
| 170 | 5235 | 10246 | 15.16 | 0.0E+00 AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 | |
| 180 | 5243 | 10253 | 9.67 | 0.0E+00 BE018970.1 | EST_HUMAN | bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z | CE22831 : |
| 180 | 5243 | 10254 | 9.67 | 0.0E+00 BE018970.1 | EST_HUMAN | bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z | CE22831 : |
| 185 | 5248 | 10257 | 4.23 | 0.0E+00 AB018327.1 | NT | Homo sapiens mRNA for KIAA0784 protein, partial cds | |
| 185 | 5248 | 10258 | 4.23 | 0.0E+00 AB018327.1 | NT | Homo sapiens mRNA for KIAA0784 protein, partial cds | |
| 186 | 5249 | 10259 | 3.83 | 0.0E+00 AB018327.1 | NT | Homo sapiens mRNA for KIAA0784 protein, partial cds | |
| 186 | 5249 | 10260 | 3.83 | 0.0E+00 AB018327.1 | NT | Homo sapiens mRNA for KIAA0784 protein, partial cds | |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 194 | 5258 | 10271 | 261.78 | 0.0E+00 | D50659.1 | NT | Human gamma-cytoplasmic actin (ACTGP9) pseudogene |
| 199 | 5263 | 10276 | 3.01 | 0.0E+00 | AF273045.1 | NT | Homo sapiens CTCL tumor antigen set 4-3 mRNA, complete cds |
| 199 | 5263 | 10277 | 3.01 | 0.0E+00 | AF273045.1 | NT | Homo sapiens CTCL tumor antigen set 4-3 mRNA, complete cds |
| 201 | 5265 | 10279 | 28.3 | 0.0E+00 | AF167174.1 | NT | Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds |
| 201 | 5265 | 10280 | 28.3 | 0.0E+00 | AF167174.1 | NT | Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds |
| 210 | 7715 | 10286 | 57.42 | 0.0E+00 | A1587308.1 | EST_HUMAN | tq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847'3' similar to gb:J03191 PROFILIN [HUMAN]; |
| 210 | 7715 | 10287 | 57.42 | 0.0E+00 | A1587308.1 | EST_HUMAN | tq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847'3' similar to gb:J03191 PROFILIN [HUMAN]; |
| 212 | 5275 | 10289 | 1.9 | 0.0E+00 | AF195658.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |
| 214 | 5277 | | 99.79 | 0.0E+00 | 4506632 | NT | Homo sapiens ribosomal protein L31 (RPL31) mRNA |
| 215 | 5278 | | 15.17 | 0.0E+00 | AF132000.1 | NT | Homo sapiens TADA1 protein mRNA, complete cds |
| 220 | 5283 | 10293 | 3.41 | 0.0E+00 | AB018264.1 | NT | Homo sapiens mRNA for KIAA0721 protein, partial cds |
| 221 | 5283 | 10293 | 3.35 | 0.0E+00 | AB018264.1 | NT | Homo sapiens mRNA for KIAA0721 protein, partial cds |
| 222 | 5284 | 10294 | 4.92 | 0.0E+00 | 6678444 | NT | Mus musculus testis-specific protein, Y-encoded-like (TspY), mRNA |
| 236 | 5298 | 10309 | 16.43 | 0.0E+00 | 5453805 | NT | Homo sapiens NS1-associated protein 1 (NSA1P1) mRNA |
| 238 | 5300 | | 17.29 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 245 | 5305 | 10315 | 3.82 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 247 | 5307 | 10318 | 1.5 | 0.0E+00 | X89772.1 | NT | H.sapiens mRNA for interferon alpha/beta receptor (long form) |
| 255 | 5315 | | 6.35 | 0.0E+00 | AF231919.1 | NT | Homo sapiens chromosome 21 unknown mRNA |
| 267 | 5326 | 10336 | 1.48 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA |
| 267 | 5326 | 10337 | 1.48 | 0.0E+00 | 4507500 | NT | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA |
| 269 | 5328 | 10339 | 2.14 | 0.0E+00 | 7706028 | NT | Homo sapiens hypothetical protein (LOC51250), mRNA |
| 280 | 5338 | | 2.81 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCRR1 mRNA, partial cds |
| 281 | 5339 | 10352 | 2.43 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCRR1 mRNA, partial cds |
| 281 | 5339 | 10353 | 2.43 | 0.0E+00 | D83327.1 | NT | Homo sapiens DCRR1 mRNA, partial cds |
| 282 | 5340 | | 0.88 | 0.0E+00 | AW845293.1 | EST_HUMAN | IL2-CT0031-181189-020-B03 C70031 Homo sapiens cDNA |
| 281 | 5348 | 10360 | 5.4 | 0.0E+00 | 4557029 | NT | Homo sapiens inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA |
| 291 | 5348 | 10361 | 5.4 | 0.0E+00 | 4557029 | NT | Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA |
| 302 | 5359 | 10371 | 5.25 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 303 | 5360 | 10372 | 4.98 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 304 | 7718 | | 46.48 | 0.0E+00 | 4506728 | NT | Homo sapiens phosphotibosylglycinate formyltransferase, phosphoribosylaminodiazole synthetase (GART) mRNA |
| 305 | 5361 | 10373 | 2.02 | 0.0E+00 | 4503914 | NT | Homo sapiens phosphotibosylglycinate formyltransferase, phosphoribosylaminodiazole synthetase (GART) mRNA |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|--|
| | | | | | | | | |
| 306 | 5362 | | 2.32 | 0.0E+00 | AA480002.1 | EST_HUMAN | zr18c06_r1_Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:753964 5' | |
| 307 | 5363 | 10374 | 20.77 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA | |
| 308 | 5363 | 10374 | 22.16 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA | |
| 312 | 5367 | 10378 | 2.2 | 0.0E+00 | AF114488.1 | NT | Homo sapiens: Intersectin short isoform (ITSN) mRNA, complete cds | |
| 325 | 5379 | 10387 | 2.91 | 0.0E+00 | O14867 | SWISSPROT | TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (IA2303) | |
| 325 | 5379 | 10388 | 2.81 | 0.0E+00 | O14867 | SWISSPROT | TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (IA2303) | |
| 326 | 5380 | 10389 | 3.75 | 0.0E+00 | 7657213 | NT | Homo sapiens: hormonally upregulated neu tumor-associated kinase (HUNK), mRNA | |
| 327 | 5380 | 10389 | 2.04 | 0.0E+00 | 7657213 | NT | Homo sapiens: hormonally upregulated neu tumor-associated kinase (HUNK), mRNA | |
| 342 | 5394 | 10401 | 2.33 | 0.0E+00 | 5174574 | NT | Homo sapiens: myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA | |
| 343 | 5395 | 10402 | 1.6 | 0.0E+00 | 4505256 | NT | Homo sapiens: moesin (MSN), mRNA | |
| 346 | 5398 | 10406 | 10.77 | 0.0E+00 | 4827057 | NT | Homo sapiens: X-box binding Protein 1 (XBP1) mRNA | |
| 349 | 5401 | 10411 | 2.29 | 0.0E+00 | U71600.1 | NT | Human zinc finger protein Zfp31 (ZFP31) mRNA, partial cds | |
| 354 | 5405 | 10415 | 2.65 | 0.0E+00 | AF231919.1 | NT | Homo sapiens: chromosome 21 unknown mRNA | |
| 354 | 5405 | 10416 | 2.65 | 0.0E+00 | AF231919.1 | NT | Homo sapiens: chromosome 21 unknown mRNA | |
| 355 | 7719 | 10417 | 3.33 | 0.0E+00 | AF231919.1 | NT | Homo sapiens: chromosome 21 unknown mRNA | |
| 357 | 5407 | 10419 | 1.13 | 0.0E+00 | 4507500 | NT | Human T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA | |
| 360 | 5410 | 10423 | 1.36 | 0.0E+00 | 4503854 | NT | Homo sapiens: GA-binding protein transcription factor, alpha subunit (60kD) (GABPA) mRNA | |
| 361 | 5411 | 10424 | 2.25 | 0.0E+00 | DB0006.1 | NT | Human mRNA for KIAA0184, gene, partial cds | |
| 362 | 5411 | 10424 | 1.75 | 0.0E+00 | D80006.1 | NT | Human mRNA for KIAA0184, gene, partial cds | |
| 364 | 5413 | 10426 | 1.21 | 0.0E+00 | 4507500 | NT | Homo sapiens: T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA | |
| 375 | 5422 | 10437 | 2.21 | 0.0E+00 | AU134963.1 | EST_HUMAN | AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5' | |
| 386 | 5461 | 10479 | 7.9 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds | |
| 387 | 5462 | 10480 | 7.2 | 0.0E+00 | AJ363014.1 | EST_HUMAN | q161h05_x1_NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199 | |
| 391 | 5429 | 10444 | 3.05 | 0.0E+00 | AW7541180.1 | EST_HUMAN | PHOSPHOR: BOSYLAMINE-GLYCINE LIGASE (HUMAN); RC2-CT0320-3d0100-016-a09 C10320 Homo sapiens cDNA | |
| 394 | 5431 | 10447 | 1.12 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 395 | 5432 | 10448 | 2.02 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 395 | 5432 | 10449 | 2.02 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 396 | 5433 | 10450 | 1.2 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 397 | 5434 | 10451 | 1.19 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 397 | 5434 | 10452 | 1.19 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 398 | 5435 | 10453 | 3.59 | 0.0E+00 | 4503680 | NT | Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA | |
| 399 | 5436 | 10454 | 3.82 | 0.0E+00 | X74870.1 | NT | H. sapiens gene for RNA pol II largest subunit, exons 23-29 | |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 399 | 5436 | 10455 | 3.82 | 0.0E+00 | X74870.1 | NT | H.sapiens gene for RNA pol II largest subunit, exons 23-29 |
| 400 | 5426 | 10454 | 3.87 | 0.0E+00 | X74870.1 | NT | H.sapiens gene for RNA pol II largest subunit, exons 23-29 |
| 400 | 5426 | 10455 | 3.87 | 0.0E+00 | X74870.1 | NT | H.sapiens gene for RNA pol II largest subunit, exons 23-29 |
| 404 | 5440 | | 114.34 | 0.0E+00 | 4506608 | NT | Homo sapiens ribosomal protein L19 (RPL19) mRNA |
| 417 | 5075 | 10059 | 1.06 | 0.0E+00 | R17795.1 | EST_HUMAN | yg08a02.1T Scares infant brain cDNA clone IMAGE:31662 5' |
| 425 | 5463 | 10481 | 2.62 | 0.0E+00 | 4503914 | NT | Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA |
| 426 | 5464 | | 36.55 | 0.0E+00 | 4506728 | NT | Homo sapiens ribosomal protein S5 (RPS5) mRNA |
| 427 | 5465 | 10482 | 3.49 | 0.0E+00 | AB028942.1 | NT | Homo sapiens mRNA for KIAA1019 protein, partial cds |
| 428 | 5466 | 10483 | 6.44 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 428 | 5466 | 10484 | 6.44 | 0.0E+00 | 4507152 | NT | Homo sapiens SON DNA binding protein (SON) mRNA |
| 429 | 5467 | 10485 | 3.81 | 0.0E+00 | AF193607.1 | NT | Mus musculus truncated SON protein (Son) mRNA, complete cds |
| 441 | 5478 | | 0.76 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 443 | 5480 | 10498 | 3.88 | 0.0E+00 | 4557879 | NT | Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA |
| 448 | 5485 | | 1.31 | 0.0E+00 | AA324262.1 | EST_HUMAN | EST27054 Cerebellum II Homo sapiens cDNA 5' end |
| 449 | 5486 | | 2.44 | 0.0E+00 | BE254447.1 | EST_HUMAN | 601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5' |
| 465 | 5502 | 10512 | 5.86 | 0.0E+00 | 4504632 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA |
| 465 | 5502 | 10513 | 5.86 | 0.0E+00 | 4504632 | NT | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA |
| 470 | 5506 | 10520 | 21.4 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 470 | 5506 | 10521 | 21.4 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 480 | 5517 | 10527 | 2.88 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 481 | 5518 | 10528 | 5.35 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 481 | 5518 | 10529 | 5.35 | 0.0E+00 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 490 | 5526 | 10534 | 3.11 | 0.0E+00 | AB033035.1 | NT | Homo sapiens mRNA for KIAA1209 protein, partial cds |
| 492 | 5528 | 10536 | 1.82 | 0.0E+00 | AU132898 | NT2RP4 | Homo sapiens cDNA clone NT2RP4000837 5' |
| 500 | 5536 | 10542 | 4.41 | 0.0E+00 | BE385144.1 | EST_HUMAN | 60127495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815756 5' |
| 501 | 7722 | 10543 | 4.79 | 0.0E+00 | AW838825.1 | EST_HUMAN | PM0-DT0061;130400-002-006 DT0065 Homo sapiens cDNA |
| 504 | 5539 | 10545 | 1.51 | 0.0E+00 | AL117233.1 | NT | Novel human gene mapping to chromosome 1 |
| 505 | 5540 | 10546 | 0.81 | 0.0E+00 | 8923955 | NT | Homo sapiens PC326 protein (PC326), mRNA |
| 508 | 5543 | | 0.68 | 0.0E+00 | BF373403.1 | EST_HUMAN | IL2-FT0159-j170800-120-F07_F1019 Homo sapiens cDNA |
| 515 | 5550 | 10555 | 4.2 | 0.0E+00 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 522 | 7723 | 10559 | 1.9 | 0.0E+00 | BE081527.1 | EST_HUMAN | QV2-BT0631-160400-142-h05 BT0635 Homo sapiens cDNA |
| 527 | 5562 | 10565 | 1.86 | 0.0E+00 | BF028005.1 | EST_HUMAN | 60176485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3986998 5' |
| 532 | 5567 | 10570 | 1.25 | 0.0E+00 | AB040999.1 | NT | Homo sapiens mRNA for KIAA1476 protein, partial cds |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 535 | 5570 | 10573 | 17.56 | 0.0E+00 | 6006030 | NT | Homo sapiens transcription elongation factor B (SII), polypeptide 4-like (TCETB1L) mRNA |
| 536 | 5571 | 10574 | 5.39 | 0.0E+00 | 4504036 | NT | Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA |
| 536 | 5571 | 10575 | 5.39 | 0.0E+00 | 4504036 | NT | Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA |
| 538 | 5573 | 10577 | 3.44 | 0.0E+00 | 8923831 | NT | Homo sapiens arilin (LOC54443), mRNA |
| 539 | 5574 | 10578 | 2.66 | 0.0E+00 | 8923831 | NT | Homo sapiens arilin (LOC54443), mRNA |
| 539 | 5574 | 10579 | 2.66 | 0.0E+00 | 8923831 | NT | Homo sapiens arilin (LOC54443), mRNA |
| 544 | 5578 | | 3.9 | 0.0E+00 | AF003528.1 | NT | Homo sapiens X-linked arthritidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 552 | 5586 | 10588 | 1.35 | 0.0E+00 | AW135324.1 | EST_HUMAN | U1-H-B11-actI-h-04-0-U1-s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3' |
| 561 | 5595 | | 4.5 | 0.0E+00 | D10083.1 | NT | Homo sapiens RGH1 gene, retrovirus-like element |
| 581 | 5613 | 10613 | 7.89 | 0.0E+00 | 5174742 | NT | Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCFS1), nuclear gene encoding mitochondrial protein, mRNA |
| 594 | 5625 | | 4.24 | 0.0E+00 | J04066.1 | NT | Human apolipoprotein AI-1 (ApoA-I) gene, exon 1 |
| 597 | 5628 | 10627 | 2.06 | 0.0E+00 | BF104988.1 | EST_HUMAN | 601822627F1 NIH_M/GC_75 Homo sapiens cDNA clone IMAGE:4045447 5' |
| 599 | 5630 | 10629 | 1.05 | 0.0E+00 | 8923831 | NT | Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA |
| 599 | 5630 | 10630 | 1.05 | 0.0E+00 | 8923831 | NT | Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA |
| 600 | 5630 | 10629 | 0.52 | 0.0E+00 | 8923831 | NT | Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA |
| 600 | 5630 | 10630 | 0.52 | 0.0E+00 | 8923831 | NT | Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA |
| 601 | 5630 | 10629 | 0.7 | 0.0E+00 | 8923831 | NT | Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA |
| 601 | 5630 | 10630 | 0.7 | 0.0E+00 | 8923831 | NT | Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA |
| 610 | 5637 | 10638 | 0.83 | 0.0E+00 | AE221712.1 | NT | Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds |
| 610 | 5637 | 10639 | 0.83 | 0.0E+00 | AE221712.1 | NT | Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds |
| 617 | 5646 | 10646 | 2.81 | 0.0E+00 | AF149773.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 619 | 5646 | 10649 | 2.39 | 0.0E+00 | AB037807.1 | NT | Homo sapiens mRNA for KIAA1386 protein, partial cds |
| 621 | 5648 | 10650 | 0.76 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 622 | 5649 | 10651 | 1.52 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 622 | 5649 | 10652 | 1.52 | 0.0E+00 | 6806918 | NT | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 629 | 5667 | 10662 | 2.63 | 0.0E+00 | AA399486.1 | EST_HUMAN | Zf60c07.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726732 5' |
| 633 | 5666 | 10666 | 6.46 | 0.0E+00 | D11078.1 | NT | Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA |
| 638 | 5666 | | 3.25 | 0.0E+00 | 4885626 | NT | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA |
| 645 | 5673 | 10678 | 2.37 | 0.0E+00 | 6006003 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2), mRNA |
| 647 | 5675 | 10681 | 2.08 | 0.0E+00 | 5031624 | NT | Human neutral amino acid transporter (ASCT1) gene, exon 8 |
| 650 | 5678 | 10685 | 3.14 | 0.0E+00 | U05235.1 | NT | Human sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds |
| 654 | 5682 | 10688 | 1.1 | 0.0E+00 | AF10839.1 | NT | Human sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 654 | 5682 | 10659 | 1.1 | 0.0E+00 | AF108389.1 | NT | Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds |
| 660 | 5687 | 10694 | 4.21 | 0.0E+00 | 4826947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 660 | 5687 | 10695 | 4.21 | 0.0E+00 | 4826947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA |
| 666 | 7726 | | | 1.79 | 0.0E+00 | X57147.1 | Human endogenous retrovirus pHE-1 (ERV9). |
| 674 | 5699 | 10708 | 21.88 | 0.0E+00 | 4504424 | NT | Homo sapiens; high-mobility group (nucleosome chromosomal) protein 1 (HMG1) mRNA |
| 678 | 5703 | 10711 | 15.74 | 0.0E+00 | AB028012.1 | NT | Homo sapiens; mRNA for KIAA1089 protein, partial cds |
| 688 | 5712 | 10726 | 6.92 | 0.0E+00 | 7657468 | NT | Homo sapiens; similar to rat integral membrane glycoprotein POM121 (POM121L1) mRNA |
| 699 | 5723 | 10739 | 47.96 | 0.0E+00 | AA614537.1 | EST_HUMAN | np49d01.s1 NC_ CGAP_Br1_Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-BU (HUMAN); |
| 703 | 6727 | 10743 | 4.04 | 0.0E+00 | M60675.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 703 | 5727 | 10744 | 4.04 | 0.0E+00 | M60675.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 713 | 5737 | 10753 | 1.32 | 0.0E+00 | 5032192 | NT | Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA |
| 719 | 5742 | 10759 | 3.44 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 719 | 5742 | 10760 | 3.44 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 721 | 5744 | 10763 | 11.53 | 0.0E+00 | 11545800 | NT | Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA |
| 727 | 5750 | 10771 | 2.72 | 0.0E+00 | BE241577.1 | EST_HUMAN | TCAAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TOAA_Homo sapiens cDNA clone TCAAAP0779 |
| 747 | 5769 | 10795 | 1.78 | 0.0E+00 | AF226890.2 | NT | Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds |
| 747 | 5769 | 10796 | 1.78 | 0.0E+00 | AF226890.2 | NT | Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds |
| 750 | 5772 | 10798 | 3.03 | 0.0E+00 | J03764.1 | NT | Human, plasminogen activator inhibitor-1 gene, exons 2 to 9 |
| 750 | 5772 | 10800 | 3.03 | 0.0E+00 | J03764.1 | NT | Human, plasminogen activator inhibitor-1 gene, exons 2 to 9 |
| 752 | 5774 | 10801 | 1.73 | 0.0E+00 | AB037760.1 | NT | Homo sapiens mRNA for KIAA1329 protein, partial cds |
| 753 | 5775 | 10802 | 1.35 | 0.0E+00 | 6912749 | NT | Human zinc finger protein 212 (ZNF212), mRNA |
| 755 | 7730 | 10804 | 4.57 | 0.0E+00 | D30612.1 | NT | Homo sapiens mRNA for repressor protein, partial cds |
| 756 | 5777 | 10805 | 5.14 | 0.0E+00 | BE869735.1 | EST_HUMAN | 601445647 1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5' |
| 760 | 5781 | 10809 | 3.62 | 0.0E+00 | R48915.1 | EST_HUMAN | Y69g08.71 Soares breast 2NbH-Bst Homo sapiens cDNA clone IMAGE:154046 5' |
| 761 | 5782 | 10810 | 5.54 | 0.0E+00 | 5032086 | NT | Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA |
| 770 | 5791 | 10819 | 1.61 | 0.0E+00 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 773 | 5795 | 10823 | 3.45 | 0.0E+00 | 7661965 | NT | Homo sapiens KIAAO170 gene product (KIAAO170), mRNA |
| 784 | 5805 | 10835 | 1.98 | 0.0E+00 | D80065.1 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 784 | 5805 | 10836 | 1.58 | 0.0E+00 | D80066.1 | NT | Human mRNA for KIAA0184 gene, partial cds |
| 789 | 5810 | 10840 | 2.89 | 0.0E+00 | X89772.1 | NT | H. sapiens mRNA for interferon alphabeta receptor (long form) |
| 793 | 5814 | 10844 | 3.13 | 0.0E+00 | AB020717.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 793 | 5814 | 10845 | 3.13 | 0.0E+00 | AB020717.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 797 | 5818 | 10849 | 10.62 | 0.0E+00 | 5174478 | NT | Hom sapiens pericentrin (PCNT) mRNA |
| 798 | 5819 | | 8.45 | 0.0E+00 | 4507500 | NT | Hom sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 814 | 5835 | 10870 | 1.57 | 0.0E+00 | 7657213 | NT | Hom sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 815 | 5836 | 10871 | 2.15 | 0.0E+00 | 7657213 | NT | Hom sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 817 | 5838 | 10873 | 1.84 | 0.0E+00 | 4557686 | NT | Hom sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA |
| 823 | 5843 | 10879 | 1.98 | 0.0E+00 | AF108830.1 | NT | Hom sapiens serine-threonine protein kinase (MNBB1) mRNA, complete cds |
| 823 | 5843 | 10880 | 1.98 | 0.0E+00 | AF108830.1 | NT | Hom sapiens serine-threonine protein kinase (MNBB1) mRNA, complete cds |
| 824 | 5844 | 10881 | 1.05 | 0.0E+00 | AF108830.1 | NT | Hom sapiens serine-threonine protein kinase (MNBB1) mRNA, complete cds |
| 829 | 5849 | 10886 | 1.72 | 0.0E+00 | 4503854 | NT | Hom sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA |
| 833 | 5852 | 10891 | 2.11 | 0.0E+00 | 4507500 | NT | Hom sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 833 | 5852 | 10892 | 2.11 | 0.0E+00 | 4507500 | NT | Hom sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA |
| 840 | 5859 | | 1.37 | 0.0E+00 | AF027153.1 | NT | Hom sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds |
| 844 | 5863 | 10903 | 4.35 | 0.0E+00 | AB028942.1 | NT | Hom sapiens mRNA for KIAA1019 protein, partial cds |
| 844 | 5863 | 10904 | 4.35 | 0.0E+00 | AB028942.1 | NT | Hom sapiens mRNA for KIAA1019 protein, partial cds |
| 845 | 5864 | 10905 | 11.54 | 0.0E+00 | 4507152 | NT | Hom sapiens SON DNA binding protein (SON) mRNA |
| 846 | 5865 | 10906 | 4.49 | 0.0E+00 | AB028942.1 | NT | Hom sapiens mRNA for KIAA1019 protein, partial cds |
| 847 | 5866 | 10907 | 28.07 | 0.0E+00 | 4506728 | NT | Hom sapiens ribosomal protein S5 (RPS5) mRNA |
| 850 | 5869 | 10910 | 1.1 | 0.0E+00 | AB020717.1 | NT | Hom sapiens mRNA for KIAA0910 protein, partial cds |
| 850 | 5869 | 10911 | 1.1 | 0.0E+00 | AB020717.1 | NT | Hom sapiens mRNA for KIAA0910 protein, partial cds |
| 851 | 5870 | 10912 | 1.78 | 0.0E+00 | AA533272.1 | EST_HUMAN | nj68d07.s1NCL CGAP_Pri0 Homo sapiens cDNA clone IMAGE:997453 |
| 851 | 5870 | 10913 | 1.78 | 0.0E+00 | AA533272.1 | EST_HUMAN | nj68d07.s1NCL CGAP_Pri0 Homo sapiens cDNA clone IMAGE:997453 |
| 852 | 5871 | | 6.52 | 0.0E+00 | BF6776394.1 | EST_HUMAN | 6020855791 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 |
| 856 | 5875 | 10914 | 1.36 | 0.0E+00 | 7657213 | NT | Hom sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 856 | 5875 | 10915 | 1.36 | 0.0E+00 | 7657213 | NT | Hom sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 857 | 5876 | 10916 | 2.29 | 0.0E+00 | 7657213 | NT | Hom sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 857 | 5876 | 10917 | 2.29 | 0.0E+00 | 7657213 | NT | Hom sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 880 | 5898 | 10940 | 1.27 | 0.0E+00 | AL163203.2 | NT | Hom sapiens chromosome 21 segment HS21C003 |
| 887 | 5905 | 10945 | 1.4 | 0.0E+00 | BE089592.1 | EST_HUMAN | QVO-BT0703-28040-211-911 BT0703 Homo sapiens cDNA |
| 887 | 5905 | 10946 | 1.4 | 0.0E+00 | BE089592.1 | EST_HUMAN | QVO-BT0703-28040-211-911 BT0703 Homo sapiens cDNA |
| 887 | 5915 | 10955 | 2.23 | 0.0E+00 | AL163203.2 | NT | Hom sapiens chromosome 21 segment HS21C003 |
| 907 | 5924 | | 92.58 | 0.0E+00 | 4504938 | NT | Hom sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA |
| 910 | 5924 | | 105.51 | 0.0E+00 | 4504938 | NT | Hom sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA |
| 911 | 5927 | 10962 | 1.55 | 0.0E+00 | AF089747.1 | NT | Hom sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds |
| 912 | 5928 | 10963 | 1.39 | 0.0E+00 | L28101.1 | NT | Hom sapiens kallistatin (P14) gene, exons 1-4, complete cds |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--|--|
| | | | | | | | | |
| 936 | 5953 | 10985 | 1.21 | 0.0E+00 | M37190_1 | NT | Human ras inhibitor mRNA, 3' end | |
| 937 | 5954 | 10986 | 6.98 | 0.0E+00 | M37190_1 | NT | Human ras inhibitor mRNA, 3' end | |
| 938 | 5955 | 10987 | 0.78 | 0.0E+00 | M37190_1 | NT | Human ras inhibitor mRNA, 3' end | |
| 939 | 5956 | 10988 | 1.55 | 0.0E+00 | 4507430 | NT | Homo sapiens: thyrotrophic embryonic factor (TEF), mRNA | |
| 939 | 5956 | 10989 | 1.55 | 0.0E+00 | 4507430 | NT | Homo sapiens: thyrotrophic embryonic factor (TEF), mRNA | |
| 947 | 7735 | 10996 | 1.94 | 0.0E+00 | AI001948_1 | EST_HUMAN | os98e03.s1NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3' | |
| 947 | 7735 | 10997 | 1.94 | 0.0E+00 | AI001948_1 | EST_HUMAN | os98e03.s1NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3' | |
| 949 | 5965 | 10999 | 7.69 | 0.0E+00 | 7657266 | NT | Homo sapiens: KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA | |
| 960 | 5975 | 11009 | 1.89 | 0.0E+00 | AB030566_1 | NT | Homo sapiens: mRNA for PSP24, complete cds | |
| 968 | 5983 | 11015 | 1.14 | 0.0E+00 | BF366974_1 | EST_HUMAN | PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA | |
| 968 | 5983 | 11016 | 1.14 | 0.0E+00 | BF366974_1 | EST_HUMAN | PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA | |
| 968 | 5983 | 11017 | 1.14 | 0.0E+00 | BF366974_1 | EST_HUMAN | PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA | |
| 969 | 5984 | 11018 | 1.55 | 0.0E+00 | X52207_1 | NT | Homo sapiens: partial c-fgr gene, exons 2 and 3 | |
| 969 | 5984 | 11019 | 1.55 | 0.0E+00 | X52207_1 | NT | Homo sapiens: partial c-fgr gene, exons 2 and 3 | |
| 978 | 5993 | 11026 | 2.93 | 0.0E+00 | 4757969 | NT | Homo sapiens: chromosome-like (CDYL) mRNA | |
| 989 | 6003 | 11034 | 3.09 | 0.0E+00 | U83668_1 | NT | Human beta-tubulin (TUB4q) gene, complete cds | |
| 990 | 6004 | 11035 | 58.93 | 0.0E+00 | U83668_1 | NT | Human beta-tubulin (TUB4q) gene, complete cds | |
| 991 | 6004 | 11035 | 27.22 | 0.0E+00 | U83668_1 | NT | Human beta-tubulin (TUB4q) gene, complete cds | |
| 994 | 6007 | | 5.92 | 0.0E+00 | AF188490_1 | NT | Homo sapiens: 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds | |
| 995 | 6007 | | 11.99 | 0.0E+00 | AF188490_1 | NT | Homo sapiens: 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds | |
| 998 | 6010 | 11040 | 1.12 | 0.0E+00 | AF111170_3 | NT | Homo sapiens: 14q32.3 Jagged2 gene, complete cds; and unknown gene | |
| 999 | 6010 | 11040 | 1.89 | 0.0E+00 | AF111170_3 | NT | Homo sapiens: 14q32.3 Jagged2 gene, complete cds; and unknown gene | |
| 1000 | 6010 | 11040 | 1.74 | 0.0E+00 | AF111170_3 | NT | Homo sapiens: 14q32.3 Jagged2 gene, complete cds; and unknown gene | |
| 1001 | 6011 | 11041 | 6.04 | 0.0E+00 | AF111170_3 | NT | Homo sapiens: 14q32.3 Jagged2 gene, complete cds; and unknown gene | |
| 1004 | 6014 | 11044 | 2.62 | 0.0E+00 | 7661685 | NT | Homo sapiens: DKK2P586M0122 protein (DKFZP586M0122), mRNA | |
| 1008 | 6018 | 11048 | 4.81 | 0.0E+00 | 5803114 | NT | Homo sapiens: inner membrane protein, mitochondrial (mitofillin) (MMT), mRNA | |
| 1009 | 6019 | | 4.43 | 0.0E+00 | AA458680_1 | EST_HUMAN | aa66g07.s1 Strategene fetal retina cDNA clone 937202 Homo sapiens cDNA clone similar to DNA-DIRECTED RNA POLYMERASE II | |
| 1012 | 6022 | 11052 | 0.8 | 0.0E+00 | N43182_1 | EST_HUMAN | SW:PRSB8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8; | |
| 1012 | 6022 | 11053 | 0.8 | 0.0E+00 | N43182_1 | EST_HUMAN | EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II | |
| 1013 | 6023 | 11054 | 1.08 | 0.0E+00 | 4759249 | NT | (alignment S* and Pro with BLASTx or p) | |
| | | | | | | | Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|--|
| | | | | | | | | |
| 1013 | 6023 | 11055 | 1.08 | 0.0E+00 | 4759249 | NT | Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA | |
| 1016 | 6026 | | 5.63 | 0.0E+00 | 8922933 | NT | Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA | |
| 1030 | 6040 | 11070 | 10 | 0.0E+00 | 4758569 | NT | Homo sapiens heat shock 70kD protein 98 (heat-shock 70kD protein 98) (HSPA9B) mRNA | |
| 1048 | 6057 | 11085 | 3.04 | 0.0E+00 | 4826672 | NT | Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA | |
| 1048 | 6057 | 11086 | 3.04 | 0.0E+00 | 4826672 | NT | Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA | |
| 1052 | 6061 | 11090 | 3.86 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA | |
| 1052 | 6061 | 11091 | 3.86 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA | |
| 1053 | 6062 | 11092 | 127.96 | 0.0E+00 | AJ245922.1 | NT | Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene) | |
| 1055 | 6064 | | 1.04 | 0.0E+00 | 8923087 | NT | Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA | |
| 1057 | 6066 | 11096 | 4.28 | 0.0E+00 | 51174384 | NT | Homo sapiens alkylation repair, alkB homolog (ALKB), mRNA | |
| 1066 | 6074 | 11107 | 3.16 | 0.0E+00 | 4758117 | NT | Homo sapiens Death associated protein 3 (DAP-3) mRNA | |
| 1079 | 6086 | 11115 | 5.76 | 0.0E+00 | BE005208.1 | EST_HUMAN | MRO-BN0115_200300-003-h08 BN0115 Homo sapiens cDNA | |
| 1102 | 6109 | 11139 | 4.27 | 0.0E+00 | 7706134 | NT | Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA | |
| 1102 | 6109 | 11140 | 4.27 | 0.0E+00 | 7706134 | NT | Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA | |
| 1115 | 6121 | 11150 | 1.67 | 0.0E+00 | 4826947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA | |
| 1115 | 6121 | 11151 | 1.67 | 0.0E+00 | 4826947 | NT | Homo sapiens protein kinase, X-linked (PRKX) mRNA | |
| 1116 | 6122 | 11152 | 46.69 | 0.0E+00 | 4506712 | NT | Homo sapiens ribosomal protein S27a (RPS27A) mRNA | |
| 1118 | 6124 | 11154 | 2.22 | 0.0E+00 | 8923290 | NT | Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA | |
| 1121 | 6127 | 11157 | 37.23 | 0.0E+00 | AB002059.1 | NT | Homo sapiens DNA for Human P2Y6, complete cds | |
| 1123 | 6129 | 11158 | 82.18 | 0.0E+00 | AB002059.1 | NT | Homo sapiens DNA for Human P2Y6, complete cds | |
| 1124 | 6130 | 11159 | 4.76 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA | |
| 1124 | 6130 | 11160 | 4.76 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA | |
| 1127 | 6132 | 11162 | 4.36 | 0.0E+00 | 7706500 | NT | Homo sapiens Nip38-binding protein NipBP (LOC51728), mRNA | |
| 1128 | 6133 | 11163 | 0.66 | 0.0E+00 | X95826.1 | NT | H.sapiens AFT4 gene | |
| 1128 | 6133 | 11164 | 0.66 | 0.0E+00 | X95826.1 | NT | H.sapiens AFT4 gene | |
| 1129 | 6134 | 11165 | 1.23 | 0.0E+00 | AI147650.1 | EST_HUMAN | qb22d10_x1_Scores_pregnant_uterus_NbHPU_Homo_sapiens cDNA clone IMAGE:16970113' | |
| 1131 | 6136 | 11167 | 3.06 | 0.0E+00 | AB020710.1 | NT | Homo sapiens mRNA for KIAA0903 protein, partial cds | |
| 1138 | 6143 | 11173 | 0.86 | 0.0E+00 | 4758081 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA | |
| 1138 | 6143 | 11174 | 0.86 | 0.0E+00 | 4758081 | NT | Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA | |
| 1139 | 6144 | 11175 | 1.05 | 0.0E+00 | 9966844 | NT | Homo sapiens chromosome 12 open reading frame 3 (C12orf3), mRNA | |
| 1150 | 6154 | 11186 | 5.48 | 0.0E+00 | 7305076 | NT | Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD26, mRNA | |
| 1150 | 6154 | 11187 | 5.48 | 0.0E+00 | 7305076 | NT | Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA | |
| 1152 | 6156 | 11189 | 0.98 | 0.0E+00 | AB037835.1 | NT | Homo sapiens mRNA for KIAA1414 protein, partial cds | |
| 1159 | 6163 | 11198 | 14.52 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA | |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|-----------------------|-------------------------|--|
| 1172 | 6175 | 11209 | 1.01 | 0.0E+00 | AF073299.1 | NT | Homo sapiens: Na+/H+ exchanger isoform 2 (NHE2) mRNA, complete cds |
| 1190 | 6191 | | 1.32 | 0.0E+00 | 7657336 | NT | Homo sapiens: mutL (E. coli) homolog 3 (MLH3), mRNA |
| 1203 | 6204 | 11241 | 0.69 | 0.0E+00 | 8922583 | NT | Homo sapiens: hypothetical protein FLJ10697 (FLJ10697), mRNA |
| 1206 | 6207 | 11244 | 0.89 | 0.0E+00 | AF264750.1 | NT | Homo sapiens: ALR-like protein mRNA, partial cds |
| 1206 | 6207 | 11245 | 0.89 | 0.0E+00 | AF264750.1 | NT | Homo sapiens: ALR-like protein mRNA, partial cds |
| 1207 | 6208 | 11246 | 1.55 | 0.0E+00 | AF264750.1 | NT | Homo sapiens: ALR-like protein mRNA, partial cds |
| 1208 | 7741 | 11247 | 1.09 | 0.0E+00 | AF264750.1 | NT | Homo sapiens: ALR-like protein mRNA, partial cds |
| 1227 | 6226 | 11272 | 4.89 | 0.0E+00 | AF109718.1 | NT | Homo sapiens: chromosome 3 subtelomeric region |
| 1228 | 6227 | 11273 | 2.52 | 0.0E+00 | 4603098 | NT | Homo sapiens: chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSFG4), mRNA |
| 1238 | 6236 | 11279 | 4.31 | 0.0E+00 | 4505740 | NT | Homo sapiens: prefoldin 4 (PFDN4) mRNA |
| 1247 | 6245 | | 2.72 | 0.0E+00 | Y18000.1 | NT | Homo sapiens: NF2 gene |
| 1255 | 6253 | 11294 | 283.18 | 0.0E+00 | 4506718 | NT | Homo sapiens: ribosomal protein S2 (RPS2) mRNA |
| 1262 | 6260 | 11303 | 5.64 | 0.0E+00 | AF084479.1 | NT | Homo sapiens: Williams-Batten syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds |
| 1268 | 6266 | 11307 | 1.42 | 0.0E+00 | AB040940.1 | NT | Homo sapiens: mRNA for KIAA1507 protein, partial cds |
| 1268 | 6266 | 11308 | 1.42 | 0.0E+00 | AB040940.1 | NT | Homo sapiens: mRNA for KIAA1507 protein, partial cds |
| 1281 | 6280 | 11321 | 2.45 | 0.0E+00 | 5174748 | NT | Homo sapiens: Wolfram syndrome (WFS) mRNA |
| 1281 | 6280 | 11322 | 2.45 | 0.0E+00 | 5174748 | NT | Homo sapiens: Wolfram syndrome (WFS) mRNA |
| 1281 | 6280 | 11323 | 2.45 | 0.0E+00 | 5174748 | NT | Homo sapiens: Wolfram syndrome (WFS) mRNA |
| 1282 | 6281 | | 2.35 | 0.0E+00 | AF096156.1 | NT | Homo sapiens: protein phosphatase 2A BR gamma subunit gene, exon 5 |
| 1292 | 7743 | 11335 | 1.16 | 0.0E+00 | 7657529 | NT | Homo sapiens: rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 1292 | 7743 | 11336 | 1.16 | 0.0E+00 | 7657529 | NT | Homo sapiens: rhabdoid tumor deletion region protein 1 (RTDR1), mRNA |
| 1296 | 6294 | 11341 | 1.37 | 0.0E+00 | 5803146 | NT | Homo sapiens: ring finger protein 9 (RNF9), mRNA |
| 1297 | 6295 | 11342 | 2.26 | 0.0E+00 | 4508004 | NT | Homo sapiens: zinc finger protein 173 (ZNF173) mRNA |
| 1299 | 6297 | 11343 | 0.67 | 0.0E+00 | 5803146 | NT | Homo sapiens: ring finger protein 9 (RNF9), mRNA |
| 1300 | 6298 | 11344 | 2.07 | 0.0E+00 | 4508004 | NT | Homo sapiens: zinc finger protein 173 (ZNF173) mRNA |
| 1302 | 6300 | 11346 | 4.17 | 0.0E+00 | AB011149.1 | NT | Homo sapiens: mRNA for KIAA0577 protein, complete cds |
| 1303 | 6301 | 11347 | 9.28 | 0.0E+00 | 7661965 | NT | Homo sapiens: KIAA0170 gene product (KIAA0170), mRNA |
| 1304 | 6302 | 11348 | 10.18 | 0.0E+00 | 7661965 | NT | Homo sapiens: KIAA0170 gene product (KIAA0170), mRNA |
| 1305 | 6303 | 11349 | 3.67 | 0.0E+00 | 8567387 | NT | Homo sapiens: period (Drosophila) homolog 3 (PER3), mRNA |
| 1305 | 6303 | 11350 | 3.67 | 0.0E+00 | 8567387 | NT | Homo sapiens: period (Drosophila) homolog 3 (PER3), mRNA |
| 1317 | 6314 | 11363 | 1.22 | 0.0E+00 | M14123.1 | NT | Human endogenous retrovirus HERV-K10 |
| 1375 | 6372 | 11421 | 1.64 | 0.0E+00 | BE257955.1 | EST_HUMAN | 601109792F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5' |
| 1375 | 6372 | 11422 | 1.64 | 0.0E+00 | BE257955.1 | EST_HUMAN | 601109792F NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5' |
| 1384 | 6381 | 11431 | 1.51 | 0.0E+00 | A1250014.1 | NT | Homo sapiens mRNA for Familial Cylindromatosis cyld gene |

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Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | | | | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|---|-------------------------|--|--|--|--|--|
| | | | | | M938B06.x1 Scores_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WPT27A1.5 CE4213; | | | | | | |
| 1392 | 6389 | 11442 | 1.16 | 0.0E+00 | A1208756.1 | EST_HUMAN | | | | | |
| 1393 | 6390 | 11443 | 28.34 | 0.0E+00 | 6042206 NT | | RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA | | | | |
| 1401 | 6398 | 11453 | 1.59 | 0.0E+00 | 4505646 NT | | Homo sapiens proprotein convertase subtilisin/kinin type 2 (PCSK2) mRNA | | | | |
| 1401 | 6398 | 11454 | 1.59 | 0.0E+00 | 4505646 NT | | Homo sapiens proprotein convertase subtilisin/kinin type 2 (PCSK2) mRNA | | | | |
| 1403 | 6400 | 11457 | 3.9 | 0.0E+00 | 7705565 NT | | Homo sapiens KIAA1114 protein (KIAA1114), mRNA | | | | |
| 1403 | 6400 | 11458 | 3.9 | 0.0E+00 | 7705565 NT | | Homo sapiens KIAA1114 protein (KIAA1114), mRNA | | | | |
| 1405 | 6402 | 11459 | 4.32 | 0.0E+00 | AJ238093.1 | NT | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements | | | | |
| 1413 | 6411 | 11470 | 3.56 | 0.0E+00 | AF035280.1 | NT | Homo sapiens alpha1-6fucosyltransferase (alpha1-6Fuct1) gene, exon 7 | | | | |
| 1434 | 6431 | 11487 | 2.12 | 0.0E+00 | AL132999.1 | NT | Novel human gene on chromosome 20 | | | | |
| 1435 | 6432 | 11488 | 1.3 | 0.0E+00 | AL137764.1 | NT | Novel human gene mapping to chromosome 1 | | | | |
| 1439 | 6436 | 11493 | 1.69 | 0.0E+00 | D87077.1 | NT | Human mRNA for KIAA0240 gene, partial cds | | | | |
| 1442 | 6439 | 11496 | 6.31 | 0.0E+00 | 6912457 NT | | Homo sapiens calneurin binding protein 1 (KIAA0330), mRNA | | | | |
| 1444 | 6441 | 11498 | 2.08 | 0.0E+00 | 7661985 NT | | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA | | | | |
| 1444 | 6441 | 11499 | 2.08 | 0.0E+00 | 7661985 NT | | Homo sapiens KIAA0170 gene product (KIAA0170), mRNA | | | | |
| 1450 | 6477 | 11533 | 3.1 | 0.0E+00 | 7706434 NT | | Homo sapiens hhDCC for homolog of Drosophila headcase (LOC511986), mRNA | | | | |
| 1493 | 6491 | 11546 | 0.99 | 0.0E+00 | AW959587.1 | EST_HUMAN | EST371757 MAGE resequences, MAGF Homo sapiens cDNA | | | | |
| 1494 | 6492 | 11547 | 2.99 | 0.0E+00 | AA:481172.1 | EST_HUMAN | BB:4403.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:8151116.5' | | | | |
| 1500 | 6498 | 11551 | 42.31 | 0.0E+00 | AF023860.1 | NT | Carcinithicus aestuans cyclophilin A mRNA, complete cds | | | | |
| 1500 | 6498 | 11552 | 42.31 | 0.0E+00 | AF023860.1 | NT | Carcinithicus aestuans cyclophilin A mRNA, complete cds | | | | |
| 1502 | 6500 | 11555 | 1.1 | 0.0E+00 | AW976097.1 | EST_HUMAN | EST388206 MAGE resequences, MAGN Homo sapiens cDNA | | | | |
| 1502 | 6500 | 11556 | 1.1 | 0.0E+00 | AW976097.1 | EST_HUMAN | EST388206 MAGE resequences, MAGN Homo sapiens cDNA | | | | |
| 1503 | 6501 | 11557 | 1.11 | 0.0E+00 | D10384.1 | NT | Bovine mRNA for neurocalcin | | | | |
| 1505 | 6503 | | 1.87 | 0.0E+00 | U778027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44) and FTF3 (FTP3) genes, complete cds | | | | |
| 1506 | 6504 | 11560 | 2.02 | 0.0E+00 | 4505404 NT | | Homo sapiens transmembrane glycoprotein (GPNMb) mRNA | | | | |
| 1506 | 6504 | 11561 | 2.02 | 0.0E+00 | 4505404 NT | | Homo sapiens transmembrane glycoprotein (GPNMb) mRNA | | | | |
| 1507 | 6505 | 11562 | 2.55 | 0.0E+00 | 7662405 NT | | Homo sapiens KIAA0957 protein (KIAA0957), mRNA | | | | |
| 1508 | 6506 | | 7.44 | 0.0E+00 | 7655972 NT | | Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA | | | | |
| 1513 | 6511 | 11568 | 3 | 0.0E+00 | M98478.1 | NT | Human transglutaminase mRNA, complete cds | | | | |
| 1516 | 6514 | 11570 | 1.08 | 0.0E+00 | 4507720 NT | | Homo sapiens titin (TTN) mRNA | | | | |
| 1516 | 6514 | 11571 | 1.08 | 0.0E+00 | 4507720 NT | | Homo sapiens titin (TTN) mRNA | | | | |
| 1517 | 7749 | | 39.26 | 0.0E+00 | 4506654 NT | | Homo sapiens ribosomal protein L5 (RPL5) mRNA | | | | |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|---|
| | | | | | | | Human laminin receptor (2H5 epitope) mRNA, 5' end | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 1518 | 6515 | 11572 | 61.77 | 0.0E+00 | M14199.1 | NT | | |
| 1530 | 6528 | 11587 | 8.55 | 0.0E+00 | 4503098 | NT | | |
| 1537 | 6535 | | 1.85 | 0.0E+00 | D00335.1 | NT | Human c-type-2 gene | H.sapiens Ht12B/e gene |
| 1545 | 6543 | 11601 | 26.28 | 0.0E+00 | Z83738.1 | NT | | |
| 1546 | 6544 | 11602 | 2.84 | 0.0E+00 | 5921460 | NT | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA |
| 1546 | 6544 | 11603 | 2.84 | 0.0E+00 | 5921460 | NT | | |
| 1547 | 6545 | 11604 | 6.07 | 0.0E+00 | AV690831.1 | EST_HUMAN | AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5' | AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5' |
| 1547 | 6545 | 11605 | 6.07 | 0.0E+00 | AV690831.1 | EST_HUMAN | | |
| 1549 | 7750 | 11608 | 1.72 | 0.0E+00 | AB040905.1 | NT | Homo sapiens mRNA for KIAA1472 protein, partial cds | Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds |
| 1553 | 6550 | 11609 | 2.77 | 0.0E+00 | AF157476.1 | NT | | |
| 1555 | 6552 | 11612 | 6.44 | 0.0E+00 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 1555 | 6552 | 11613 | 6.44 | 0.0E+00 | 7662183 | NT | | |
| 1557 | 6554 | 11614 | 84.9 | 0.0E+00 | 5729876 | NT | Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA | Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA |
| 1557 | 6554 | 11615 | 84.9 | 0.0E+00 | 5729876 | NT | | |
| 1559 | 6556 | 11617 | 2.3 | 0.0E+00 | M01803.1 | NT | Homo sodium channel mRNA | |
| 1572 | 6569 | 11631 | 9.86 | 0.0E+00 | H26973.1 | EST_HUMAN | y076c05_s1 Ecores adult brain N2b4/HB55Y Homo sapiens cDNA clone IMAGE:1838483' | |
| 1579 | 6576 | 11639 | 1.95 | 0.0E+00 | AB046829.1 | NT | Homo sapiens mRNA for KIAA1609 protein, partial cds | |
| 1579 | 6576 | 11640 | 1.95 | 0.0E+00 | AB046829.1 | NT | Homo sapiens mRNA for KIAA1609 protein, partial cds | |
| 1598 | 6594 | 11655 | 4.22 | 0.0E+00 | AW444637.1 | EST_HUMAN | U1-H-B13-4W-c-04-U1s1 NCI_CGAP_SubS Homo sapiens cDNA clone IMAGE:2733294 3 | |
| 1625 | 6622 | 11690 | 8.38 | 0.0E+00 | BE144364.1 | EST_HUMAN | MRO-HT0161-191199-004-b11 HT0166 Homo sapiens cDNA | |
| 1625 | 6622 | 11691 | 8.38 | 0.0E+00 | BE144364.1 | EST_HUMAN | MRO-HT0161-191199-004-b11 HT0166 Homo sapiens cDNA | |
| 1629 | 6626 | 11695 | 3.34 | 0.0E+00 | A1768104.1 | EST_HUMAN | wg1807_x1_Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q6Z788 (262788 CS2/HIS2 ZINC FINGER PROTEIN_N; | |
| 1630 | 6627 | 11696 | 1.18 | 0.0E+00 | 4758513 | NT | Homo sapiens hemopoietic-derived zinc finger protein (HD-ZNF1) mRNA | |
| 1631 | 6628 | 11697 | 2.39 | 0.0E+00 | AF057777.1 | NT | Homo sapiens T-cell receptor gamma V1 gene region | |
| 1634 | 6631 | 11700 | 2.07 | 0.0E+00 | M29580.1 | NT | Human zinc-finger protein 7 (ZFP7) mRNA, complete cds | |
| 1634 | 6631 | 11701 | 2.07 | 0.0E+00 | M29580.1 | NT | Human zinc-finger protein 7 (ZFP7) mRNA, complete cds | |
| 1636 | 6633 | 11703 | 26.94 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA | |
| 1637 | 6634 | 11704 | 1.45 | 0.0E+00 | 7657065 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA | |
| 1641 | 6638 | 11707 | 2.18 | 0.0E+00 | BE222374.1 | EST_HUMAN | hu11d05_x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:Q65147 095147 | MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ; |
| 1641 | 6638 | 11708 | 2.18 | 0.0E+00 | BE222374.1 | EST_HUMAN | hu11d05_x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:Q65147 095147 | MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ; |
| 1643 | 6639 | 11710 | 1.29 | 0.0E+00 | 4557810 | NT | Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA | |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 1646 | 6642 | 11713 | 8.67 | 0.0E+00 | H30132.1 | EST HUMAN | ye55e08.r1 Spares breast 3NbHBst Homo sapiens cDNA clone [IMAGE: 182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| 1646 | 6642 | 11714 | 8.67 | 0.0E+00 | H30132.1 | EST HUMAN | ye55e08.r1 Spares breast 3NbHBst Homo sapiens cDNA clone [IMAGE: 182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); |
| 1648 | 6644 | 11716 | 19.26 | 0.0E+00 | Z80780.1 | NT | H.sapiens H2Bfh gene |
| 1648 | 6644 | 11717 | 19.26 | 0.0E+00 | Z80780.1 | NT | H.sapiens H2Bfh gene |
| 1651 | 6647 | | 64.75 | 0.0E+00 | 5031748 | NT | Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA |
| 1660 | 6656 | 11730 | 5.23 | 0.0E+00 | 8923841 | NT | Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA |
| 1663 | 6659 | 11733 | 1.85 | 0.0E+00 | 5453855 | NT | Homo sapiens pericentriolar material 1 (PCM1) mRNA |
| 1669 | 6665 | 11741 | 1.1 | 0.0E+00 | 4826973 | NT | Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA |
| 1675 | 6671 | 11748 | 7.62 | 0.0E+00 | AB026542.1 | NT | Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds |
| 1677 | 6673 | | 1.82 | 0.0E+00 | S94400.1 | NT | TCR zeta (human, Genomic)mRNA, 365 nt, segment 1 of 8] |
| 1686 | 6682 | 11757 | 1.82 | 0.0E+00 | 4557538 | NT | Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26a2) mRNA |
| 1693 | 7753 | 11764 | 1.05 | 0.0E+00 | '11545911 | NT | Homo sapiens NOD2 protein (NOD2), mRNA |
| 1706 | 6701 | 11778 | 2.59 | 0.0E+00 | AF273841.1 | NT | Homo sapiens SmCY (SmCY) gene, complete cds |
| 1747 | 7754 | | 150.64 | 0.0E+00 | 4506718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 1752 | 6748 | 11826 | 3.32 | 0.0E+00 | 4557556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 1752 | 6748 | 11827 | 3.32 | 0.0E+00 | 4557556 | NT | Homo sapiens E1A binding protein p300 (EP300) mRNA |
| 1755 | 6748 | 11831 | 2.75 | 0.0E+00 | U63963.1 | NT | Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds |
| 1759 | 7755 | 11836 | 8.02 | 0.0E+00 | 4505332 | NT | Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA |
| 1771 | 6763 | 11851 | 22.06 | 0.0E+00 | U14967.1 | NT | Human ribosomal protein L21 mRNA, complete cds |
| 1773 | 6765 | 11854 | 12.68 | 0.0E+00 | AB002331.1 | NT | Human mRNA for KIAA0333 gene, partial cds |
| 1774 | 6766 | 11855 | 13.86 | 0.0E+00 | 4502264 | NT | Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA |
| 1774 | 6766 | 11856 | 13.86 | 0.0E+00 | 4502264 | NT | Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA |
| 1774 | 6766 | 11857 | 13.86 | 0.0E+00 | 4502264 | NT | Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA |
| 1778 | 6780 | 11872 | 1.29 | 0.0E+00 | 4504626 | NT | Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products |
| 1778 | 6780 | 11873 | 1.29 | 0.0E+00 | 4504626 | NT | Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products |
| 1798 | 6789 | 11878 | 5.58 | 0.0E+00 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 1798 | 6789 | 11879 | 5.58 | 0.0E+00 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 1807 | 6798 | 11888 | 3.27 | 0.0E+00 | AB032978.1 | NT | Homo sapiens mRNA for KIAA1152 protein, partial cds |
| 1807 | 6798 | 11889 | 3.27 | 0.0E+00 | AB032978.1 | NT | Homo sapiens mRNA for KIAA1152 protein, partial cds |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1811 | 6801 | 11891 | 3.31 | 0.0E+00 | 4826783 | NT | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA |
| 1811 | 6801 | 11892 | 3.31 | 0.0E+00 | 4826783 | NT | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA |
| 1812 | 6802 | 11893 | 8.06 | 0.0E+00 | U07147.1 | NT | Human retinal degeneration slow (RDS) gene, exon 1 |
| 1812 | 6802 | 11894 | 8.06 | 0.0E+00 | U07147.1 | NT | Human retinal degeneration slow (RDS) gene, exon 1 |
| 1815 | 6805 | 11891 | 1.53 | 0.0E+00 | AW2077280.1 | EST_HUMAN | U+H-B1-afn-f-07-0-Ul s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3' |
| 1815 | 6805 | 11898 | 1.53 | 0.0E+00 | AW2077280.1 | EST_HUMAN | U+H-B1-afn-f-07-0-Ul s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3' |
| 1837 | 6827 | 11915 | 2.87 | 0.0E+00 | BE277465.1 | EST_HUMAN | 601179164f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5' |
| 1837 | 6827 | 11916 | 2.87 | 0.0E+00 | BE277465.1 | EST_HUMAN | 601179164f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5' |
| 1878 | 6867 | 11955 | 1.79 | 0.0E+00 | 7657390 | NT | Homo sapiens nuclear protein (NP220), mRNA |
| 1878 | 6867 | 11956 | 1.79 | 0.0E+00 | 7657390 | NT | Homo sapiens nuclear protein (NP220), mRNA |
| 1881 | 6870 | 11958 | 2.53 | 0.0E+00 | 4506384 | NT | Human sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products |
| 1881 | 6870 | 11959 | 2.53 | 0.0E+00 | 4506384 | NT | Human sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products |
| 1888 | 6877 | 11967 | 1.87 | 0.0E+00 | AB037788.1 | NT | Human sapiens mRNA for KIAA1367 protein, partial cds |
| 1891 | 6880 | 11960 | 1.55 | 0.0E+00 | AF157476.1 | NT | Human sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds |
| 1892 | 7753 | 11970 | 1.49 | 0.0E+00 | M98478.1 | NT | Human trans-glutaminase mRNA, complete cds |
| 1892 | 7753 | 11971 | 1.49 | 0.0E+00 | M98478.1 | NT | Human trans-glutaminase mRNA, complete cds |
| 1897 | 6885 | 11978 | 1.31 | 0.0E+00 | 4507464 | NT | Human sapiens transforming growth factor, beta 3 (TGFB3), mRNA |
| 1897 | 6885 | 11979 | 1.31 | 0.0E+00 | 4507464 | NT | Human sapiens transforming growth factor, beta 3 (TGFb3), mRNA |
| 1900 | 6887 | 11981 | 1.17 | 0.0E+00 | 7657038 | NT | Human sapiens glutathione S-transferase theta 6 (GST6), mRNA |
| 1902 | 6889 | | 6.49 | 0.0E+00 | AF240786.1 | NT | Human sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 1907 | 6894 | | 3.82 | 0.0E+00 | M55532.1 | NT | Human topoisomerase I pseudogene 1 |
| 1908 | 7759 | 11988 | 1.74 | 0.0E+00 | 5901905 | NT | Human sapiens butyrophilin, subfamily 3, member A2 (BTNSA2), mRNA |
| 1910 | 6896 | 11990 | 4.05 | 0.0E+00 | BEO18066.1 | EST_HUMAN | bb73f1.1.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5' |
| 1916 | 6902 | 11995 | 1.47 | 0.0E+00 | 4809282 | NT | Human sapiens histidine ammonia-lyase (HAL) mRNA |
| 1916 | 6902 | 11996 | 1.47 | 0.0E+00 | 4809282 | NT | Human sapiens histidine ammonia-lyase (HAL) mRNA |
| 1926 | 6912 | 12007 | 9.5 | 0.0E+00 | 4826638 | NT | Human sapiens actinin, alpha 4 (ACTN4) mRNA |
| 1926 | 6912 | 12008 | 9.5 | 0.0E+00 | 4826638 | NT | Human sapiens actinin, alpha 4 (ACTN4) mRNA |
| 1940 | 6926 | 12023 | 1.41 | 0.0E+00 | M33782.1 | NT | Human TFEB protein mRNA, partial cds |
| 1940 | 6926 | 12024 | 1.41 | 0.0E+00 | M33782.1 | NT | Human TFEB protein mRNA, partial cds |
| 1942 | 6928 | 12025 | 1.95 | 0.0E+00 | AW193024.1 | EST_HUMAN | x69b01.x1 NCI CGAP_Par1 Homo sapiens cDNA clone IMAGE:2878913 3' |
| 1942 | 6928 | 12026 | 1.95 | 0.0E+00 | AW193024.1 | EST_HUMAN | x69b01.x1 NCI CGAP_Par1 Homo sapiens cDNA clone IMAGE:2878913 3' |

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Table 4

Single Exon Probes Expressed in HBL1100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 1943 | 6929 | 12027 | 8.45 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1943 | 6929 | 12028 | 8.45 | 0.0E+00 | 6912457 | NT | Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA |
| 1945 | 6931 | 12030 | 1.25 | 0.0E+00 | 7662095 | NT | Homo sapiens KIAA0408 gene product (KIAA0408), mRNA |
| 1946 | 6932 | 12031 | 1.88 | 0.0E+00 | AB011149.1 | NT | Homo sapiens mRNA for KIAA0577 protein, complete cds |
| 1947 | 6933 | 12032 | 1.43 | 0.0E+00 | Z47556.1 | NT | H.sapiens genes for semenogelin I and semenogelin II |
| 1947 | 6933 | 12033 | 1.43 | 0.0E+00 | Z47556.1 | NT | H.sapiens genes for semenogelin I and semenogelin II |
| 1954 | 6940 | 12042 | 3.49 | 0.0E+00 | AB040946.1 | NT | Homo sapiens mRNA for KIAA1513 protein, partial cds |
| 1971 | 6956 | 12060 | 0.94 | 0.0E+00 | AF273841.1 | NT | Homo sapiens SMCY (SMCY) gene, complete cds |
| 1971 | 6956 | 12061 | 0.94 | 0.0E+00 | AF273841.1 | NT | Homo sapiens SMCY (SMCY) gene, complete cds |
| 2000 | 6983 | 12087 | 1.1 | 0.0E+00 | 7708742 | NT | Homo sapiens TP53TC3a (TP53TC3a), mRNA |
| 2004 | 6987 | 12091 | 13.6 | 0.0E+00 | BE743215.1 | EST_HUMAN | 6015738951 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5' |
| 2004 | 6987 | 12092 | 13.6 | 0.0E+00 | BE743215.1 | EST_HUMAN | 6015738951 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5' |
| 2006 | 6989 | 12093 | 1.98 | 0.0E+00 | 4503648 | NT | Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA |
| 2007 | 6990 | 12094 | 1.02 | 0.0E+00 | BE207688.1 | EST_HUMAN | 6018619741 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081483 5' |
| 2008 | 6991 | 12095 | 5.35 | 0.0E+00 | AU140831.1 | EST_HUMAN | AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5' |
| 2010 | 6993 | 12097 | 1.29 | 0.0E+00 | AA077589.1 | EST_HUMAN | 7B22E10 Chromosome 7 Fetal Brain cDNA Library-Homo sapiens cDNA clone 7B22E10 |
| 2010 | 6993 | 12098 | 1.29 | 0.0E+00 | AA077589.1 | EST_HUMAN | 7B22E10 Chromosome 7 Fetal Brain cDNA Library-Homo sapiens cDNA clone 7B22E10 |
| 2012 | 6995 | 12101 | 2.47 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein ROM121 (POM121L1), mRNA |
| 2014 | 6997 | 12101 | 1.21 | 0.0E+00 | 45885853 | NT | Homo sapiens phosphodiesterase 6A, cGMP specific, rod, alpha (PDE6A), mRNA |
| 2015 | 6998 | 12101 | 1.06 | 0.0E+00 | Z42399.1 | EST_HUMAN | HSCOIC021 normalized infant brain cDNA Homo sapiens cDNA clone c-Dic022 |
| 2017 | 7000 | | 1.43 | 0.0E+00 | A1244247.1 | EST_HUMAN | qv90f08_x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element. |
| 2021 | 7004 | 12109 | 6.29 | 0.0E+00 | BE877225.1 | EST_HUMAN | 601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5' |
| 2023 | 7006 | 12111 | 4.71 | 0.0E+00 | BF315325.1 | EST_HUMAN | 601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5' |
| 2023 | 7006 | 12112 | 4.71 | 0.0E+00 | BF315325.1 | EST_HUMAN | 601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5' |
| 2028 | 7011 | 12118 | 2.79 | 0.0E+00 | BE697125.1 | EST_HUMAN | RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA |
| 2028 | 7011 | 12119 | 2.79 | 0.0E+00 | BE697125.1 | EST_HUMAN | RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA |
| 2033 | 7016 | 12125 | 2.04 | 0.0E+00 | L00620.1 | NT | Human plasmna membrane calcium ATPase Isoform 2 (APT2B2) mRNA, complete cds |
| 2033 | 7016 | 12126 | 2.04 | 0.0E+00 | L00620.1 | NT | Human plasmna membrane calcium ATPase Isoform 2 (APT2B2) mRNA, complete cds |
| 2036 | 7019 | 12129 | 1.7 | 0.0E+00 | 4758489 | NT | Homo sapiens GTP binding protein 1 (GTPBP1) mRNA |
| 2055 | 7037 | | 2.76 | 0.0E+00 | BE767964.1 | EST_HUMAN | QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA |
| 2056 | 7038 | | 1.41 | 0.0E+00 | AF018963.1 | NT | Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds |
| 2058 | 7040 | 12149 | 4.46 | 0.0E+00 | BF027562.1 | EST_HUMAN | 601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5' |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------------------|--|
| 2059 | 7041 | 12150 | 1.77 | 0.0E+00 | BE072624.1 | EST_HUMAN | PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA genes, complete cds |
| 2061 | 7043 | 12151 | 2.11 | 0.0E+00 | AF240786.1 | NT | IL3-CT0219-271089-022-G10 CT0219 Homo sapiens cDNA |
| 2062 | 7044 | 12152 | 3.64 | 0.0E+00 | AW752/08.1 | EST_HUMAN | QV-BT065-010389-002-BT065 Homo sapiens cDNA |
| 2064 | 7046 | 12154 | 4.62 | 0.0E+00 | AI904640.1 | EST_HUMAN | QV-BT065-010389-002-BT065 Homo sapiens cDNA |
| 2064 | 7046 | 12155 | 4.62 | 0.0E+00 | AI904640.1 | EST_HUMAN | QV-BT065-010389-002-BT065 Homo sapiens cDNA |
| 2116 | 7096 | | 1.21 | 0.0E+00 | L14787.1 | NT | Human DNA-binding protein mRNA, 3' end |
| 2122 | 7102 | 12214 | 1.98 | 0.0E+00 | BE274696.1 | EST_HUMAN | 601122338F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5' |
| 2124 | 7104 | 12217 | 1.01 | 0.0E+00 | D87685.1 | NT | Human mRNA for KIAA0244 gene, partial cds |
| 2125 | 7105 | 12218 | 42.14 | 0.0E+00 | AV738288.C3 | Homo sapiens cDNA clone CBNBDE08 5' | AV738288.C3 Homo sapiens cDNA clone CBNBDE08 5' |
| 2125 | 7105 | 12219 | 42.14 | 0.0E+00 | AV738288.1 | EST_HUMAN | AV738288.C3 Homo sapiens cDNA clone CBNBDE08 5' |
| 2127 | 7107 | 12221 | 3.7 | 0.0E+00 | AA93169.1 | EST_HUMAN | oc32e01.s1.NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3' |
| 2129 | 7109 | | 1.02 | 0.0E+00 | M198285.1 | NT | Human apolipoprotein B-100 (apoB) gene, exons 22 through 29 |
| 2132 | 7112 | 12225 | 52.74 | 0.0E+00 | BF344434.1 | EST_HUMAN | 602014829F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5' |
| 2133 | 7113 | 12226 | 55.46 | 0.0E+00 | BE748899.1 | EST_HUMAN | 601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3' |
| 2136 | 7116 | 12229 | 4.45 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA |
| 2136 | 7116 | 12230 | 4.45 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA |
| 2140 | 7764 | 12235 | 4.41 | 0.0E+00 | BF313617.1 | EST_HUMAN | 601980267F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5' |
| 2143 | 7122 | 12238 | 2.4 | 0.0E+00 | BE018750.1 | EST_HUMAN | bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 |
| 2145 | 7124 | 12240 | 2.17 | 0.0E+00 | AA042813.1 | EST_HUMAN | TRANSSCRIPTION FACTOR S-II-RELATED PROTEIN ; |
| 2145 | 7124 | 12241 | 2.17 | 0.0E+00 | AA042813.1 | EST_HUMAN | zk53c07_s1 Soares_pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to |
| 2153 | 7132 | 12249 | 2.86 | 0.0E+00 | AL163204.2 | NT | gb:X65857_>ds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOTE (HUMAN); |
| 2153 | 7132 | 12250 | 2.86 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21CC004 |
| 2154 | 7133 | 12251 | 2.34 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2154 | 7133 | 12252 | 2.34 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2159 | 7138 | | 2.31 | 0.0E+00 | U36254.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 18 |
| 2160 | 7139 | 12257 | 1.43 | 0.0E+00 | AA282281.1 | EST_HUMAN | Zr12b10.r1.NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:7128891 5' |
| 2167 | 7146 | 12263 | 2.22 | 0.0E+00 | BE897487.1 | EST_HUMAN | 601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5' |
| 2180 | 7159 | 12279 | 8.49 | 0.0E+00 | 4557556 | NT | Hom sapiens E1A binding protein p300 (EP300) mRNA |
| 2185 | 7164 | 12284 | 1.93 | 0.0E+00 | 7662401 | NT | Hom sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2191 | 7170 | 12291 | 6.09 | 0.0E+00 | BE895281.1 | EST_HUMAN | 601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918867 5' |

Table 4
Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2195 | 7174 | 12295 | 2.37 | 0.0E+00 | BE905563.1 | EST_HUMAN | 601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5' |
| 2195 | 7174 | 12296 | 2.37 | 0.0E+00 | BE905563.1 | EST_HUMAN | 601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5' |
| 2197 | 7175 | 12298 | 3.61 | 0.0E+00 | AB037784.1 | NT | Homo sapiens mRNA for KIAA1363 protein, partial cds |
| 2237 | 7214 | 12331 | 3.29 | 0.0E+00 | 11545748 | NT | Homo sapiens is differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA |
| 2237 | 7214 | 12332 | 3.29 | 0.0E+00 | 11545748 | NT | Homo sapiens is differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA |
| 2238 | 7215 | 12333 | 2.27 | 0.0E+00 | AI076404.1 | EST_HUMAN | ox209c07_X1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3' |
| 2241 | 7218 | 12336 | 3.84 | 0.0E+00 | AA428010.1 | EST_HUMAN | zv78a11.11_Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5' |
| 2241 | 7218 | 12337 | 3.84 | 0.0E+00 | AA428010.1 | EST_HUMAN | zv78a11.11_Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5' |
| 2243 | 7220 | 12339 | 3.72 | 0.0E+00 | BF347039.1 | EST_HUMAN | 602021846F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157339 5' |
| 2248 | 7225 | 12345 | 1.02 | 0.0E+00 | 6325466 | NT | Homo sapiens flavin containing monooxygenase 3 (FMOC3), mRNA |
| 2255 | 7232 | 12351 | 2.79 | 0.0E+00 | BE676095.1 | EST_HUMAN | 7122a02.X1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94839 O94939 |
| 2258 | 7235 | 12353 | 16.03 | 0.0E+00 | AF044571.1 | NT | KIAA0857 PROTEIN ; |
| 2259 | 7236 | 12354 | 1.78 | 0.0E+00 | AI625542.1 | EST_HUMAN | Homo sapiens phosphotyrosine kinase alpha subunit (PHKα2), gene, exon 32 |
| 2261 | 7238 | 12355 | 1.15 | 0.0E+00 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 2264 | 7241 | 12357 | 3.07 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2264 | 7241 | 12358 | 3.07 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 2267 | 7244 | 12361 | 3.48 | 0.0E+00 | 5803178 | NT | Homo sapiens sperm specific antigen 2 (SSFA2), mRNA |
| 2267 | 7244 | 12362 | 3.48 | 0.0E+00 | 5803178 | NT | Homo sapiens sperm specific antigen 2 (SSFA2), mRNA |
| 2273 | 7249 | 12365 | 2.22 | 0.0E+00 | 7662007 | NT | Homo sapiens KIAA0218 gene product (KIAA0218), mRNA |
| 2273 | 7249 | 12366 | 2.22 | 0.0E+00 | 7662007 | NT | Homo sapiens KIAA0218 gene product (KIAA0218), mRNA |
| 2277 | 7253 | 12371 | 1.4 | 0.0E+00 | D83778.1 | NT | Human mRNA for KIAA0194 gene, partial cds |
| 2277 | 7253 | 12372 | 1.4 | 0.0E+00 | D83778.1 | NT | Human mRNA for KIAA0194 gene, partial cds |
| 2287 | 7263 | 12380 | 2.25 | 0.0E+00 | 5174678 | NT | Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA |
| 2291 | 7266 | 12384 | 3.96 | 0.0E+00 | AU131142.1 | EST_HUMAN | AU131142.NT2RP3.Homo sapiens cDNA clone NT2RP3002064 5' |
| 2292 | 7267 | 12385 | 47.81 | 0.0E+00 | BE794026.1 | EST_HUMAN | 601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5' |
| 2293 | 7268 | 12385 | 2.44 | 0.0E+00 | AW867076.1 | EST_HUMAN | MR1-SN003-120400-002_and SNI0033.Homo sapiens cDNA |
| 2294 | 7269 | 12386 | 4.95 | 0.0E+00 | 7662017 | NT | Homo sapiens KIAA0244 protein (KIAA0244), mRNA |
| 2295 | 7270 | 12387 | 2.03 | 0.0E+00 | 4758497 | NT | Homo sapiens hexose-6-phosphate dehydrogenase (glucose-1-dehydrogenase) (H6PD), mRNA |
| 2295 | 7270 | 12388 | 2.03 | 0.0E+00 | 4758497 | NT | Homo sapiens hexose-6-phosphate dehydrogenase (glucose-1-dehydrogenase) (H6PD), mRNA |
| 2296 | 7271 | | 4.1 | 0.0E+00 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 42 (CYP3A45) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 2298 | 7273 | 12390 | 21.5 | 0.0E+00 | AU118082.1 | EST_HUMAN | AU118082.HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5' |

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Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2298 | 7273 | 12391 | 21.5 | 0.0E+00 | AU118082.1 | EST_HUMAN | AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5' |
| 2298 | 7273 | 12392 | 21.5 | 0.0E+00 | AU118082.1 | EST_HUMAN | AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5' |
| 2299 | 7274 | 12393 | 1.24 | 0.0E+00 | 8923089 NT | | Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA |
| 2316 | 7291 | | 1.51 | 0.0E+00 | BE814424.1 | EST_HUMAN | MRO-BN00j-0-090600-0229-d12 BN0070 Homo sapiens cDNA |
| 2348 | 7322 | 12441 | 0.99 | 0.0E+00 | AU119582.1 | EST_HUMAN | AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5' |
| 2349 | 7323 | | 3.28 | 0.0E+00 | AI042335.1 | EST_HUMAN | oxf0b02_x1 Soares_NHNMpu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662 |
| 2350 | 7324 | 12442 | 1.18 | 0.0E+00 | 8923620 NT | | O08662_23(KDA PHOSPHATIDYLINOSITOL 4-KINASE,) |
| 2354 | 7328 | | 4.15 | 0.0E+00 | BE895605.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA |
| 2365 | 7339 | | 3.39 | 0.0E+00 | AB005622.1 | EST_HUMAN | 601432608f1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5' |
| 2369 | 7342 | 12460 | 5.53 | 0.0E+00 | 6006002 NT | | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA |
| 2372 | 7343 | 12463 | 1.57 | 0.0E+00 | D85606.1 | NT | Homo sapiens gene for cholecystokinin type-A receptor, complete cds |
| 2372 | 7344 | 12464 | 1.57 | 0.0E+00 | D85606.1 | NT | Homo sapiens gene for cholecystokinin type-A receptor, complete cds |
| 2380 | 7352 | 12473 | 1.34 | 0.0E+00 | AF106275.1 | NT | Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6 |
| 2384 | 7355 | 12477 | 0.95 | 0.0E+00 | BF345274.1 | EST_HUMAN | 602018058f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158670 5' |
| 2390 | 7361 | 12484 | 6.99 | 0.0E+00 | 5729777 NT | | Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA |
| 2398 | 7369 | 12490 | 16.53 | 0.0E+00 | BF569144.1 | EST_HUMAN | 602184558f1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3' |
| 2407 | 7378 | 12497 | 2.46 | 0.0E+00 | AW466922.1 | EST_HUMAN | ha04h04x41 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3' |
| 2409 | 7380 | 12498 | 2.09 | 0.0E+00 | AW501010.1 | EST_HUMAN | U-HF-BP01-als-c-07-Q-U_f1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072730 5' |
| 2433 | 7404 | | 2.13 | 0.0E+00 | AWB13853.1 | EST_HUMAN | RC3-ST0187-3013030-016-c04 ST0197 Homo sapiens cDNA |
| 2438 | 7409 | 12526 | 27.9 | 0.0E+00 | BE789542.1 | EST_HUMAN | 60159253f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5' |
| 2439 | 6887 | 11981 | 1.18 | 0.0E+00 | 7657038 NT | | Homo sapiens death receptor 6 (DR6), mRNA |
| 2440 | 7410 | 12527 | 1.33 | 0.0E+00 | BF509482.1 | EST_HUMAN | UH-BI4-ac22-b-08-0-U_f1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3' |
| 2443 | 7413 | 12529 | 3.32 | 0.0E+00 | Z32684.2 | NT | Homo sapiens mRNA for membrane transport protein (XK gene) |
| 2445 | 7415 | | 3.21 | 0.0E+00 | 5453871 NT | | Homo sapiens platelet-derived growth factor receptor-like (PDGFR α) mRNA |
| 2448 | 7418 | 12533 | 1.05 | 0.0E+00 | BE910378.1 | EST_HUMAN | 60150356f1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5' |
| 2449 | 7419 | 12534 | 2.35 | 0.0E+00 | 7657468 NT | | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 2450 | 7420 | 12535 | 0.91 | 0.0E+00 | BE150865.1 | EST_HUMAN | RC4-HT02f1-6-160200-013-d05 HT0276 Homo sapiens cDNA |
| 2451 | 7421 | 12536 | 3.02 | 0.0E+00 | U93239.1 | NT | Human Sec62 (Sec62) mRNA, complete cds |
| 2457 | 7427 | 12542 | 2.2 | 0.0E+00 | BE886490.1 | EST_HUMAN | 60150822f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5' |
| 2461 | 7430 | 12547 | 4.05 | 0.0E+00 | BE875511.1 | EST_HUMAN | 60148924f1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5' |
| 2461 | 7430 | 12548 | 4.05 | 0.0E+00 | BE875511.1 | EST_HUMAN | 60148924f1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5' |
| 2462 | 7431 | 12549 | 1.27 | 0.0E+00 | AF114027.1 | EST_HUMAN | AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF8 |
| 2464 | 7433 | 12552 | 1 | 0.0E+00 | AF245505.1 | NT | Homo sapiens adican mRNA, complete cds |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|--|
| 2480 | 7449 | 12560 | 1.91 | 0.0E+00 | BE536921.1 | EST_HUMAN | 601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161' 5' |
| 2485 | 7453 | 12567 | 3.77 | 0.0E+00 | AU143277.1 | EST_HUMAN | AU143277 Y79AA11 Homo sapiens cDNA clone Y79AA1001673' 5' |
| 2485 | 7453 | 12568 | 3.77 | 0.0E+00 | AU143277.1 | EST_HUMAN | AU143277 Y79AA11 Homo sapiens cDNA clone Y79AA1001673' 5' |
| 2486 | 7454 | 12569 | 3.86 | 0.0E+00 | BE292896.1 | EST_HUMAN | 601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955' 5' |
| 2486 | 7454 | 12570 | 3.86 | 0.0E+00 | BE292898.1 | EST_HUMAN | 601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955' 5' |
| 2487 | 7455 | 12571 | 0.93 | 0.0E+00 | BF223041.1 | EST_HUMAN | 7q27h12-X1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:00246 O00246 |
| 2490 | 7458 | 12573 | 5.96 | 0.0E+00 | AF245505.1 | NT | Homo sapiens adican mRNA, complete cds |
| 2508 | 7476 | 12591 | 0.91 | 0.0E+00 | BE296613.1 | EST_HUMAN | 60117363F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159' 5' |
| 2522 | 7708 | 12608 | 1.49 | 0.0E+00 | AB037836.1 | NT | Homo sapiens mRNA for KIAA1415 protein, partial cds |
| 2522 | 7708 | 12609 | 1.49 | 0.0E+00 | AB037836.1 | NT | Homo sapiens mRNA for KIAA1415 protein, partial cds |
| 2523 | 7489 | | 1.95 | 0.0E+00 | BF513835.1 | EST_HUMAN | Ui-H-BW1-amp-f-12-0-U1-s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631' 3' |
| 2528 | 7494 | 12614 | 1.25 | 0.0E+00 | BF672818.1 | EST_HUMAN | 602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612' 5' |
| 2530 | 7496 | | 1.1 | 0.0E+00 | BE616895.1 | EST_HUMAN | 601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621788' 5' |
| 2539 | 7504 | 12623 | 2.22 | 0.0E+00 | AB037742.1 | NT | Homo sapiens mRNA for KIAA1321 protein, partial cds |
| 2540 | 7505 | 12624 | 2.36 | 0.0E+00 | 5032150 | NT | Homo sapiens TATA box binding protein (TBP)-associated Factor, RNA polymerase II, I, 28kD (TAF2) |
| 2542 | 7507 | 12626 | 5.06 | 0.0E+00 | AB037859.1 | NT | Homo sapiens mRNA for KIAA1438 protein, partial cds |
| 2543 | 7508 | 12627 | 1.42 | 0.0E+00 | BE795445.1 | EST_HUMAN | 601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304' 5' |
| 2543 | 7508 | 12628 | 1.42 | 0.0E+00 | BE795445.1 | EST_HUMAN | 601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304' 5' |
| 2546 | 7511 | 12629 | 1.35 | 0.0E+00 | BE29328.1 | EST_HUMAN | 601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051358' 5' |
| 2553 | 7518 | | 6.42 | 0.0E+00 | BE792472.1 | EST_HUMAN | 601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222' 5' |
| 2555 | 7520 | 12637 | 1.06 | 0.0E+00 | AB020710.1 | NT | Homo sapiens mRNA for KIAA0930 protein, partial cds |
| 2563 | 7527 | 12645 | 2.7 | 0.0E+00 | 4504686 | NT | Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA |
| 2574 | 7537 | 12653 | 4 | 0.0E+00 | AF173227.1 | NT | Homo sapiens guanylate cyclase-activating protein 2 (GUCATB) gene, exon 1 |
| 2577 | 7540 | 12654 | 1.3 | 0.0E+00 | AB011108.1 | NT | Homo sapiens mRNA for KIAA0536 protein, partial cds |
| 2580 | 7543 | 12657 | 1.88 | 0.0E+00 | AU133385.1 | EST_HUMAN | AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964' 5' |
| 2581 | 7544 | 12658 | 1.75 | 0.0E+00 | M69225.1 | NT | Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds |
| 2584 | 7547 | 12661 | 2.23 | 0.0E+00 | AU130403.1 | EST_HUMAN | AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779' 5' |
| 2584 | 7547 | 12662 | 2.23 | 0.0E+00 | AU130403.1 | EST_HUMAN | AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779' 5' |
| 2587 | 7550 | 12665 | 1.36 | 0.0E+00 | AW887015.1 | EST_HUMAN | RC1-OT0016-220300-011-d07 OT00086 Homo sapiens cDNA |
| 2590 | 7553 | 12668 | 1.01 | 0.0E+00 | BF000018.1 | EST_HUMAN | 7h15h05X NCI CGAP_C016 Homo sapiens cDNA clone IMAGE:3916099' 3' |
| 2591 | 7554 | 12669 | 5.22 | 0.0E+00 | BE383165.1 | EST_HUMAN | 601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923' 5' |
| 2592 | 7555 | | 8.33 | 0.0E+00 | BE531263.1 | EST_HUMAN | 601278317F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267' 5' |

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Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 2616 | 7578 | 12690 | 1.38 | 0.0E+00 | 8922843 | NT | Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA |
| 2626 | 7586 | 12698 | 1.22 | 0.0E+00 | AB037732.1 | NT | Homo sapiens mRNA for KIAA1311 protein, partial cds |
| 2650 | 7610 | | 27.94 | 0.0E+00 | AA316723.1 | EST_HUMAN | EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29 |
| 2651 | 7611 | 12721 | 1.31 | 0.0E+00 | BE794884.1 | EST_HUMAN | 601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5' |
| 2655 | 7615 | 12726 | 5.13 | 0.0E+00 | U36253.1 | NT | Human beta-prime-adaptin (BAM22) gene, exon 5 |
| 2656 | 7616 | 12727 | 5.03 | 0.0E+00 | 76695717 | NT | Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA |
| 2657 | 7617 | 12728 | 2.44 | 0.0E+00 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FLI-1) gene, complete cds |
| 2658 | 7618 | 12729 | 1.27 | 0.0E+00 | AB051826.1 | NT | Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds |
| 2664 | 7623 | 12735 | 26.29 | 0.0E+00 | BE796316.1 | EST_HUMAN | 60158199F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5' |
| 2665 | 7624 | 12736 | 1.5 | 0.0E+00 | BF680632.1 | EST_HUMAN | 602155922F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5' |
| 2668 | 7778 | 12740 | 24.53 | 0.0E+00 | BE563433.1 | EST_HUMAN | 601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5' |
| 2669 | 7627 | | 2.28 | 0.0E+00 | AV721647 | HTB | Homo sapiens cDNA clone HTB3YE09 5' |
| 2671 | 7629 | 12743 | 2.82 | 0.0E+00 | 5174486 | NT | Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA |
| 2671 | 7629 | 12744 | 2.82 | 0.0E+00 | 5174486 | NT | Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA |
| 2672 | 7630 | 12745 | 1.27 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 2672 | 7630 | 12746 | 1.27 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 2673 | 7631 | 12747 | 2.26 | 0.0E+00 | AF290195.1 | NT | Homo sapiens hypertension-related calcium-regulated gene PD1 (KIAA0757) mRNA |
| 2674 | 7632 | | 51.51 | 0.0E+00 | AV651066 | EST_HUMAN | AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3' |
| 2675 | 7633 | 12748 | 3.33 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250800-439-608 TN0141 Homo sapiens cDNA |
| 2675 | 7633 | 12749 | 3.33 | 0.0E+00 | BF377897.1 | EST_HUMAN | CM1-TN0141-250800-439-608 TN0141 Homo sapiens cDNA |
| 2682 | 7640 | 12756 | 19.56 | 0.0E+00 | BE747183.1 | EST_HUMAN | 601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5' |
| 2687 | 7645 | 12760 | 3.09 | 0.0E+00 | BF037713.1 | EST_HUMAN | 601462038F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3865497 5' |
| 2695 | 7653 | | 0.93 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 2696 | 7654 | 12768 | 2.53 | 0.0E+00 | BF514110.1 | EST_HUMAN | UI-H-BW1-antw-e-07-0-U1 s1 NCI_OGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3' |
| 2703 | 7660 | | 2.14 | 0.0E+00 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 2708 | 7665 | 12776 | 1.05 | 0.0E+00 | 7705275 | NT | Homo sapiens angiopoietin-3 (ANG-3), mRNA |
| 2708 | 7665 | 12777 | 1.05 | 0.0E+00 | 7705275 | NT | Homo sapiens angiopoietin-3 (ANG-3), mRNA |
| 2709 | 7666 | 12778 | 2.68 | 0.0E+00 | BF677684.1 | EST_HUMAN | 602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5' |
| 2715 | 7672 | 12786 | 1.43 | 0.0E+00 | 7427522 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 2719 | 7676 | 12789 | 26.73 | 0.0E+00 | AV725534.1 | EST_HUMAN | AV725534 HTC Homo sapiens cDNA clone HTCCA03 5' |
| 2719 | 7676 | 12790 | 26.73 | 0.0E+00 | AV725534.1 | EST_HUMAN | AV725534 HTC Homo sapiens cDNA clone HTCCA03 5' |
| 2721 | 7678 | | 11.75 | 0.0E+00 | AI879163.1 | EST_HUMAN | au55d04.Y Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW.R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ; |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|---|-------------------------|---|
| 2724 | 7681 | 12795 | 2.71 | 0.0E+00 | BF530661.1 | EST_HUMAN | 602071957F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4214679 5' |
| 2725 | 7682 | 12796 | 58.63 | 0.0E+00 | BE872768.1 | EST_HUMAN | 601450912F1 NIH MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5' |
| 2727 | 7684 | 12797 | 2.21 | 0.0E+00 | AU131494 NT_2RP3 Homo sapiens cDNA clone NT_2RP3002672 5' | EST_HUMAN | AU131494 NT_2RP3 Homo sapiens cDNA clone NT_2RP3002672 5' |
| 2727 | 7684 | 12798 | 2.2 | 0.0E+00 | AU131494 NT_2RP3 Homo sapiens cDNA clone NT_2RP3002672 5' | EST_HUMAN | AU131494 NT_2RP3 Homo sapiens cDNA clone NT_2RP3002672 5' |
| 2728 | 7685 | 12789 | 68.47 | 0.0E+00 | BE300344.1 | EST_HUMAN | 600944794F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5' |
| 2728 | 7685 | 12800 | 68.47 | 0.0E+00 | BE300344.1 | EST_HUMAN | 600944794F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5' |
| 2734 | 5251 | 10262 | 2.82 | 0.0E+00 | S76830.1 | NT | glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3068 nt] |
| 2737 | 7692 | | 3.43 | 0.0E+00 | AB033281.1 | NT | Homo sapiens BTRGP2 mRNA for F-box and WD-repeats protein Isoform C, complete cds |
| 2743 | 5747 | 10768 | 1.92 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 2743 | 5747 | 10769 | 1.92 | 0.0E+00 | AF264750.1 | NT | Homo sapiens ALR-like protein mRNA, partial cds |
| 2747 | 6032 | 11062 | 2.78 | 0.0E+00 | 4503202 | NT | Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) |
| 2747 | 6032 | 11063 | 2.78 | 0.0E+00 | 4503202 | NT | Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) |
| 2752 | 7783 | 12808 | 5.17 | 0.0E+00 | X85980.1 | NT | H. sapiens serine hydroxymethyltransferase pseudogene |
| 2763 | 7784 | | 1.34 | 0.0E+00 | AF068624.1 | NT | Homo sapiens 5'-aminolevulinate synthase 2 (ALAS2) gene, complete cds |
| 2765 | 7786 | | 1.35 | 0.0E+00 | AB040960.1 | NT | Homo sapiens mRNA for KIAA1527 protein, partial cds |
| 2771 | 7792 | | | | | | Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes |
| 2772 | 7793 | 12813 | 2.35 | 0.0E+00 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 2775 | 7796 | 12815 | 1.41 | 0.0E+00 | M91803.1 | NT | Human sodium channel mRNA |
| 2777 | 7798 | 12817 | 1.16 | 0.0E+00 | M80902.1 | NT | Human AH4K nucleoprotein mRNA, 5' end |
| 2781 | 7802 | | 1.42 | 0.0E+00 | X73428.1 | NT | H. sapiens Id3 gene for HLH type transcription factor |
| 2783 | 7804 | | 2.78 | 0.0E+00 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 2784 | 7805 | 12821 | 1.41 | 0.0E+00 | 7019584 | NT | Homo sapiens zinc finger protein 221 (ZNF221), mRNA |
| 2784 | 7805 | 12822 | 1.41 | 0.0E+00 | 7019584 | NT | Homo sapiens zinc finger protein 221 (ZNF221), mRNA |
| 2784 | 7805 | 12823 | 1.41 | 0.0E+00 | 7019584 | NT | Homo sapiens zinc finger protein 221 (ZNF221), mRNA |
| 2787 | 7808 | 12825 | 0.96 | 0.0E+00 | M98478.1 | NT | Human trans-glutaminase mRNA, complete cds |
| 2792 | 7812 | 12829 | 36.19 | 0.0E+00 | D508657.1 | NT | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene |
| 2792 | 7812 | 12830 | 36.19 | 0.0E+00 | D508657.1 | NT | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene |
| 2795 | 7815 | 12833 | 4.89 | 0.0E+00 | AL096857.1 | NT | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes |
| 2796 | 7816 | | 6.12 | 0.0E+00 | Y10658.1 | NT | H. sapiens mRNA for nuclear DNA helicase II |
| 2797 | 7817 | | 1.14 | 0.0E+00 | AF152303.1 | NT | Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds |
| 2798 | 7818 | 12834 | 71.64 | 0.0E+00 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|--|---|
| 2798 7818 | 12835 | 71.64 | 0.0E+00 | | 4503470 NT | | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 2810 7830 | 12846 | 2.53 | 0.0E+00 | | 4507280 NT | | Homo sapiens serine/threonine kinase 9 (STK9) mRNA |
| 2813 7833 | 12850 | 1 | 0.0E+00 | AL04759.1 | EST_HUMAN | DKFZp586G0621 [r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621] | |
| 2814 7834 | | 2.12 | 0.0E+00 | | 4503098 NT | | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 2817 7837 | 12852 | 5.88 | 0.0E+00 | BEO81898.1 | EST_HUMAN | QY2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA | |
| 2817 7837 | 12853 | 5.88 | 0.0E+00 | BEO81898.1 | EST_HUMAN | QY2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA | |
| 2822 7843 | 12861 | 0.85 | 0.0E+00 | | 6806918 NT | | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 2822 7843 | 12862 | 0.85 | 0.0E+00 | | 6806918 NT | | Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA |
| 2825 7846 | 12866 | 3.1 | 0.0E+00 | AL163206.2 | NT | | Homo sapiens chromosome 21 segment HS21C006 |
| 2825 7846 | 12867 | 3.1 | 0.0E+00 | AL163206.2 | NT | | Homo sapiens chromosome 21 segment HS21C006 |
| 2826 7847 | 12868 | 1.03 | 0.0E+00 | AA215579.1 | EST_HUMAN | zg86b11_s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:6835173' similar to contains Alu repetitive element | |
| 2834 7854 | | 4.09 | 0.0E+00 | Y19210.1 | NT | | Homo sapiens fibb5 gene for hair keratin, exons 1 to 9 |
| 2836 7856 | 12875 | 1.08 | 0.0E+00 | | 4758279 NT | | Homo sapiens EphA4 (EPHA4) mRNA |
| 2837 7857 | 12876 | 50.46 | 0.0E+00 | | 4503470 NT | | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 2838 7858 | 12877 | 2.63 | 0.0E+00 | AL561002.1 | EST_HUMAN | tn18d07_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247_O16247_F44E7.2 PROTEIN; | |
| 2838 7858 | 12878 | 2.63 | 0.0E+00 | AL561002.1 | EST_HUMAN | tn18d07_x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247_O16247_F44E7.2 PROTEIN; | |
| 2840 7860 | 12880 | 1.19 | 0.0E+00 | P52740 | SWISSPROT | ZINC FINGER PROTEIN_132 | |
| 2841 7861 | 12881 | 1.05 | 0.0E+00 | AF152338.1 | NT | Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds | |
| 2857 7877 | 12893 | 2.2 | 0.0E+00 | AB033093.1 | NT | Homo sapiens mRNA for KIAA267 protein, partial cds | |
| 2857 7877 | 12894 | 2.2 | 0.0E+00 | AB033093.1 | NT | Homo sapiens mRNA for KIAA267 protein, partial cds | |
| 2858 7878 | 12895 | 5.42 | 0.0E+00 | AB040941.1 | NT | Homo sapiens mRNA for KIAA1508 protein, partial cds | |
| 2858 7878 | 12896 | 5.42 | 0.0E+00 | AB040941.1 | NT | Homo sapiens mRNA for KIAA1508 protein, partial cds | |
| 2861 7881 | 12899 | 2.79 | 0.0E+00 | | 7661903 NT | Homo sapiens KIAA0100 gene product (KIAA0100), mRNA | |
| 2861 7881 | 12900 | 2.79 | 0.0E+00 | | 7661903 NT | Homo sapiens KIAA0100 gene product (KIAA0100), mRNA | |
| 2862 7882 | 12901 | 3.2 | 0.0E+00 | | 5174574 NT | | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (Drosophila) homolog; translocated to, 4 (MLLT4) mRNA |
| 2862 7882 | 12902 | 3.2 | 0.0E+00 | | 5174574 NT | | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (Drosophila) homolog; translocated to, 4 (MLLT4) mRNA |
| 2867 7886 | 12906 | 0.99 | 0.0E+00 | BF110702.1 | EST_HUMAN | 7n40d03_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG:17293 PROTEIN ; | |

Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|---|--|
| 2867 | 7886 | 12907 | 0.99 | 0.0E+00 | BF110702.1 | EST_HUMAN | 7n40d03_x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 |
| 2875 | 7894 | 12917 | 2.17 | 0.0E+00 | 4505054 NT | Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA | |
| 2875 | 7894 | 12918 | 2.17 | 0.0E+00 | 4505054 NT | Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA | |
| 2882 | 7901 | 12923 | 1.65 | 0.0E+00 | 4758827 NT | Homo sapiens neurexin III (NRXN3) mRNA | |
| 2883 | 7902 | | 1.14 | 0.0E+00 | X98494.1 NT | H. sapiens mRNA for M phase phosphoprotein 10 | |
| 2886 | 7905 | 12926 | 0.93 | 0.0E+00 | AB033034.1 NT | Homo sapiens mRNA for KIAA1208 protein, partial cds | |
| 2888 | 7907 | 12927 | 0.94 | 0.0E+00 | X15309.1 NT | H. sapiens Ni-H gene, exon 4 | |
| 2888 | 7907 | 12928 | 0.94 | 0.0E+00 | X15309.1 NT | H. sapiens Ni-H gene, exon 4 | |
| 2890 | 7909 | 12930 | 8.37 | 0.0E+00 | AF106275.1 NT | Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6 | |
| 2904 | 7923 | | 1.38 | 0.0E+00 | AI149880.1 EST_HUMAN | qf43f03_x1_Scares testis NHT Homo sapiens cDNA clone IMAGE:1752809 3' | |
| 2912 | 7931 | 12930 | 1.21 | 0.0E+00 | 4506118 NT | Homo sapiers prosper-related homeobox 1 (PROX1) mRNA | |
| 2913 | 7932 | 12951 | 4.29 | 0.0E+00 | AB004884.1 NT | Homo sapiers mRNA for PKU-alpha, partial cds | |
| 2924 | 7943 | 12959 | 2.03 | 0.0E+00 | 7662273 NT | Homo sapiers KIAA0737 gene product (KIAA0737), mRNA | |
| 2925 | 7944 | 12950 | 2.05 | 0.0E+00 | 5729755 NT | Homo sapiers calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA | |
| 2925 | 7944 | 12961 | 2.05 | 0.0E+00 | 5729755 NT | Homo sapiers calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA | |
| 2935 | 7954 | 12971 | 1.3 | 0.0E+00 | AF114488.1 NT | Homo sapiers Intersectin short isoform (ITSN) mRNA, complete cds | |
| 2935 | 7954 | 12972 | 1.3 | 0.0E+00 | AF114488.1 NT | Homo sapiers Intersectin short isoform (ITSN) mRNA, complete cds | |
| 2958 | 7977 | 12992 | 1.23 | 0.0E+00 | M74099.1 NT | Human displacement protein (CCAA1) mRNA | |
| 2967 | 7985 | 12999 | 0.84 | 0.0E+00 | AW976266.1 EST_HUMAN | EST388375 MAGE sequences, MAGN Homo sapiens cDNA | |
| 2970 | 7983 | | 4.06 | 0.0E+00 | AF195953.1 NT | Homo sapiers membrane-bound aminopeptidase P (XNPEP2) gene, complete cds | |
| 2973 | 7991 | 13005 | 6.1 | 0.0E+00 | 5579469 NT | Homo sapiers heat shock 70kD protein 1 (HSPA1A), mRNA | |
| 2973 | 7991 | 13006 | 6.1 | 0.0E+00 | 5579469 NT | Homo sapiers heat shock 70kD protein 1 (HSPA1A), mRNA | |
| 2975 | 7993 | | 6.5 | 0.0E+00 | AL259403.1 NT | Isoform 2 of a novel human mRNA from chromosome 22 | |
| 2979 | 7997 | 13010 | 1.96 | 0.0E+00 | AF017433.1 NT | Homo sapiers putative transcription factor CR53 (CRS3) mRNA, partial cds | |
| 2982 | 8000 | | | | | Homo sapiers transcription factor GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel &> | |
| 3002 | 8020 | 13033 | 3.21 | 0.0E+00 | X03529.1 NT | Human germline gene 16.1 for Ig lambda L-chain C region (Ig-L-C16.1) | |
| 3008 | 8025 | | 1.61 | 0.0E+00 | AF199355.1 NT | Homo sapiers F-box protein FB1.5 (FB1.5) mRNA, complete cds | |
| 3012 | 8029 | 13040 | 1.43 | 0.0E+00 | AF064589.1 NT | Homo sapiers melanoma-associated antigen (MAGE-C1) gene, complete cds | |
| 3033 | 8050 | 13058 | 3.49 | 0.0E+00 | AF285208.1 NT | Homo sapiers SWI-SNF complex protein p270 mRNA, partial cds | |
| 3034 | 8051 | 13060 | 5.9 | 0.0E+00 | AF149773.1 NT | Homo sapiers NOD1 protein (NOD1) gene, exons 1, 2, and 3 | |
| 3038 | 8055 | 13063 | 3.23 | 0.0E+00 | 7682139 NT | Homo sapiers KIAA0469 gene product (KIAA0469), mRNA | |

Single Exon Probes Expressed In HBL100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLASTE Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|-------------------------------------|-----------------------|---|--|
| 3039 8056 | 13064 | 1.38 | 0.0E+00 | AF042076.1 | NT | | Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds |
| 3068 8084 | 13098 | 3.44 | 0.0E+00 | 4826783 | NT | | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNCB1) mRNA |
| 3077 8093 | 13107 | 28.05 | 0.0E+00 | L20841.1 | NT | | Human ferritin heavy chain mRNA, complete cds |
| 3080 8096 | 13110 | 1.09 | 0.0E+00 | AB011121.1 | NT | | Homo sapiens mRNA for KIAA0549 protein, partial cds |
| 3080 8096 | 13111 | 1.09 | 0.0E+00 | AB011121.1 | NT | | Homo sapiens mRNA for KIAA0549 protein, partial cds |
| 3087 8103 | 13118 | 33.16 | 0.0E+00 | T94870.1 | EST_HUMAN | ye32f03.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539 | |
| 3102 8118 | 13136 | 1.16 | 0.0E+00 | BF242336.1 | EST_HUMAN | S29539 BASIC PROTEIN, 23K - ; | |
| 3104 8120 | 13137 | 1.26 | 0.0E+00 | AI968036.1 | EST_HUMAN | 6018785071 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:410743 5' | |
| 3109 8125 | 13144 | 4.08 | 0.0E+00 | X98922.1 | NT | wu12h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3' | |
| 3109 8125 | 13145 | 4.08 | 0.0E+00 | X98922.1 | NT | H_sapiens mRNA for gamma-glutamyltransferase | |
| 3120 8136 | 13157 | 1.48 | 0.0E+00 | 4758827 | NT | H_sapiens mRNA for gamma-glutamyltransferase | |
| 3120 8136 | 13158 | 1.48 | 0.0E+00 | 4758827 | NT | Homo sapiens neurexin III (NRXN3) mRNA | |
| 3127 8143 | 13164 | 9.09 | 0.0E+00 | 4504658 | NT | Homo sapiens neurexin III (NRXN3) mRNA | |
| 3145 8161 | 13182 | 12.76 | 0.0E+00 | M28699.1 | NT | Homo sapiens nucleolar phosphoprotein B23 (NP23) mRNA, complete cds | |
| 3149 8165 | 13185 | 10.04 | 0.0E+00 | 4502098 | NT | Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA | |
| 3155 8171 | 13193 | 0.8 | 0.0E+00 | 4758055 | NT | Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA | |
| 3155 8171 | 13194 | 0.8 | 0.0E+00 | 4758055 | NT | Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA | |
| 3157 8173 | 13195 | 2.91 | 0.0E+00 | AA774783.1 | EST_HUMAN | aa87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3' | |
| 3165 8181 | 13203 | 5.5 | 0.0E+00 | AF286598.1 | NT | Homo sapiens angiostatin binding protein 1 mRNA, complete cds | |
| 3165 8181 | 13204 | 5.5 | 0.0E+00 | AF286598.1 | NT | Homo sapiens angiostatin binding protein 1 mRNA, complete cds | |
| 3175 8191 | 13212 | 1.57 | 0.0E+00 | 4557590 | NT | Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA | |
| 3180 8196 | 13219 | 0.98 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA | |
| | | | | | | | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,> |
| 3187 8203 | 13225 | 1.67 | 0.0E+00 | AF019413.1 | NT | Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds | |
| 3190 8206 | 13228 | 3.59 | 0.0E+00 | AF055084.1 | NT | Homo sapiens KIAA0440 protein (KIAA0440) mRNA | |
| 3193 8209 | 13230 | 1.14 | 0.0E+00 | 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440) mRNA | |
| 3193 8209 | 13231 | 1.14 | 0.0E+00 | 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440) mRNA | |
| 3201 10045 | 13238 | 2.89 | 0.0E+00 | 4502014 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA | |
| 3201 10045 | 13239 | 2.89 | 0.0E+00 | 4502014 | NT | Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA | |
| 3218 8233 | 13254 | 2.91 | 0.0E+00 | AF265208.1 | NT | Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds | |

Table 4
Single Exon Probes Expressed in HBL1100 Cells

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|--|-------------------------|--|
| 3219 | 8234 | 13255 | 1.97 | 0.0E+00 | 8923624 | NT | Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA |
| 3231 | 8246 | 13268 | 1.1 | 0.0E+00 | 7657038 | NT | Homo sapiens death receptor 6 (DR6), mRNA |
| 3250 | 8263 | 13284 | 6 | 0.0E+00 | AI589294.1 | EST_HUMAN | I58908_x2 NCI_CGAP_Pari Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT |
| 3257 | 8270 | 13292 | 2.09 | 0.0E+00 | AF128838.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, contains Alu repetitive element; |
| 3257 | 8270 | 13293 | 2.09 | 0.0E+00 | AF128838.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6 |
| 3258 | 8271 | 13294 | 0.78 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 3258 | 8271 | 13295 | 0.78 | 0.0E+00 | 7657213 | NT | Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA |
| 3261 | 8274 | 13297 | 1.16 | 0.0E+00 | 4502582 | NT | Homo sapiens caspase-8, apoptosis-related cysteine protease (CASP8), mRNA |
| 3261 | 8274 | 13298 | 1.16 | 0.0E+00 | 4502582 | NT | Homo sapiens caspase-8, apoptosis-related cysteine protease (CASP8), mRNA |
| 3264 | 8277 | 13300 | 11.21 | 0.0E+00 | AF111163.1 | NT | Homo sapiens pyrin (M6PF) gene, complete cds |
| 3266 | 8279 | 13302 | 1.25 | 0.0E+00 | AB040940.1 | NT | Homo sapiens mRNA for KIAA1507 protein, partial cds |
| 3279 | 8291 | 13316 | 0.86 | 0.0E+00 | AI632569.1 | EST_HUMAN | wb10f04_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR-Q91929 Q91929 |
| 3312 | 8323 | 13346 | 3.08 | 0.0E+00 | AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM20001735 5' | ZINC FINGER PROTEIN : | |
| 3319 | 8329 | 13349 | 0.95 | 0.0E+00 | 7363436 | NT | Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA |
| 3319 | 8329 | 13350 | 0.95 | 0.0E+00 | 7363436 | NT | Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA |
| 3322 | 8332 | 13352 | 1.91 | 0.0E+00 | 7706239 | NT | Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA |
| 3323 | 8333 | 13353 | 1.03 | 0.0E+00 | AF211189.1 | NT | Homo sapiens T-type calcium channel alpha1 subunit Alpha1- α isoform (CACNA1) mRNA, complete cds |
| 3327 | 8337 | | 0.97 | 0.0E+00 | AW867015.1 | EST_HUMAN | MR1-SN033-100400-001-008 SN033 Homo sapiens cDNA |
| 3340 | 8349 | 13366 | 1.39 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 3340 | 8349 | 13367 | 1.39 | 0.0E+00 | 7662401 | NT | Homo sapiens KIAA0952 protein (KIAA0952), mRNA |
| 3341 | 8350 | 13368 | 1.13 | 0.0E+00 | 4502398 | NT | Homo sapiens beaded filament structural protein 1 filensin (BFSP-1) mRNA |
| 3343 | 8352 | 13369 | 2.13 | 0.0E+00 | 5803067 | NT | Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA |
| 3352 | 7817 | 12723 | 1.45 | 0.0E+00 | AF110763.1 | NT | Homo sapiens skeletal muscle LIM-protein 1 (FLH1) gene, complete cds |
| 3357 | 8365 | 13382 | 2.22 | 0.0E+00 | 7657038 | NT | Homo sapiens death receptor 6 (DR6), mRNA |
| 3358 | 8366 | 13383 | 1.37 | 0.0E+00 | 5453965 | NT | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA |
| 3358 | 8366 | 13384 | 1.37 | 0.0E+00 | 5453965 | NT | Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA |
| 3361 | 8369 | 13389 | 0.96 | 0.0E+00 | AJ277276.1 | NT | Homo sapiens mRNA for rapa-2 (rapa gene) |
| 3362 | 8370 | 13390 | 4.78 | 0.0E+00 | K02380.1 | NT | Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC Incompatibility determinants |

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Table 4

Single Exon Probes Expressed in HBL100 Cells

| Probe Seq ID NO: | Exon ORF SEQ ID NO: | Top Similar BLAST E Value | Expression Signal | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|---------------------|---------------------------|-------------------|-----------------------|-------------------------|---|
| 3364 8372 | 13392 | 1.12 | 0.0E+00 | 7427522 NT | | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 3367 8375 | 13395 | 1.1 | 0.0E+00 | 4557746 NT | | Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA |
| 3373 8381 | 13400 | 4.09 | 0.0E+00 | AI935159.1 EST_HUMAN | | wp14d10_x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE ; |
| 3373 8381 | 13401 | 4.09 | 0.0E+00 | AI935159.1 EST_HUMAN | | wp14d10_x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE ; |
| 3377 8385 | 13406 | 1.61 | 0.0E+00 | A1278120.1 NT | | [Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)] |
| 3395 8393 | 13416 | 5.22 | 0.0E+00 | 6552332 NT | | [Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)], mRNA |
| 3395 8393 | 13417 | 5.22 | 0.0E+00 | 6552332 NT | | [Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)], mRNA |
| 3391 8399 | 13425 | 1.11 | 0.0E+00 | M14123.1 NT | | Human endogenous retrovirus HERV-K10 |
| 3397 8405 | 13431 | 6.63 | 0.0E+00 | U43293.1 NT | | Human MDS1A (AML-1/MDS1 fusion) mRNA, partial cds |
| 3401 8410 | 13435 | 0.99 | 0.0E+00 | 95568718 NT | | Homo sapiens hypothetical protein (AF038169), mRNA |
| 3401 8410 | 13436 | 0.99 | 0.0E+00 | 95568718 NT | | Homo sapiens hypothetical protein (AF038169), mRNA |
| 3405 8414 | 13441 | 2.65 | 0.0E+00 | AF045452.1 NT | | Homo sapiens cell-line K1 transcriptional regulatory protein p54 mRNA, complete cds |
| 3405 8414 | 13442 | 2.65 | 0.0E+00 | AF045452.1 NT | | Homo sapiens cell-line K1 transcriptional regulatory protein p54 mRNA, complete cds |
| 3413 8422 | 13451 | 1.04 | 0.0E+00 | AF231922.1 NT | | Homo sapiens chromosome 21 unknown mRNA |
| 3423 8431 | 13457 | 1.44 | 0.0E+00 | 4508028 NT | | Homo sapien's zinc finger protein 45 (La Kruppel-associated box (KRB) domain polypeptide) (ZNF45) mRNA |
| 3426 8434 | 13459 | 2.04 | 0.0E+00 | BE304791.1 EST_HUMAN | | 601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5' |
| 3426 8434 | 13460 | 2.04 | 0.0E+00 | BE304791.1 EST_HUMAN | | 601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5' |
| 3429 8437 | 13463 | 1.11 | 0.0E+00 | 4826795 NT | | Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA |
| 3431 8439 | 13468 | 1.05 | 0.0E+00 | O14867 SWISSPROT | | TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303) |
| 3436 8444 | 13470 | 0.83 | 0.0E+00 | AI384007.1 EST_HUMAN | | te35g12_Xt Scores_NIHIMPU_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O000498 |
| 3439 8447 | 13473 | 1.05 | 0.0E+00 | M10976.1 NT | | O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN : |
| 3454 8462 | 13489 | 1.53 | 0.0E+00 | AB032979.1 NT | | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 3454 8462 | 13490 | 1.53 | 0.0E+00 | AB032979.1 NT | | Homo sapiens mRNA for KIAA1153 protein, partial cds |
| 3463 8471 | 13496 | 0.86 | 0.0E+00 | AV701869.1 EST_HUMAN | | Hom sapiens potassium voltage-gated channel ADBDAH06 5' |
| 3465 8473 | 13497 | 1.06 | 0.0E+00 | 45016884 NT | | Homo sapiens semenogelin II (SEMG2) mRNA |
| 3467 8475 | | 2.85 | 0.0E+00 | AF078868.1 NT | | Homo sapiet is homologous yeast-44.2 protein mRNA, complete cds |
| 3475 8483 | 13503 | 1.11 | 0.0E+00 | AL133204.1 NT | | Novel human gene mapping to chromosome X |
| 3477 8485 | 13504 | 0.77 | 0.0E+00 | AB040909.1 NT | | Homo sapiens mRNA for KIAA1476 protein, partial cds |
| 3485 8493 | 13510 | 1.54 | 0.0E+00 | 8923087 NT | | Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA |
| 3493 8501 | 13515 | 0.94 | 0.0E+00 | 6997248 NT | | Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA |

Table 4
Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO. | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal Value | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------------|----------------------------------|-----------------------|-------------------------|--|
| 3493 | 8501 | 13516 | 0.94 | 0.0E+00 | 6897248 | NT | Homo sapiens <i>sal (Drosophila)-like 1 (SALL1)</i> , mRNA |
| 3494 | 8502 | | 1.7 | 0.0E+00 | AI081907.1 | EST_HUMAN | ox77c11.x1_Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:1662358 3' similar to WP:T19B4.4 CE131742; |
| 3496 | 8504 | 13519 | 1.01 | 0.0E+00 | 6325463 | NT | Homo sapiens <i>buhophilin, subfamily 3, member A3 (BTN3A3)</i> , mRNA |
| 3500 | 8508 | | 4.62 | 0.0E+00 | AW852217.1 | EST_HUMAN | QV0-C70225-230300-1169-e01 CT0225 Homo sapiens cDNA |
| 3504 | 8512 | 13527 | 1.42 | 0.0E+00 | 45044294 | NT | Homo sapiens <i>H3 histone family, member K (H3FK)</i> , mRNA |
| 3508 | 8516 | | 5.83 | 0.0E+00 | AF118846.1 | NT | Homo sapiens <i>gamma-glutamyltransferase synthetase (GLCLC)</i> gene, partial cds |
| 3509 | 8517 | 13528 | 7.79 | 0.0E+00 | BF676393.1 | EST_HUMAN | 602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5' |
| 3513 | 8521 | | 1.01 | 0.0E+00 | AA988715.1 | EST_HUMAN | cq94h06.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER28.b2 MER29 repetitive element; |
| 3522 | 8529 | 13539 | 1.4 | 0.0E+00 | AW857977.1 | EST_HUMAN | QV0-D70047-170200-123-g01 DT0047 Homo sapiens cDNA |
| 3535 | 8541 | 13547 | 0.96 | 0.0E+00 | BF672054.1 | EST_HUMAN | 602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283645 5' |
| 3535 | 8541 | 13548 | 0.96 | 0.0E+00 | BF672054.1 | EST_HUMAN | 602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283645 5' |
| 3536 | 8542 | | 1.13 | 0.0E+00 | 4826967 | NT | Homo sapiens <i>retinoblastoma-binding protein 2 (RBBP2)</i> , mRNA |
| 3538 | 8544 | 13550 | 0.75 | 0.0E+00 | AW854693.1 | EST_HUMAN | hi84g01.x1_SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879024 3' |
| 3538 | 8544 | 13551 | 0.75 | 0.0E+00 | AW854693.1 | EST_HUMAN | hi84g01.x1_SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879024 3' |
| 3541 | 8547 | 13555 | 0.72 | 0.0E+00 | | 7662319 | NT |
| 3546 | 8553 | 13560 | 2.09 | 0.0E+00 | | 4557752 | NT |
| 3546 | 8553 | 13561 | 2.09 | 0.0E+00 | | 4557752 | NT |
| 3562 | 8569 | 13574 | 2.29 | 0.0E+00 | D87327.1 | NT | Homo sapiens mRNA for <i>G protein-coupled inward rectifier potassium channel, complete cds</i> |
| 3566 | 8573 | | 14.47 | 0.0E+00 | 7665491 | NT | Homo sapiens <i>midline 1 (OptizBBB syndrome) (MID1)</i> mRNA |
| 3583 | 8590 | 13594 | 3.35 | 0.0E+00 | AB026542.1 | NT | Homo sapiens <i>midline 1 (OptizBBB syndrome) (MID1)</i> mRNA |
| 3584 | 8591 | 13595 | 1.92 | 0.0E+00 | AB007866.2 | NT | Homo sapiens mRNA for <i>G protein-coupled inward rectifier potassium channel, complete cds</i> |
| 3586 | 8593 | 13596 | 4.2 | 0.0E+00 | AF124250.1 | NT | Homo sapiens mRNA for <i>WASP-family protein, complete cds</i> |
| 3586 | 8593 | 13597 | 4.2 | 0.0E+00 | AF124250.1 | NT | Homo sapiens mRNA for <i>WAVE2</i> mRNA for <i>WASP-family protein, complete cds</i> |
| 3592 | 8599 | 13605 | 1.04 | 0.0E+00 | AA852743.1 | EST_HUMAN | NHTBCae15j09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09 |
| 3592 | 8599 | 13606 | 1.04 | 0.0E+00 | AA852743.1 | EST_HUMAN | NHTBCae15j09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09 |
| 3595 | 8602 | 13608 | 1.83 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 3595 | 8602 | 13609 | 1.83 | 0.0E+00 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 3596 | 8603 | 13610 | 0.93 | 0.0E+00 | AB002331.1 | NT | Human mRNA for <i>KIAA0333</i> gene, partial cds |
| 3596 | 8603 | 13611 | 0.93 | 0.0E+00 | AB002331.1 | NT | Human mRNA for <i>KIAA0333</i> gene, partial cds |
| 3599 | 8606 | 13614 | 1.43 | 0.0E+00 | AW851714.1 | EST_HUMAN | MR2-C70222-281098-005-e05 CT0222 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 3601 | 8608 | 13616 | 1.91 | 0.0E+00 | 5729928 | NT | Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA |
| 3603 | 8610 | 13618 | 1.09 | 0.0E+00 | AB01839.1 | NT | Homo sapiens mRNA for KIAA0796 protein, partial cds |
| 3605 | 8612 | 13620 | 1 | 0.0E+00 | O14867 | SWISSPROT | TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (H42303) |
| 3607 | 8614 | 13622 | 0.53 | 0.0E+00 | AB02077.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 3607 | 8614 | 13623 | 0.53 | 0.0E+00 | AB02077.1 | NT | Homo sapiens mRNA for KIAA0910 protein, partial cds |
| 3618 | 8625 | 13632 | 1.01 | 0.0E+00 | 5729733 | NT | Homo sapiens activator of S phase kinase (ASK) mRNA |
| 3618 | 8625 | 13633 | 1.01 | 0.0E+00 | 5729733 | NT | Homo sapiens activator of S phase kinase (ASK) mRNA |
| 3623 | 8630 | 13635 | 4.46 | 0.0E+00 | AW298134.1 | EST_HUMAN | UI-H-BW0_8j5-e-12-0-1II_s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3' |
| 3623 | 8630 | 13636 | 4.46 | 0.0E+00 | AW298134.1 | EST_HUMAN | UI-H-BW0_8j5-e-12-0-1II_s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3' |
| 3645 | 8651 | 13657 | 1.21 | 0.0E+00 | AB004630.1 | NT | Human gene for Type XIX collagen α1 chain, exon 6 |
| 3646 | 8652 | 13658 | 0.9 | 0.0E+00 | AA463659.1 | EST_HUMAN | ee05g011_x1_Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812406 5' similar to SW_KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1]; |
| 3650 | 8656 | 13662 | 1.09 | 0.0E+00 | AB020770.1 | NT | Homo sapiens mRNA for KIAA0803 protein, partial cds |
| 3653 | 8659 | 13664 | 4.19 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 3674 | 8679 | 13682 | 7.89 | 0.0E+00 | 7662183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 3677 | 8682 | 13685 | 75.43 | 0.0E+00 | 4506718 | NT | Homo sapiens ribosomal protein S2 (RPS2) mRNA |
| 3683 | 8687 | 13689 | 1.39 | 0.0E+00 | 7657065 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 3683 | 8687 | 13690 | 1.39 | 0.0E+00 | 7657065 | NT | Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA |
| 3729 | 8733 | | 0.98 | 0.0E+00 | AF195658.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |
| 3730 | 8734 | 13731 | 2.82 | 0.0E+00 | AF179733.1 | NT | Pan troglodytes olfactory receptor (PTR208) gene, partial cds |
| 3733 | 8737 | 13735 | 2.36 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 3733 | 8737 | 13736 | 2.36 | 0.0E+00 | 7657468 | NT | Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA |
| 3734 | 8738 | 13737 | 1.15 | 0.0E+00 | AF020091.1 | NT | Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds |
| 3738 | 8742 | 13742 | 1.16 | 0.0E+00 | 4759011 | NT | Homo sapiens RAB9, member RAS oncogene family (RAB9), mRNA |
| 3741 | 8745 | 13745 | 1.16 | 0.0E+00 | AF127851.1 | NT | Gorilla gorilla olfactory receptor (GGO71) gene, partial cds |
| 3741 | 8745 | 13746 | 1.16 | 0.0E+00 | AF127851.1 | NT | Gorilla gorilla olfactory receptor (GGO71) gene, partial cds |
| 3742 | 8746 | 13747 | 1.18 | 0.0E+00 | AI377699.1 | EST_HUMAN | le62f10.x1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3' |
| 3743 | 8747 | | 1.17 | 0.0E+00 | AF152496.1 | NT | Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds |
| 3744 | 8748 | 13748 | 1.26 | 0.0E+00 | 4758199 | NT | Homo sapiens desmoplakin (DP1, DPL) (DSP) mRNA |
| 3747 | 8751 | 13750 | 36.36 | 0.0E+00 | S78985.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds |
| 3749 | 8753 | 13752 | 2.74 | 0.0E+00 | 7710148 | NT | Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA |
| 3750 | 8754 | 13753 | 1.32 | 0.0E+00 | 7682183 | NT | Homo sapiens KIAA0569 gene product (KIAA0569), mRNA |
| 3752 | 8756 | 13754 | 1.1 | 0.0E+00 | AF068601.2 | NT | Homo sapiens myosin light chain kinase Isoform 2 (MLCK) mRNA, complete cds |

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar BLAST E Value | (Top) Hit No. | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------|---------------|-----------------------|---|--------------------|
| 3752 8756 | 13755 | 1.1 | 0.0E+00 | AF069601.2 | NT | | Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds | |
| 3753 8757 | 13756 | 1.03 | 0.0E+00 | 4504534 | NT | | Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA | |
| 3759 8762 | 13762 | 0.81 | 0.0E+00 | 6912735 | NT | | Homo sapiens transient receptor potential channel 5 (TRPC5) mRNA | |
| 3764 8767 | 13770 | 7.3 | 0.0E+00 | 4503178 | NT | | Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA | |
| 3764 8767 | 13771 | 7.3 | 0.0E+00 | 4503178 | NT | | Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA | |
| 3766 8769 | 13774 | 4.16 | 0.0E+00 | U09412.1 | NT | | Human zinc finger protein ZNF134 mRNA, complete cds | |
| 3767 8770 | 13775 | 1.26 | 0.0E+00 | AF114488.1 | NT | | Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds | |
| 3770 8773 | 13777 | 1.15 | 0.0E+00 | 4826783 | NT | | Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA | |
| 3773 8776 | 13780 | 2.04 | 0.0E+00 | 4759171 | NT | | Homo sapiens SC35-interacting protein 1 (SRRP1) mRNA | |
| 3784 8787 | 13791 | 2.48 | 0.0E+00 | AI864727.1 | EST_HUMAN | | Homo sapiens Lyn12 Homo sapiens cDNA clone IMAGE:2411085 3' similar to TR:O43340 | |
| 3787 8790 | 13795 | 20.27 | 0.0E+00 | 4506742 | NT | | wk01101_x1_NCI_CGAP_Lyn12 Homo sapiens cDNA clone R28c130_2.; contains element PTK7 repetitive element; | |
| 3789 8792 | 13797 | 1.47 | 0.0E+00 | AI040338.1 | EST_HUMAN | | O43340 R28c130_2.; contains element PTK7 repetitive element; | |
| 3794 8797 | 13803 | 0.97 | 0.0E+00 | 6005887 | NT | | Homo sapiens ribosomal protein S8 (RPS8) mRNA | |
| 3794 8797 | 13804 | 0.97 | 0.0E+00 | 6005887 | NT | | Homo sapiens ribosomal protein S8 (RPS8) mRNA | |
| 3795 8798 | 13805 | 1.95 | 0.0E+00 | 4504138 | NT | | DKFZp434N413_r1_434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434N0413_5' | |
| 3796 8799 | 13808 | 0.87 | 0.0E+00 | 6005887 | NT | | Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA | |
| 3800 8803 | 13811 | 1.69 | 0.0E+00 | 4506758 | NT | | Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA | |
| 3808 8811 | 13817 | 2.31 | 0.0E+00 | 4585842 | NT | | Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA | |
| 3812 8815 | 13821 | 1.87 | 0.0E+00 | 4505078 | NT | | Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA | |
| 3824 8826 | 13833 | 1.91 | 0.0E+00 | AF129533.1 | NT | | Homo sapiens HBPI7 heparin-binding and FGF-binding protein gene, complete cds | |
| 3829 8831 | 13838 | 3.61 | 0.0E+00 | BE378602.1 | EST_HUMAN | | Homo sapiens ryanodine receptor 3 (RYR3) mRNA | |
| 3836 8838 | 13844 | 2.13 | 0.0E+00 | AW580740.1 | EST_HUMAN | | Homo sapiens partial cds | |
| 3837 8839 | 13845 | 1.01 | 0.0E+00 | BE26498.1 | EST_HUMAN | | PM3-LT0031-100-003-h09 L70031 Homo sapiens cDNA clone IMAGE:3537774_5' | |
| 3837 8839 | 13846 | 1.01 | 0.0E+00 | BE29498.1 | EST_HUMAN | | 6011938271_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774_5' | |
| 3868 8869 | 13872 | 4.2 | 0.0E+00 | AF116185.1 | NT | | 6011938271_1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774_5' | |
| 3868 8869 | 13873 | 4.2 | 0.0E+00 | AF116195.1 | NT | | Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds | |
| 3878 8879 | | 4.42 | 0.0E+00 | M23910.1 | NT | | Homo sapiens class II lymphocyte antigen DP-w4-beta-2 pseudogene, exon 2 | |
| 3881 8882 | | 5.98 | 0.0E+00 | AL163303.2 | NT | | Homo sapiens chromosomes 21 segment HS21C103 | |
| 3887 8888 | 13887 | 0.93 | 0.0E+00 | AL118494.1 | NT | | Novel human gene mapping to chromosome 20 | |
| 3891 8891 | 13889 | 2.94 | 0.0E+00 | AL163284.2 | NT | | Homo sapiens chromosome 21 segment HS21C068 | |
| 3899 8899 | 13897 | 2.2 | 0.0E+00 | AL163268.2 | NT | | Homo sapiens elongation factor 1 alpha 1 (EEF1A1) mRNA | |
| 3911 8911 | | 113.41 | 0.0E+00 | 4503470 | NT | | Homo sapiens eukaryotic translation initiation factor 2B subunit 1 (EIF2B1) mRNA | |

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Table 4
Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|-------------------------|--------------------|
| 3914 | 8914 | | | 1.34 | 0.0E+00 | AI657076.1 | EST_HUMAN |
| 3916 | 8916 | 13910 | | 2.58 | 0.0E+00 | U09366.1 | NT |
| 3933 | 8932 | 13925 | | 12.81 | 0.0E+00 | AB015610.1 | NT |
| 3941 | 8939 | | | 3.58 | 0.0E+00 | AJ238617.1 | NT |
| 3951 | 8949 | 13938 | | 1.39 | 0.0E+00 | AB002314.2 | NT |
| 3952 | 8950 | 13939 | | 1.76 | 0.0E+00 | AL183203.2 | NT |
| 3953 | 8951 | 13940 | | 2.58 | 0.0E+00 | AJ277276.1 | NT |
| 3953 | 8951 | 13941 | | 2.58 | 0.0E+00 | AJ277276.1 | NT |
| 3961 | 8959 | 13948 | | 14.88 | 0.0E+00 | 5032026 | NT |
| 3961 | 8959 | 13949 | | 14.88 | 0.0E+00 | 5032026 | NT |
| 3969 | 8968 | 13957 | | 1.91 | 0.0E+00 | 4503914 | NT |
| 3973 | 8971 | 13959 | | 4.78 | 0.0E+00 | 4885306 | NT |
| 3974 | 8972 | 13960 | | 1.41 | 0.0E+00 | AB006665.1 | NT |
| 3977 | 8975 | 13961 | | 0.8 | 0.0E+00 | 4758807 | NT |
| 3978 | 8976 | 13962 | | 7.12 | 0.0E+00 | 11419297 | NT |
| 3979 | 8977 | 13963 | | 3.68 | 0.0E+00 | AL0966857.1 | NT |
| 3980 | 8978 | | | 0.98 | 0.0E+00 | AA018975.1 | EST_HUMAN |
| 3986 | 8984 | 13970 | | 3.76 | 0.0E+00 | AF165527.1 | NT |
| 3991 | 10050 | 13974 | | 1.98 | 0.0E+00 | AF157476.1 | NT |
| 3995 | 6121 | 11150 | | 1.11 | 0.0E+00 | 4826947 | NT |
| 3995 | 6121 | 11151 | | 1.11 | 0.0E+00 | 4826947 | NT |
| 4000 | 8996 | 13984 | | 1.04 | 0.0E+00 | 4503854 | NT |
| 4000 | 8996 | 13985 | | 1.04 | 0.0E+00 | 4503854 | NT |
| 4003 | 8999 | 13987 | | 1.39 | 0.0E+00 | 8922391 | NT |
| 4003 | 8999 | 13988 | | 1.39 | 0.0E+00 | 8922391 | NT |
| 4006 | 9002 | 13989 | | 1.03 | 0.0E+00 | AB020702.1 | NT |
| 4012 | 9008 | 13997 | | 6.13 | 0.0E+00 | AI982597.1 | EST_HUMAN |
| 4012 | 9008 | 13998 | | 6.13 | 0.0E+00 | AI982597.1 | EST_HUMAN |
| 4014 | 9010 | | | 2.24 | 0.0E+00 | BE184856.1 | EST_HUMAN |
| 4014 | 9010 | 14001 | | 2.24 | 0.0E+00 | BE184856.1 | EST_HUMAN |
| 4018 | 9014 | | | 10.6 | 0.0E+00 | BE274217.1 | EST_HUMAN |

Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4024 | 9020 | 14007 | 1.02 | 0.0E+00 | 4507476 | NT | Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) |
| 4025 | 9021 | 14008 | 2.26 | 0.0E+00 | 5728725 | NT | Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA |
| 4032 | 9028 | | 6.78 | 0.0E+00 | AW675599.1 | EST_HUMAN | ba51f04_x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:28000095 3' similar to SW:TH12_BOVIN |
| 4037 | 9033 | 14021 | 0.95 | 0.0E+00 | AW408788.1 | EST_HUMAN | Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ; U+HF-BM0adv-c-02-0U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5' |
| 4039 | 9035 | 14024 | 1.51 | 0.0E+00 | 8922466 | NT | Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA |
| 4039 | 9035 | 14025 | 1.51 | 0.0E+00 | 8922466 | NT | Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA |
| 4048 | 9044 | | 2.18 | 0.0E+00 | 5174632 | NT | Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDRE-J) mRNA |
| 4068 | 9062 | 14049 | 9.69 | 0.0E+00 | AA401438.1 | EST_HUMAN | zu68h07_s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Aliu repetitive element;contains element MER35 repetitive element; |
| 4068 | 9062 | 14050 | 9.69 | 0.0E+00 | AA401438.1 | EST_HUMAN | zu68h07_s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Aliu repetitive element;contains element MER35 repetitive element; |
| 4072 | 9066 | 14056 | 1.32 | 0.0E+00 | AF157476.1 | NT | Homo sapiens DNA polymerase zeta catalytic subunit (REV5) mRNA, complete cds |
| 4085 | 9079 | 14063 | 0.94 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4085 | 9079 | 14069 | 0.94 | 0.0E+00 | 4507720 | NT | Homo sapiens titin (TTN) mRNA |
| 4087 | 9081 | 14072 | 1.45 | 0.0E+00 | 7662125 | NT | Homo sapiens KIAA0440 protein (KIAA0440), mRNA |
| 4101 | 9095 | 14079 | 1.28 | 0.0E+00 | 4758199 | NT | Homo sapiens desmopletin (DPI, DPlI) (DSP) mRNA |
| 4101 | 9095 | 14080 | 1.28 | 0.0E+00 | 4758199 | NT | Homo sapiens desmopletin (DPI, DPlI) (DSP) mRNA |
| 4109 | 9103 | | 0.71 | 0.0E+00 | AL165303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 4135 | 9130 | 14113 | 1.99 | 0.0E+00 | AJ003145.1 | NT | Homo sapiens mRNA for olfactory receptor protein, pseudogene |
| 4151 | 9146 | 14130 | 2.21 | 0.0E+00 | J02610.1 | NT | Human apolipoprotein B-100 mRNA, complete cds |
| 4164 | 9159 | 14146 | 0.86 | 0.0E+00 | AW9336689.1 | EST_HUMAN | PM2-DT0123-080300-004-a08 DT0123 Homo sapiens cDNA, partial cds |
| 4171 | 9166 | 14153 | 4.94 | 0.0E+00 | AF174590.1 | NT | Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds |
| 4177 | 9171 | | 3.4 | 0.0E+00 | A1189844.1 | EST_HUMAN | qd23f06_x1 Soares_placenta_8to9weeks_2NbHIF8ic9W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20,b2 MER20 repetitive element; |
| 4180 | 9173 | | 5.07 | 0.0E+00 | U14520.1 | NT | Human Cbf-A3 (Cbfb3) gene, partial cds |
| 4183 | 9176 | 14160 | 0.82 | 0.0E+00 | 5174574 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (itthorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA |
| 4198 | 9191 | 14173 | 1.19 | 0.0E+00 | 6563384 | NT | Homo sapiens protein kinase C, nu (PRKCN), mRNA |
| 4198 | 9191 | 14174 | 1.19 | 0.0E+00 | 6563384 | NT | Homo sapiens protein kinase C, nu (PRKCN), mRNA |
| 4205 | 9198 | 14180 | 1.28 | 0.0E+00 | U10991.1 | NT | Human G2 protein mRNA, partial cds |
| 4205 | 9198 | 14181 | 1.28 | 0.0E+00 | U10991.1 | NT | Human G2 protein mRNA, partial cds |

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Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4215 | 9208 | 14187 | 10.08 | 0.0E+00 | 6912281 | NT | Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR) mRNA |
| 4235 | 9229 | | 1.05 | 0.0E+00 | AF153047.2 | NT | Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds |
| 4245 | 9239 | 14222 | 5.12 | 0.0E+00 | L14561.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 4249 | 9243 | 14227 | 4.71 | 0.0E+00 | Z80780.1 | NT | H. sapiens H2af/h gene |
| 4249 | 9243 | 14228 | 4.71 | 0.0E+00 | Z80780.1 | NT | H. sapiens H2af/h gene |
| 4250 | 9244 | 14229 | 1.5 | 0.0E+00 | AW166933.1 | EST_HUMAN | xg88e10x1_NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:PP97365 P97365 |
| 4256 | 9250 | 14235 | 2.06 | 0.0E+00 | X60483.1 | NT | H. sapiens H4/d gene for H4 histone |
| 4256 | 9250 | 14236 | 2.06 | 0.0E+00 | X60483.1 | NT | H. sapiens H4/d gene for H4 histone |
| 4261 | 9254 | 14242 | 11.18 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390) mRNA |
| 4261 | 9254 | 14243 | 11.18 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390) mRNA |
| 4274 | 9267 | 14258 | 11.95 | 0.0E+00 | 4885126 | NT | Homo sapiens caudal type homeo box transcription factor 4 (CDX4) mRNA |
| 4275 | 9268 | 14259 | 1.08 | 0.0E+00 | AJ271736.1 | NT | Homo sapiens Xq pseudoautosomal region; segment 2/2 |
| 4276 | 9269 | | 0.98 | 0.0E+00 | AL165207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 4309 | 9301 | 14286 | 1.08 | 0.0E+00 | 7019456 | NT | Homo sapiens myosin regulatory light chain interacting protein (MIR) mRNA |
| 4320 | 9312 | | 6.33 | 0.0E+00 | AF185953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 4325 | 9317 | 14299 | 2.96 | 0.0E+00 | AJ249765.1 | NT | Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10 |
| 4325 | 9317 | 14300 | 2.96 | 0.0E+00 | AJ249765.1 | NT | Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10 |
| 4330 | 9321 | 14306 | 0.81 | 0.0E+00 | W26179.1 | EST_HUMAN | 24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 4330 | 9321 | 14307 | 0.81 | 0.0E+00 | W26179.1 | EST_HUMAN | 24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 4344 | 9335 | | 2.03 | 0.0E+00 | AF200629.1 | NT | Homo sapiens HPS1 gene, intron 5 |
| 4362 | 9353 | | 0.76 | 0.0E+00 | M14123.1 | NT | Human endogenous retrovirus HERV-K10 |
| 4372 | 9364 | 14344 | 2.57 | 0.0E+00 | AW084964.1 | EST_HUMAN | xg68e08_x1_NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2588446 3' similar to SW.AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION PROTEIN AHNK ; |
| 4374 | 10052 | | 1.15 | 0.0E+00 | 8051619 | NT | Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA |
| 4375 | 9366 | 14346 | 0.91 | 0.0E+00 | AF016050.1 | NT | Homo sapiens: vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds |
| 4378 | 9369 | | 7.59 | 0.0E+00 | AL163207.2 | NT | Homo sapiens: chromosome 21 segment HS21C007 |
| 4380 | 9371 | 14350 | 1.24 | 0.0E+00 | AW381570.1 | EST_HUMAN | PM1-HT0305-101189-002-d03 HT0305 Homo sapiens cDNA |
| 4386 | 9377 | 14357 | 1.16 | 0.0E+00 | AJ278120.1 | NT | Homo sapiens: mRNA for putative ankyrin-repeat containing protein (ORF1) |
| 4386 | 9377 | 14358 | 1.16 | 0.0E+00 | AJ278120.1 | NT | Homo sapiens: mRNA for putative ankyrin-repeat containing protein (ORF1) |
| 4388 | 9379 | 14360 | 1.24 | 0.0E+00 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 4389 | 9380 | 14361 | 3.1 | 0.0E+00 | AF108830.1 | NT | Homo sapiens: serine-threonine protein kinase (MNKH) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|--------------------------------------|-----------------------|-------------------------|--------------------|--|
| | | | | | | | |
| 4598 | 9389 | 14372 | 1.05 | 0.0E+00 | S78684.1 | NT | Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon |
| 4599 | 9390 | 14373 | 1.06 | 0.0E+00 | AF111163.1 | NT | Homo sapiens pyrin (MEFFV) gene, complete cds |
| 4599 | 9390 | 14374 | 1.06 | 0.0E+00 | AF111163.1 | NT | Homo sapiens pyrin (MEFFV) gene, complete cds |
| 4409 | 10053 | 14384 | 3.16 | 0.0E+00 | 6005973 | NT | Homo sapiens zinc finger protein 195 (ZNF195), mRNA |
| 4413 | 9403 | 14388 | 5.97 | 0.0E+00 | AF208161.1 | NT | Homo sapiens syncytin precursor, mRNA, complete cds |
| 4418 | 9408 | 14395 | 1.83 | 0.0E+00 | AF152237.1 | NT | Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds |
| 4421 | 9411 | 14399 | 1.07 | 0.0E+00 | 5454175 | NT | Homo sapiens zinc finger protein 211 (ZNF211), mRNA |
| 4431 | 9421 | 14407 | 50.75 | 0.0E+00 | 4503470 | NT | Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA |
| 4438 | 9428 | 14412 | 1.01 | 0.0E+00 | 4505016 | NT | Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products |
| 4442 | 9432 | 14415 | 1.5 | 0.0E+00 | 4503098 | NT | Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA |
| 4446 | 9436 | 14420 | 1.11 | 0.0E+00 | 4502556 | NT | Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA |
| 4449 | 9439 | | 1.16 | 0.0E+00 | BE871980.1 | EST_HUMAN | 601447892F1 NIH_MGC_C_65 Homo sapiens cDNA clone IMAGE:3852127 5' |
| 4452 | 9442 | | 2.72 | 0.0E+00 | L36485.1 | NT | Homo sapiens kuronate sulphate sulphatase (IDS) gene, complete cds |
| 4454 | 9444 | 14423 | 11.71 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390), mRNA |
| 4454 | 9444 | 14424 | 11.71 | 0.0E+00 | 7662091 | NT | Homo sapiens KIAA0390 gene product (KIAA0390), mRNA |
| 4471 | 9461 | 14440 | 2.89 | 0.0E+00 | AF143314.1 | NT | Homo sapiens PTEN (PTEN) gene, exons 3 through 5 |
| 4473 | 9463 | 14442 | 10.04 | 0.0E+00 | AJ245418.1 | NT | Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex) |
| 4473 | 9463 | 14443 | 10.04 | 0.0E+00 | AJ245418.1 | NT | Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex) |
| 4475 | 9465 | 14444 | 0.8 | 0.0E+00 | AB018383.1 | NT | Homo sapiens mRNA for KIAA0795 protein, partial cds |
| 4490 | 9480 | | 1.45 | 0.0E+00 | AA174072.1 | EST_HUMAN | Zp180g.s13;Strategic fetal retina S67202 Homo sapiens cDNA clone IMAGE:6098854 3' |
| 4492 | 9482 | | 1.39 | 0.0E+00 | 7657410 | NT | Homo sapiens odd (odd Oz/en-m, Drosophila) homolog 1 (ODZ1), mRNA |
| 4494 | 9484 | | 2.8 | 0.0E+00 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4495 | 9485 | 14463 | 1.18 | 0.0E+00 | AF184110.1 | NT | Homo sapiens cyclophilin-related protein (NKRTR) gene, complete cds |
| 4496 | 9486 | 14464 | 5.1 | 0.0E+00 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 4497 | 9487 | | 1.83 | 0.0E+00 | AB037521.1 | NT | Homo sapiens gene for natriuretic protein, partial cds |
| 4499 | 9489 | 14465 | 0.9 | 0.0E+00 | AF195658.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |
| 4502 | 9492 | 14469 | 1.33 | 0.0E+00 | AB007862.2 | NT | Homo sapiens mRNA for KIAA0406 protein, partial cds |
| 4507 | 9497 | 14475 | 11.33 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 4507 | 9497 | 14476 | 11.33 | 0.0E+00 | 4557887 | NT | Homo sapiens keratin 18 (KRT18) mRNA |
| 4508 | 9498 | 14477 | 2.06 | 0.0E+00 | AF167441.1 | NT | Mus musculus E-cadherin binding protein E7 mRNA, complete cds |
| 4518 | 9508 | 14489 | 0.94 | 0.0E+00 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |

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Table 4
Single Exon Probes Expressed in HBL100

| Probe SEQ ID No. | Exon SEQ ID NO. | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor | |
|------------------|-----------------|----------------|-------------------|----------------------------------|-----------------------|---|---|--|
| | | | | | | | | |
| 4518 | 9508 | 14480 | 0.94 | 0.0E+00 | L78810.1 | NT | Homo sapiens ADPIATP carrier protein (ANT-2) gene, complete cds | |
| 4518 | 9508 | 14491 | 0.94 | 0.0E+00 | L78810.1 | NT | Homo sapiens ADPIATP carrier protein (ANT-2) gene, complete cds | |
| 4519 | 9509 | 14492 | 1.58 | 0.0E+00 | AB028970.1 | NT | Homo sapiens mRNA for KIAA1047 protein, partial cds | |
| 4519 | 9509 | 14493 | 1.58 | 0.0E+00 | AB028970.1 | NT | Homo sapiens mRNA for KIAA1047 protein, partial cds | |
| 4524 | 9514 | 14499 | 3.45 | 0.0E+00 | Y18890.1 | NT | Human endogenous retrovirus type K (HERV-K), gag, pol and env genes | |
| 4530 | 9520 | 14507 | 1.32 | 0.0E+00 | BE081527.1 | EST_HUMAN | QV2-BT0635-160-400-142-h05 BT0635 Homo sapiens cDNA | |
| 4531 | 9521 | 14508 | 1.01 | 0.0E+00 | AA418246.1 | EST_HUMAN | Z96607.s1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:767605'3' | |
| 4536 | 9526 | | 2.02 | 0.0E+00 | AF086641.1 | NT | Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region | |
| 4541 | 9530 | 14517 | 2.53 | 0.0E+00 | AB037820.1 | NT | Homo sapiens mRNA for KIAA1399 protein, partial cds | |
| 4541 | 9530 | 14518 | 2.53 | 0.0E+00 | AB037820.1 | NT | Homo sapiens mRNA for KIAA1399 protein, partial cds | |
| 4542 | 9531 | 14519 | 2.25 | 0.0E+00 | M74099.1 | NT | Human displacement protein (CCATT) mRNA | |
| 4544 | 9533 | 14521 | 2.86 | 0.0E+00 | 6453812 | NT | Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA | |
| 4544 | 9533 | 14522 | 2.86 | 0.0E+00 | 6453812 | NT | Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA | |
| 4549 | 9537 | 1.17 | 0.0E+00 | BE278730.1 | EST_HUMAN | 601156935f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3506521'5' | | |
| 4550 | 9558 | 14546 | 1.12 | 0.0E+00 | 5729817 | NT | Homo sapiens ectopic viral integration site 2B (EV12B), mRNA | |
| 4570 | 9558 | 14547 | 1.12 | 0.0E+00 | 5729817 | NT | Homo sapiens ectopic viral integration site 2B (EV12B), mRNA | |
| 4575 | 9563 | 14551 | 5.79 | 0.0E+00 | M80902.1 | NT | Human AhR/AK nucleoprotein mRNA, 5' end | |
| 4578 | 9566 | 14554 | 2.21 | 0.0E+00 | M69197.1 | NT | Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds | |
| 4578 | 9566 | 14555 | 2.21 | 0.0E+00 | M69197.1 | NT | Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds | |
| 4581 | 9569 | 14558 | 1.86 | 0.0E+00 | AF184110.1 | NT | Homo sapiens cyclophilin-1 related protein (NKTR) gene, complete cds | |
| 4582 | 9570 | 14559 | 0.68 | 0.0E+00 | 7662479 | NT | Homo sapiens KIAA1084 protein (KIAA1084), mRNA | |
| 4583 | 9571 | 14560 | 2.97 | 0.0E+00 | 7662181 | NT | Homo sapiis KIAA0553 gene product (KIAA0553), mRNA | |
| 4590 | 9578 | 14568 | 1.07 | 0.0E+00 | U07563.1 | NT | Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds | |
| 4594 | 9582 | 14572 | 1.24 | 0.0E+00 | AL096857.1 | NT | Novel human mRNA from chromosome 1, which has similarities to BAT2 genes | |
| 4599 | 9587 | | 1.15 | 0.0E+00 | X58467.1 | NT | Human CTF2D7AP pseudogene for cytochrome P450 2D6 | |
| 4615 | 9600 | 14586 | 1.22 | 0.0E+00 | AF026801.1 | NT | Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26 | |
| 4617 | 9602 | 14588 | 1.69 | 0.0E+00 | 6677700 | NT | Homo sapiens G-protein coupled receptor (RE2), mRNA | |
| 4617 | 9602 | 14589 | 1.69 | 0.0E+00 | 6677700 | NT | Homo sapiens G-protein coupled receptor (RE2), mRNA | |
| 4618 | 9603 | 14590 | 0.75 | 0.0E+00 | 7019320 | NT | Homo sapiens proteinxx008 (AD013), mRNA | |
| 4618 | 9603 | 14591 | 0.75 | 0.0E+00 | 7019320 | NT | Homo sapiens proteinxx008 (AD013), mRNA | |
| 4641 | 9626 | 14618 | 1.65 | 0.0E+00 | AW444637.1 | EST_HUMAN | U1-H-B13-45iv-c-04-0-U.1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733294'3' | |
| 4647 | 9632 | 14627 | 1.01 | 0.0E+00 | AF303134.1 | NT | Homo sapiens aldehyde dehydrogenase 12 (ALDH12), mRNA, complete cds | |

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Table 4

Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|---------------------|-------------------|--------------------------------------|-----------------------|--|--------------------|
| 4649 9634 | | 1.44 | 0.0E+00 AF083242.1 | NT | Homo sapiens HSPOC024-iso mRNA, complete cds | |
| 4688 9673 | 14655 | 0.68 | 0.0E+00 J00191.1 | NT | Human MHC class I transplantation antigen (hla) gene | |
| 4688 9673 | 14656 | 0.68 | 0.0E+00 J00191.1 | NT | Human MHC class I transplantation antigen (hla) gene | |
| 4694 9679 | | 6.96 | 0.0E+00 AF240786.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) | |
| 4698 9683 | 14666 | 2.39 | 0.0E+00 X87205.1 | NT | M. fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa genes, complete cds | |
| 4700 9685 | 14668 | 1.77 | 0.0E+00 AF084479.1 | NT | Homo sapiens Williams-Bauren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds | |
| 4701 9686 | 14669 | 1.47 | 0.0E+00 AF097416.1 | NT | Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds | |
| 4702 9687 | 14670 | 4.25 | 0.0E+00 4503768 | NT | Homo sapiens fragile X mental retardation 2 (FMR2) mRNA | |
| 4704 9689 | 14672 | 13.59 | 0.0E+00 4885048 | NT | Homo sapiens actin, alpha, cardiac muscle (ACTC) mRNA | |
| 4706 9691 | 14674 | 2.35 | 0.0E+00 89221180 | NT | Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312) mRNA | |
| 4709 9694 | 14678 | 7.7 | 0.0E+00 89230580 | NT | Homo sapiens hypothetical protein FLJ20073 (FLJ20073) mRNA | |
| 4712 9697 | 14681 | 2.67 | 0.0E+00 7661979 | NT | Homo sapiens KIAA0187 gene product (KIAA0187) mRNA | |
| 4713 9698 | 14682 | 1.91 | 0.0E+00 M94081.1 | NT | Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments, and Tcr-C-alpha gene, exons 1-4 | |
| 4713 9698 | 14683 | 1.91 | 0.0E+00 M94081.1 | NT | Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments, and Tcr-C-alpha gene, exons 1-4 | |
| 4715 9700 | 14685 | 1.8 | 0.0E+00 X94628.1 | NT | H.sapiens MeCP-2 gene | |
| 4715 9700 | 14686 | 1.8 | 0.0E+00 X94628.1 | NT | H.sapiens MeCP-2 gene | |
| 4718 9703 | 14689 | 1.97 | 0.0E+00 AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 | |
| 4727 9712 | 14697 | 1.27 | 0.0E+00 5032150 | NT | Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, II, III (TAF2) | |
| 4732 9717 | 14702 | 3.92 | 0.0E+00 X92841.1 | NT | H.sapiens MiCA gene | |
| 4734 9719 | 14704 | 1.63 | 0.0E+00 4585642 | NT | Homo sapiens zinc finger protein (KIAA0412) mRNA | |
| 4735 9720 | 14705 | 1.08 | 0.0E+00 AB037884.1 | NT | Homo sapiens mRNA for KIAA0443 protein, partial cds | |
| 4736 9721 | 14706 | 0.92 | 0.0E+00 AB014533.1 | NT | Homo sapiens mRNA for KIAA0633 protein, partial cds | |
| 4737 9722 | 14707 | 2.29 | 0.0E+00 6677648 | NT | Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA | |
| 4738 9723 | 14708 | 1.04 | 0.0E+00 5174560 | NT | Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA | |
| 4740 9725 | 14710 | 1.45 | 0.0E+00 4758199 | NT | Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA | |
| 4744 9729 | 14716 | 38.01 | 0.0E+00 AF055066.1 | NT | Homo sapiens MHC class 1 region | |
| 4746 9731 | | 2.39 | 0.0E+00 4505508 | NT | Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA | |
| 4747 9732 | 14719 | 2.63 | 0.0E+00 AF091711.1 | NT | Homo sapiens splice variant AKAP250 mRNA, partial cds | |
| 4760 9744 | 14730 | 1.02 | 0.0E+00 D63562.1 | NT | Homo sapiens COL4A6 gene for a6(IV) collagen, exon 44 and partial cds | |

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Table 4
Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4762 | 9746 | 14732 | 1.96 | 0.0E+00 | 4503684 | NT | Homo sapiens: farnesyldiphosphate synthase (farnesylyltransferase, geranyltransferase) (FDPS) mRNA |
| 4764 | 9748 | 14735 | 1.13 | 0.0E+00 | AI249062.1 | EST_HUMAN | dimethylallyltransferase, geranyltransferase (IMAGE:1849839 3' similar to qn68d08_x1_Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1849839 3' |
| 4764 | 9748 | 14736 | 1.13 | 0.0E+00 | AI249062.1 | EST_HUMAN | SW_ATPN_BOVIN_Q28852 ATP SYNTHASE G CHAIN, MITOCHONDRIAL; qn68d08_x1_Soares_fetal_liver_spleen_1INF1S_S1 Homo sapiens cDNA clone IMAGE:1849839 3' similar to SW_ATPN_BOVIN_Q28852 ATP SYNTHASE G CHAIN, MITOCHONDRIAL; qm15f05_x1_NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632 Q61632 |
| 4768 | 9752 | | 1.07 | 0.0E+00 | AI291129.1 | EST_HUMAN | EN_2/LACZ FUSION PROTEIN; |
| 4775 | 9779 | 14762 | 1.2 | 0.0E+00 | AL163224.2 | NT | Homo sapiens: chromosome 21 segment HS21C084 |
| 4801 | 9785 | 14767 | 1.02 | 0.0E+00 | 7662319 | NT | Homo sapiens: KIAA0866 gene product (KIAA0866), mRNA |
| 4808 | 9792 | 14774 | 0.86 | 0.0E+00 | AA205437.1 | EST_HUMAN | zq66b016_s1 Stratagene neuroepithelium (#83723) Homo sapiens cDNA clone IMAGE:546547 3' |
| 4813 | 9797 | | 6.57 | 0.0E+00 | U14967.1 | NT | Human ribosomal protein L21 mRNA, complete cds |
| 4823 | 9807 | 14789 | 1.6 | 0.0E+00 | M10976.1 | NT | Human endogenous retroviral DNA (4-1), complete retroviral segment |
| 4825 | 9809 | | 2.99 | 0.0E+00 | BE408863.1 | EST_HUMAN | 601303729FL NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5' |
| 4829 | 9813 | 14794 | 3.55 | 0.0E+00 | 4758199 | NT | Homo sapiens desmoplakin (DPL, DPPL) (DSP) mRNA |
| 4836 | 9820 | 14797 | 2.16 | 0.0E+00 | AB028966.1 | NT | Homo sapiens mRNA for KIAA1043 protein, partial cds |
| 4848 | 9830 | 14804 | 2.53 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 4848 | 9830 | 14805 | 2.53 | 0.0E+00 | 8923441 | NT | Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA |
| 4862 | 9843 | 14815 | 1 | 0.0E+00 | AA601246.1 | EST_HUMAN | no14g9_s1_NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 |
| 4862 | 9843 | 14816 | 1 | 0.0E+00 | AA601246.1 | EST_HUMAN | E239140 SPALT PROTEIN; |
| 4862 | 9843 | | | | | | no14g9_s1_NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 |
| 4862 | 9843 | 14817 | 1 | 0.0E+00 | AA601246.1 | EST_HUMAN | E239140 SPALT PROTEIN; |
| 4864 | 9844 | 14818 | 1.59 | 0.0E+00 | AF181463.1 | NT | Homo sapiens HSPC114 mRNA, complete cds |
| 4864 | 9844 | 14819 | 1.59 | 0.0E+00 | AF181463.1 | NT | Homo sapiens HSPC114 mRNA, complete cds |
| 4867 | 5275 | 10229 | 0.81 | 0.0E+00 | AF195658.1 | NT | Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds |
| 4870 | 9849 | | 0.92 | 0.0E+00 | 4758225 | NT | Homo sapiens E2F transcription factor 2 (E2F2) mRNA |
| 4881 | 9860 | 14831 | 1.28 | 0.0E+00 | AF016705.1 | NT | Homo sapiens E6-AP Ubiquitin-protein ligase (UBE3A) gene, exon 3 |
| 4883 | 9862 | 14833 | 1.27 | 0.0E+00 | U53388.1 | NT | Homo sapiens MHC class 1 region |
| 4887 | 9866 | | 1.11 | 0.0E+00 | AL1763209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 4890 | 9869 | | 27.33 | 0.0E+00 | D50657.1 | NT | Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene |
| 4913 | 9892 | 14866 | 3.61 | 0.0E+00 | X52988.1 | NT | Bacillus amiloliquefaciens sacB gene for levan sucrose (EC 2.4.1.10) |
| 4927 | 9904 | 14882 | 2.48 | 0.0E+00 | AF272663.1 | NT | Homo sapiens gophyrin mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in HBL100

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------|-----------------|----------------|-------------------|--------------------------------------|-----------------------|-------------------------|---|
| 4930 | 9907 | 14884 | 1.13 | 0.0E+00 | 5454153 | NT | Homo sapien: cyclophilin (USA-CYP) mRNA |
| 4936 | 9913 | 14891 | 0.99 | 0.0E+00 | AA683268.1 | EST_HUMAN | aa92B04.51 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:10203673 |
| 4951 | 9928 | 14906 | 0.95 | 0.0E+00 | 4557362 | NT | Homo sapien: PR domain containing 1, with ZNF-domain (PRDM1) mRNA |
| 4957 | 9934 | 14912 | 0.72 | 0.0E+00 | Y08632.1 | NT | Human endogenous retrovirus-K, LTR U5 and gag gene |
| 4965 | 9942 | 14919 | 0.92 | 0.0E+00 | AF124250.1 | NT | Homo sapien: SH2-containing protein Nsp2 mRNA, complete cds |
| 4980 | 9955 | 14933 | 0.92 | 0.0E+00 | 7662421 | NT | Homo sapien: KIAA0971 protein (KIAA0971), mRNA |
| 4981 | 9956 | 14934 | 0.67 | 0.0E+00 | 4826795 | NT | Homo sapien: potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA |
| 4990 | 9963 | 14940 | 1.07 | 0.0E+00 | AF108830.1 | NT | Homo sapien: serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 4990 | 9963 | 14941 | 1.07 | 0.0E+00 | AF108830.1 | NT | Homo sapien: serine-threonine protein kinase (MNBH) mRNA, complete cds |
| 5009 | 9980 | 14955 | 1.27 | 0.0E+00 | 7657203 | NT | Homo sapien: acidic 82 kDa protein mRNA (HSUJ5552), mRNA |
| 5034 | 10005 | 14976 | 1.17 | 0.0E+00 | 4758621 | NT | Homo sapien: coagulation factor C (Limulus polyphemus) homology (COCH), mRNA |
| 5049 | 10020 | 14989 | 0.99 | 0.0E+00 | 6677700 | NT | Homo sapien: G-protein coupled receptor (RE2), mRNA |
| 5049 | 10020 | 14990 | 0.99 | 0.0E+00 | 6677700 | NT | Homo sapien: G-protein coupled receptor (RE2), mRNA |
| 5053 | 10024 | 14993 | 0.74 | 0.0E+00 | 7657336 | NT | Homo sapien: mutL (E. coli) homolog 3 (MLH3), mRNA |
| 5068 | 10037 | 15004 | 0.75 | 0.0E+00 | AL044081.1 | EST_HUMAN | DKEZ4434.2428_17434 (synonym: hts3) Homo sapiens cDNA clone DKF4434.2428 5' |

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Breast comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 5,074 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,075 - 10,058.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 5% of said single exon nucleic acid probes lack 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 10% of said single exon nucleic acid probes lack 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in 15 that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon 20 and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 25 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast 30 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 5,074 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Breast.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 5,075 - 10,058 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,059 - 15,009, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

10
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16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30
35

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human Breast, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said probe is
20 a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

30 identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 10,058 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 10,058.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 10,059 - 15,009.

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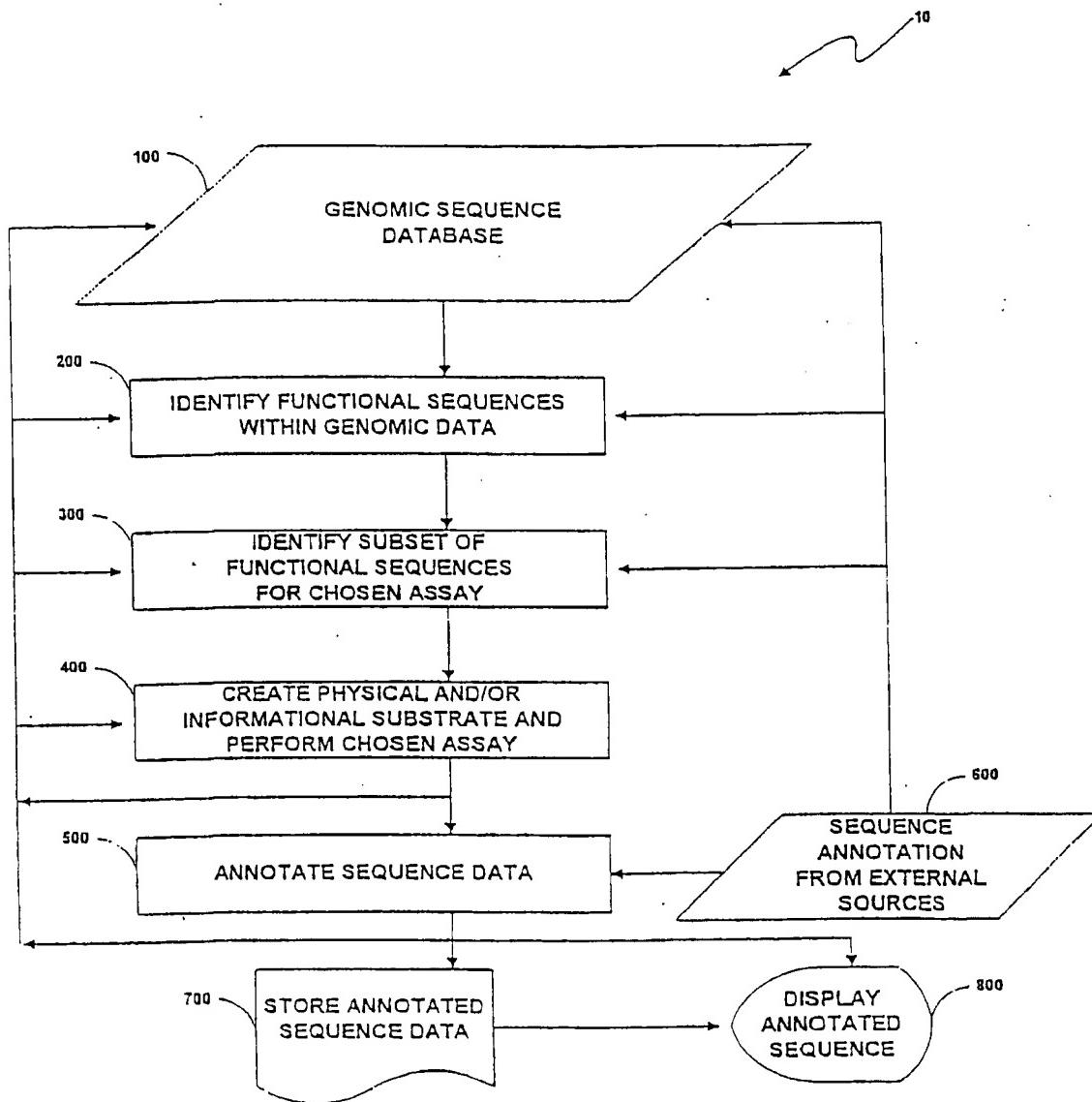


Fig. 1

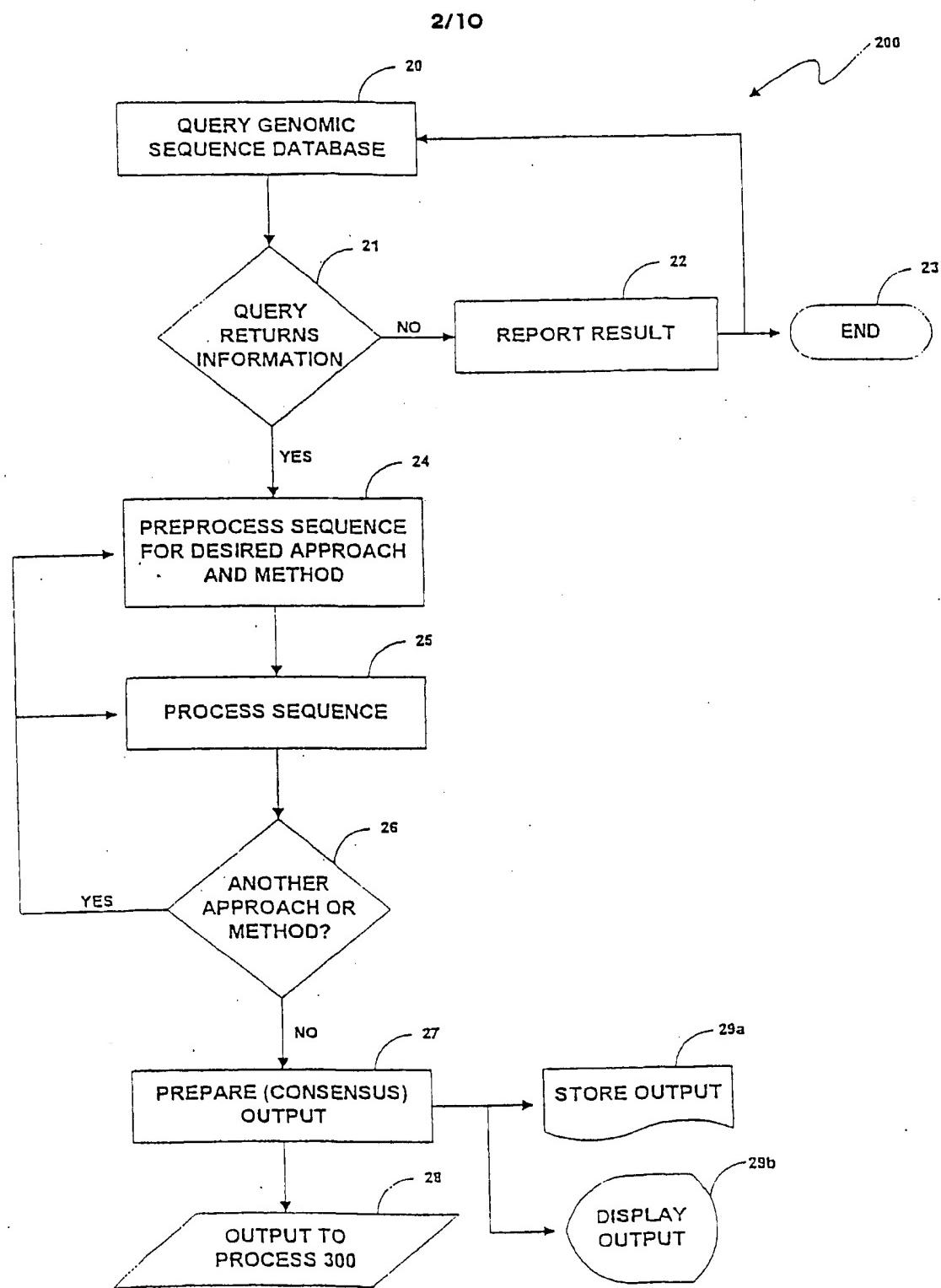


Fig. 2

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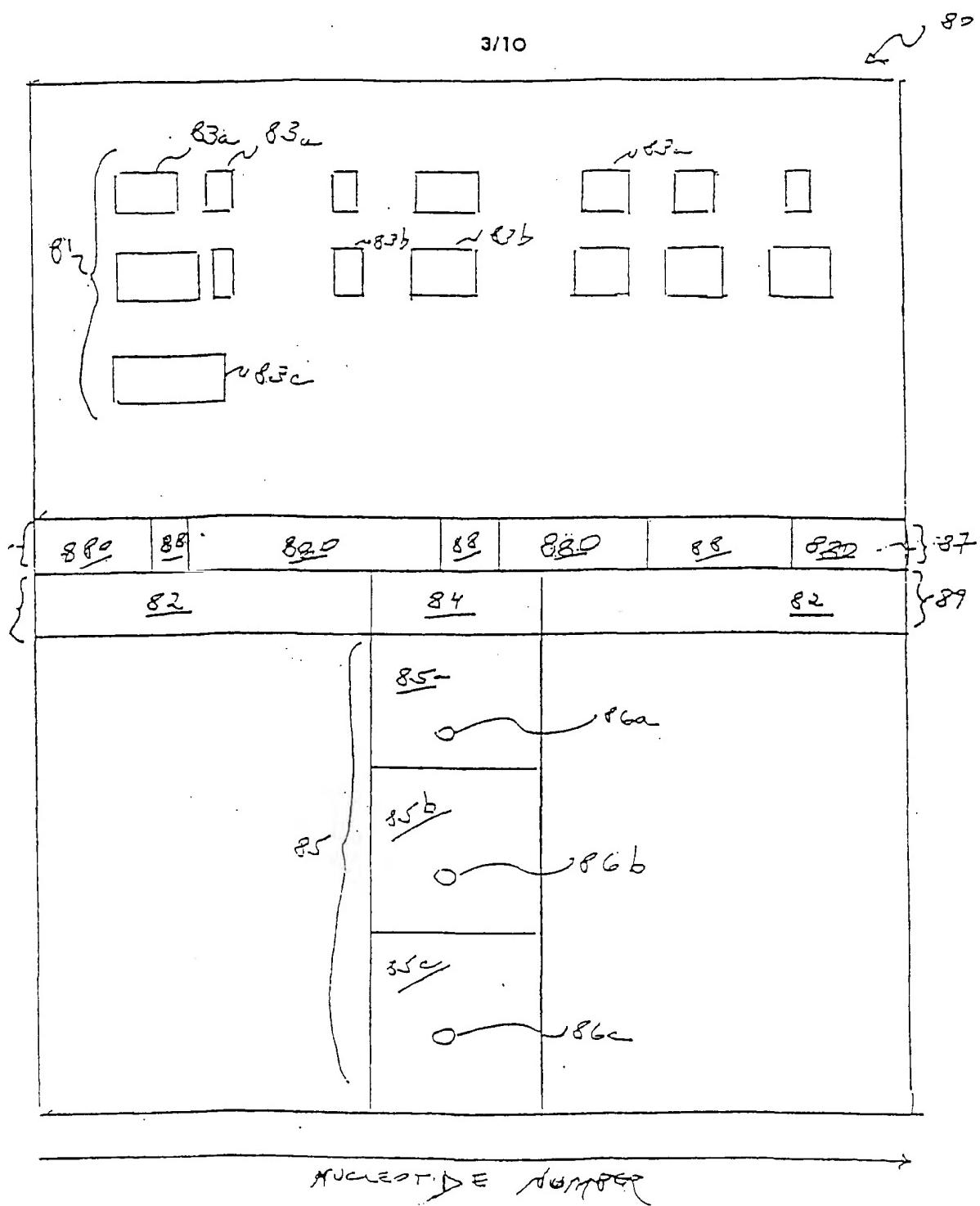


Fig. 3

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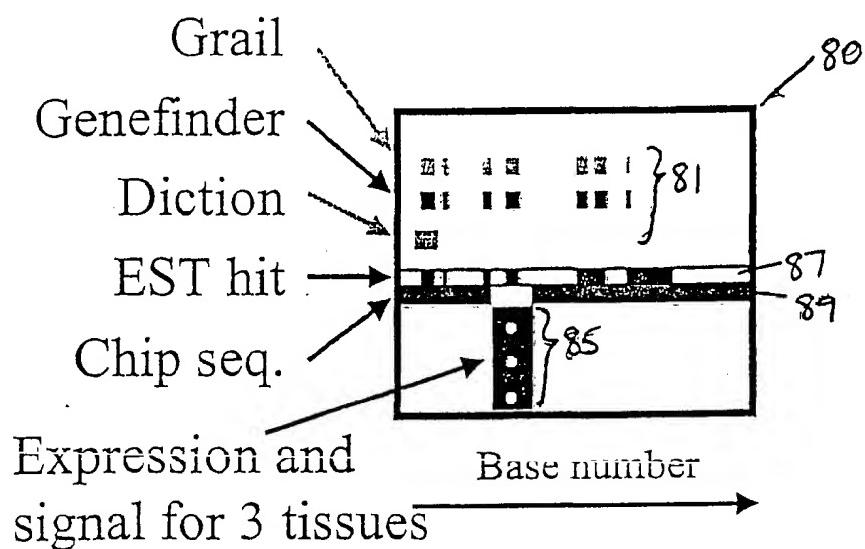


Fig. 4

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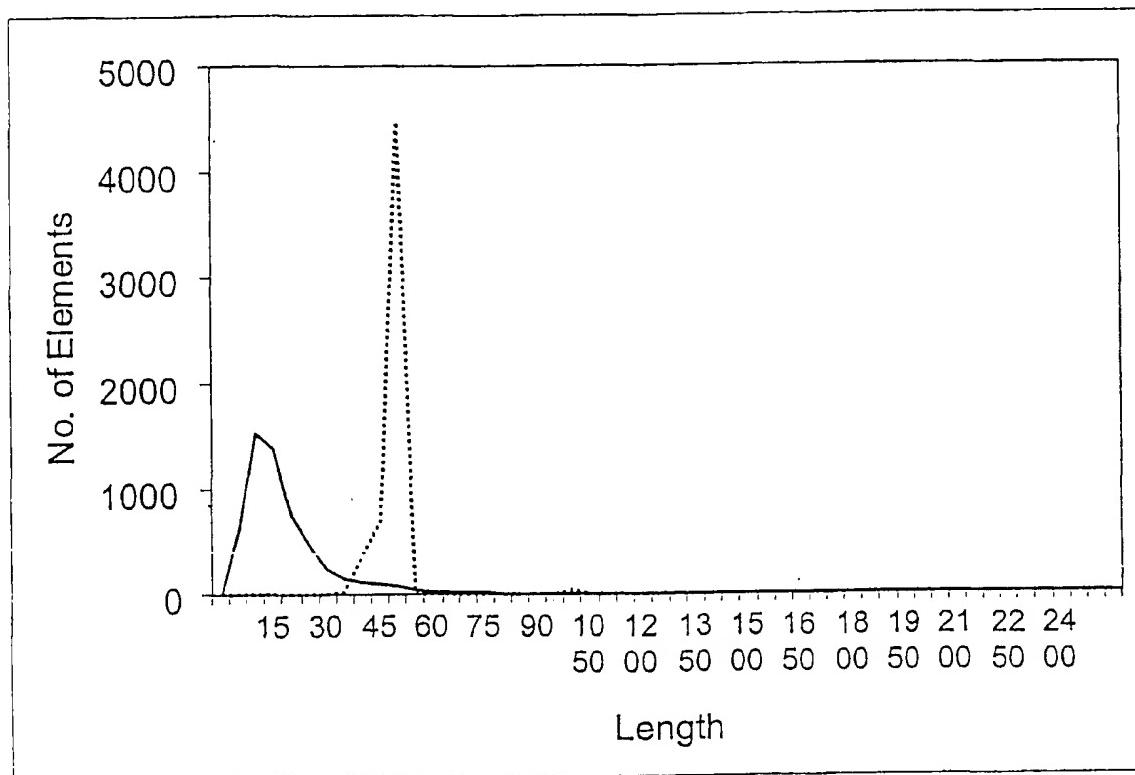


Fig. 5

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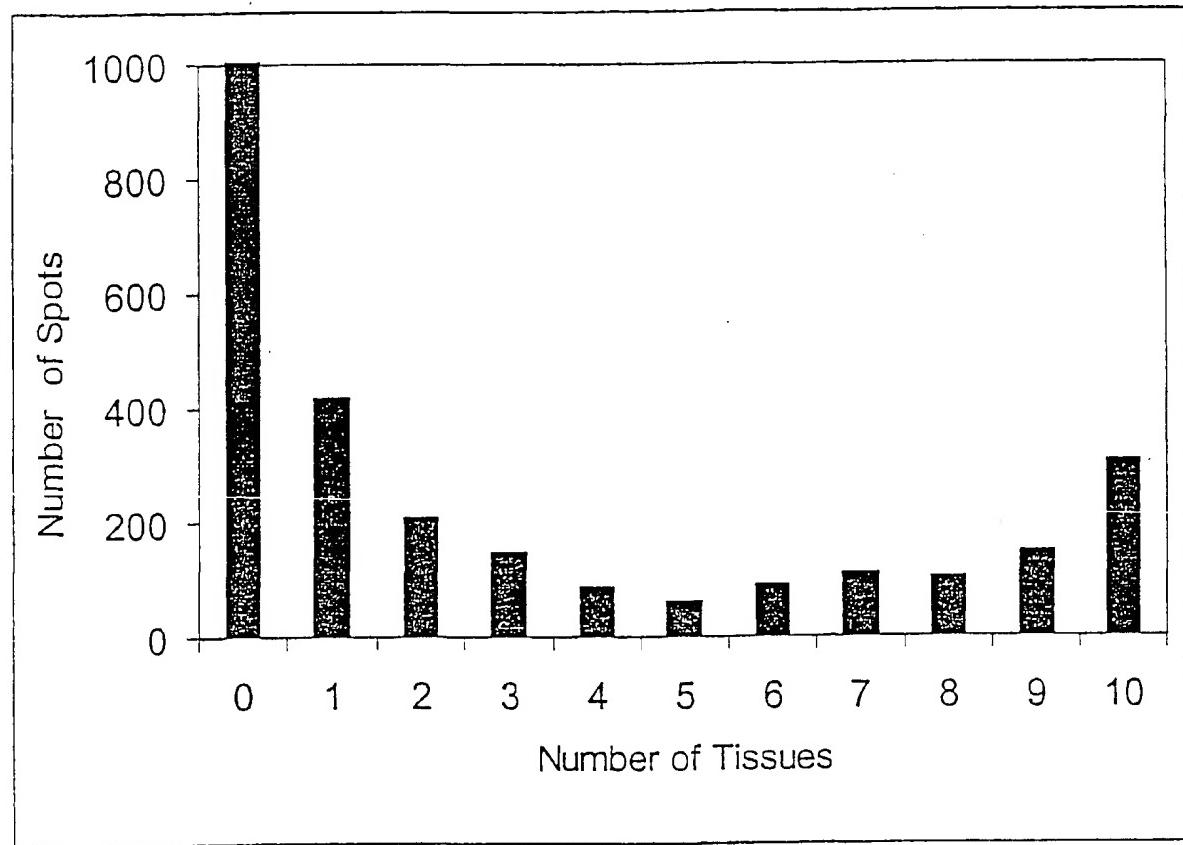


Fig. 6

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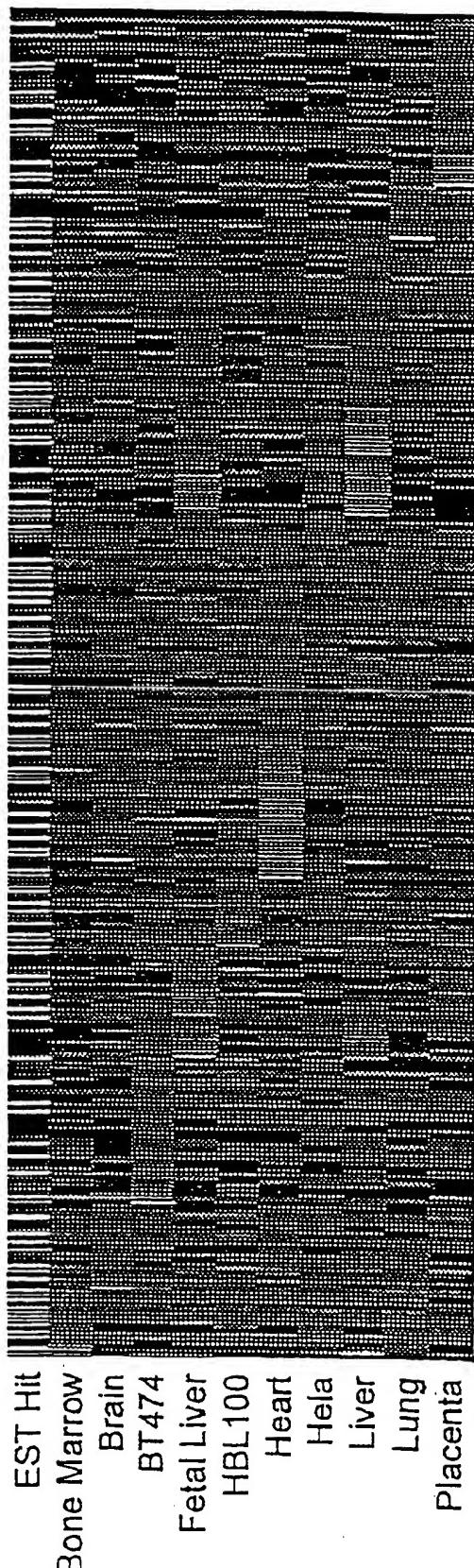


Fig. 7a

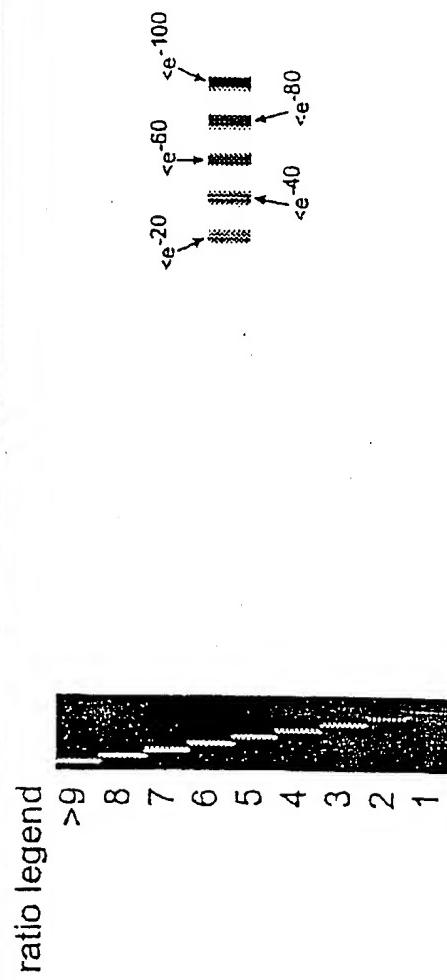


Fig. 7b

Fig. 7c

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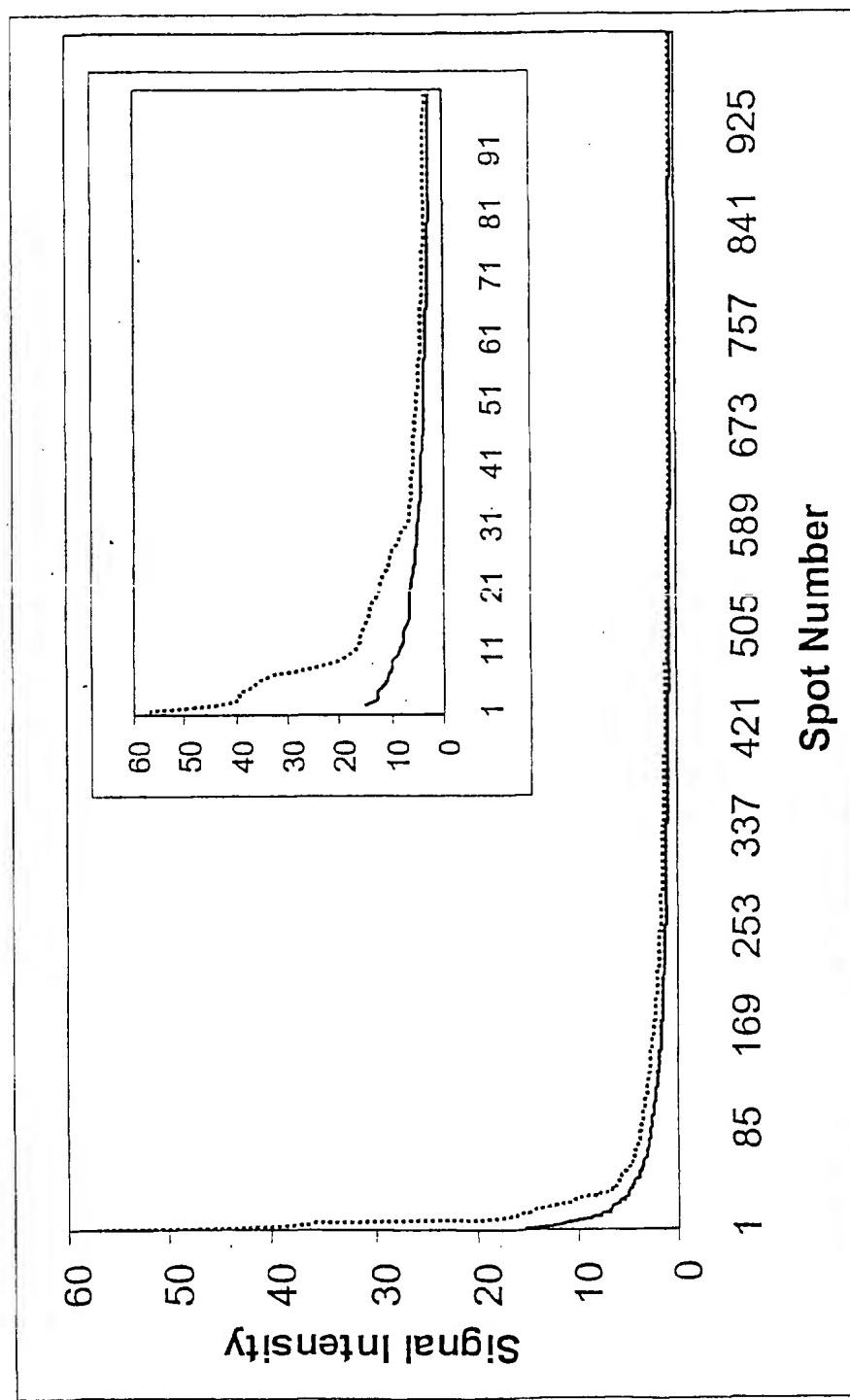


Fig. 8

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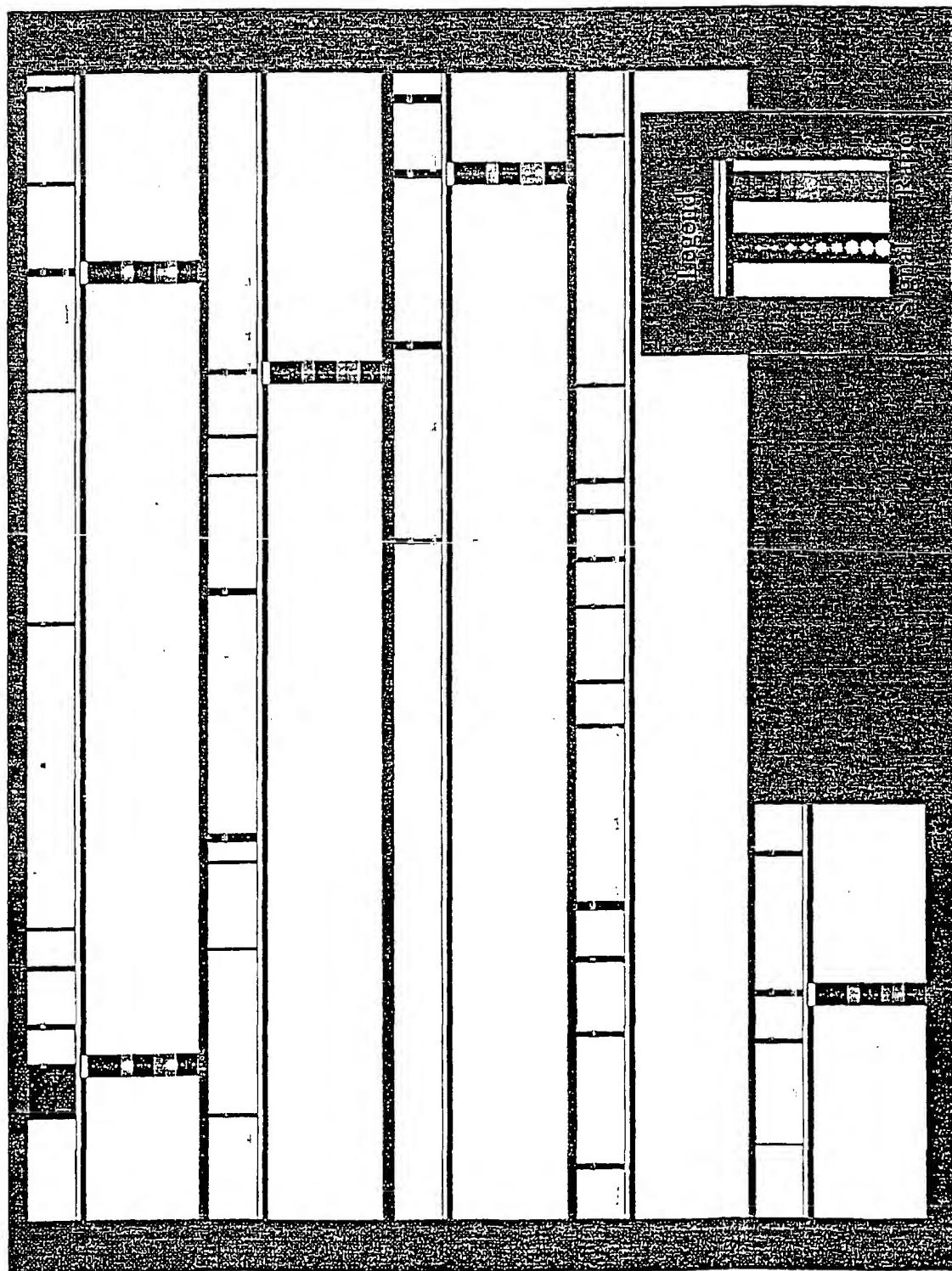
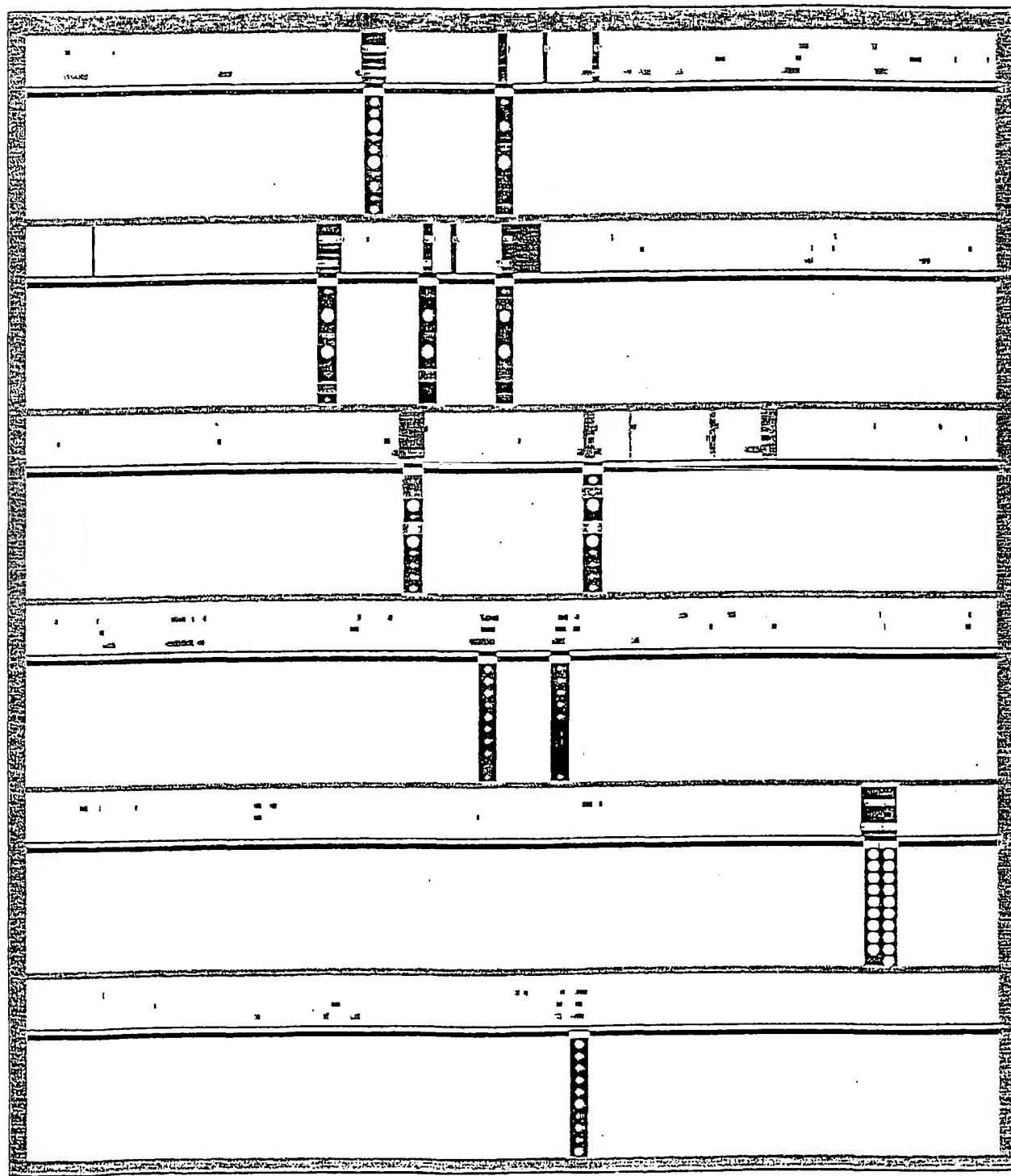


Fig. 9

10/10

Fig. 10



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HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
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patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND HBL 100 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human HBL 100 cells is described. Also described are single exon nucleic acid probes expressed in the HBL 100 cells and their use in methods for detecting gene expression.

INTERNATIONAL SEARCH REPORT

In' nal Application No
PCT/US 01/00661

A. CLASSIFICATION OF SUBJECT MATTER
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According to International Patent Classification (IPC) or to both national classification and IPC

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| X | STAUDER R ET AL: "Different CD44 splicing patterns define prognostic subgroups in multiple myeloma." BLOOD, (1996). VOL. 88, NO. 8, PP. 3101-8. JOURNAL CODE: A8G. ISSN: 0006-4971., XP001033913 Basel Institute for Immunology, Switzerland. the whole document --- | 13 |
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Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

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- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *8* document member of the same patent family

Date of the actual completion of the international search

2 August 2002

Date of mailing of the international search report

03.09.02

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Luzzatto, E

INTERNATIONAL SEARCH REPORT

II Initial Application No

PCT/US 01/00661

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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| X | WO 99 23252 A (BAKKENIST CHRISTOPHER JAMES ;MCGEE JAMES O DONNELL (GB); ISIS INNO) 14 May 1999 (1999-05-14) page 5, line 10 -page 9, line 6 page 22, line 1 -page 23, line 23; figure 4 --- | 1-27 |
| X | WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) page 2, line 10 -page 4, line 15 page 16, line 4 - line 23 page 18, line 4 - line 18 page 24, line 20 - line 36 page 43, line 1 - line 21 page 58, line 34 -page 63, line 15; figure 5 --- | 1,12,13 |
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INTERNATIONAL SEARCH REPORT

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| In | national Application No |
| PCT/US 01/00661 | |

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/00661

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Character of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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| X | <p>DATABASE EBI 'Online! 9 May 1997 (1997-05-09)</p> <p>MARRA M. ET AL.: "THe WashU-HHMI mouse EST project; vc72c02.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 780098"</p> <p>Database accession no. AA414703</p> <p>XP002208274</p> <p>abstract</p> <p>---</p> | 13,14, 18,20,21 |
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00661

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (partially)

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 1 (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 5075 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 1), microarrays comprising said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons (claim 23) and a method for assigning exons to a single gene (claim 24) comprising using the said arrays, the peptide encoded by SEQ ID 1 or 5075 (claims 26-27) having the sequence SEQ ID 10059 (see ISA form 206), which is the translation from SEQ ID 5075 (see p. 74 of the description).

2. Claims: 1-27(partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 5076 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sequence, a method for measuring gene expression, a method for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 13116 having the sequence SEQ ID 10060, which is the translation from SEQ ID 5076 (see p. 74 of the description) (see however last paragraph of the reasoning hereinafter).

...Inventions 3-5074: similar subject-matter as above related to SEQ IDs 3-5074.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject-matter for which a search has been performed and which has been identified as inventions 1 and 2.

1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description pages 10, l. 10-17 and 69, l. 14-26).

2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID 1 and 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and conciseness (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID 1 and 2 as such.

3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID 1 and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. 10059 and 10060 (Art. 6 PCT).

4) Claims 15-21 relate to nucleic probes, solely defined in that they code for a polypeptide having the sequence SEQ ID 10059 or 10060. However, a peptide is potentially coded by an extremely large number of nucleic acid sequences. Hence, claims 15-21 lack clarity and conciseness to such an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID 1, 2, 5075 and 5076.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

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Information on patent family members

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